

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 312 shows 95.6% identity over a 451 aa overlap with a predicted ORF (ORF 312.ng) from *N. gonorrhoeae*:

m312/g312

m312.pep	MSIQSGEILETVKMVADQNFDVRTITIGIDLHDCISSDINVLNQNIYNKITTGVKDLVTT
g312	MSIQSGEILETVKMVADRNFDVRTITIGIDLHDCISTDIDVLNQNIYNKITTGVKDLVAT
m312.pep	AKYLSAKYGVPIVNQRISVTPIAQIAAATHADSYVSVSAQTLDKAAKAIGVSFIGGFSALV
g312	AKHLSAKYGVPIVNQRISVTPIAQIAAATKADSYVSVSAQTLDKAAKAIGVSFIGGFSALV
m312.pep	QKGMSPSDEVLIRSIPEAMKTTDIVCXSNIGSTRAGINMDAVKLAGEVTKRTAEITPEG
g312	QKGMSPSDEVLIRSVPEAMKTTDIVCSSINIGSTRAGINMDAVKLAGEVTKRTAEITPEG
m312.pep	FGCAKIVVFCNAVEDNPFAXAGAFHSGS--DAVINVGVSFGPGVVKAALENS DATLTLEVAE
g312	FGCAKIVVFCNAVEDNPFMAGAFHSGSEADAVINVGVSFGPGVVKAALENS DAVSLTEVAE
m312.pep	VVKKTAFKTRVGELIGREASKMLNIPFGILDLS--PTPPVGDVSARILEEMGLSVCGTH
g312	VVKKTAFKTRVGELIGREASKMLNIPFGILDLSLAPTPAVGDSVARILEEMGLSVCGTH
m312.pep	GTTAALALLNDVAVKKGMMASSAVGGLSGAFIPVSEDEGMIXAAEAGVLTLDKLEAMTAV
g312	GTTAALALLNDVAVKKGMMASSAVGGLSGAFIPVSEDEGMIAAAEAGVLTLDKLEAMTAV
m312.pep	CSVGLDMIAVPGDTPAHTISGIIADEAAIGMINSKTTAVRIIPVTGKTVGDTVEFGGLLG
g312	CSVGLDMIAVPGDTPAHTISGIIADEAAIGMINSKTTAVRIIPVTGKTVGDSVEFGGLLG
m312.pep	YAPVMPVKEGSCEVFVNRGGRI PAPVQSMKNX
g312	YAPVMPAKEGSCEVFVNRGGRI PAPVQSMKNX

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1305>:

a312.seq

1	ATGAGTATCC	AATCCGGCGA	AATTTTAGAA	ACCGTCAAAA	TGGTTGCCGA
51	CCAGAATTTC	GATGTCCGCA	CCATTACCAT	CGGCATTGAT	TTGCACGACT
101	GCATCAGCAC	CGACATCGAC	GTGTTGAACC	AAAATATTTA	CAACAAAATT
151	ACCACGGTCG	GCAAAGACTT	GGTGGCGACA	GCAAAATATC	TGTCTGCCAA
201	ATACGGCGTG	CCGATTGTGA	ATCAGCGCAT	TTCTGTCACG	CCGATTGCCC
251	AAATCGCGGC	GGCCACCCAT	GCTGATTCTT	ACGTCAGCGT	GGCGCAAAT

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301 TTGGATAAGG CTGCCAAAGC CATCGGCGTG TCTTTTATTG GCGGCTTTTC
351 CGCGCTGGTG CAAAAGGTA TGTGCGCTTC TGACGAGGTG TTAATCCGTT
401 CCATTCCCGA AGCGATGAAG ACTACTGATA TCGTGTGCAG CTCCATCAAT
451 ATCGGCAGTA CGCGCGCCGG TATCAATATG GACGCGGTCA GACTGGCGGG
501 CGAAACCATC AAACGCACGG CTGAAATCAC ACTAGAAGGT TTCGGCTGCG
551 CAAAATCGT CGTGTCTGTC AACGCGGTGG AAGACAACCC GTTTATGGCG
601 GGCGCGTTTC ACGGCTCAGG CGAAGCGGAT GCTGTGATTA ATGTCGCGGT
651 ATCCGGCCCCG GGTGTCGTAA AAGCCGCGTT GGAATTCG GATGCAACGA
701 CATTGACUGA AGTTGCGGAA GTTGTGAAGA AAACCGCCTT CAAAATTACC
751 CGCGTGGGCG AACTCATCGG CCGCGAAGCC TCAAAAATGC TGAATATCCC
801 GTTTGGTATT CTCGACTTGT CGCTGGCACC GACCCCTGCC GTCGGCGACT
851 CCGTGGCGCG CATTCTTGAA GAAATGGGTT TGAGCGTCTG CCGTACGCAC
901 GGCACAACAG CAGCTTGGC ATTGCTGAAC GATGCCGTGA AAAAGGGCGG
951 CATGATGGCT TCGAGCGCGG TTGGCGGTTT GAGTGGCGCG TTTATCCCCG
1001 TTTCCGAAGA CGAAGGTATG ATTGCCGCGG CCGAAGCAGG CGTGCTGACG
1051 TTGGATAAAC TCGAAGCGAT GACCGCCGTT TGTTGCGTGC GCTGGATAT
1101 GATTGCCGTT CCCGGCGACA CACCCGCGCA CACCATTTC GGCATCATTG
1151 CCGACGAAGC CGCCATCGGC ATGATCAACA GCAAAACCAC TGCCGTGCGC
1201 ATTATCCGG TAACCGGTAA AACCGTCGGC GACAGCGTCG AGTTCGGCGG
1251 CCTGTTGGGC TACGCGCCTG TAATGCCGGT AAAAGAAGGC TCATGCGAAG
1301 TGTTCTGCAA CCGGGCGCGC AGGATTCCTG CACCGGTTCA ATCGATGAAA
1351 AACTGA

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This corresponds to the amino acid sequence <SEQ ID 1306; ORF 312.a>:

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a312.pep
1  MSIQSGEILE TVKMOVADQNF DVRTITIGID LHCISTDID VLNQNIYNKI
51  TTVGKDLVAT AKYLSAKYGV PIVNQRISVT PIAQIAAATH ADSYVSVAQT
101 LDKAAGAIGV SFIGGFSALV QKGMSPSDEV LIRSIPEAMK TTDIVCSSIN
151 IGSTRAGINM DAVRLAGETI KRTAEITLEG FGCAKIVVFC NAVEDNPFMA
201 GAFHGSSEAD AVINVGVSGP GVVKAALENS DATTLTEVAE VVKKTAFKIT
251 RVGELIGREA SKMLNIPFGI LDLSLAPTPA VGDSVARILE EMGLSVCETH
301 GTTAALALLN DAVKKGGGMA SSAVGGLSGA FIPVSEDEGM IAAAEAGVLT
351 LDKLEAMTAV CSVGLDMIIV PGDTPAHTIS GIIADEAAIG MINSKTTAVR
401 IIPVTGKTVG DSVEFGGLLG YAPVMPVKEG SCEVFVNRGG RIPAPVQSMK
451 N*

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m312/a312 96.7% identity in 451 aa overlap

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              10      20      30      40      50      60
m312.pep    MSIQSGEILETVKMOVADQNF DVRTITIGIDLHCISSDINVLNQNINYNKITT VVGKDLVTT
              |||
a312        MSIQSGEILETVKMOVADQNF DVRTITIGIDLHCISTDIDVLNQNINYNKITT VVGKDLVAT
              10      20      30      40      50      60

              70      80      90      100     110     120
m312.pep    AKYLSAKYGVPIVNQRISVTPIAQIAAATHADS YVSVAQTLDKAAGAIGVSFIGGFSALV
              |||
a312        AKYLSAKYGVPIVNQRISVTPIAQIAAATHADS YVSVAQTLDKAAGAIGVSFIGGFSALV
              70      80      90      100     110     120

              130     140     150     160     170     180
m312.pep    QKGMSPSDEV LIRSIPEAMKTTDIVCX SINIGSTRAGINMDAVKLAGETVKRTAEITPEG
              |||
a312        QKGMSPSDEV LIRSIPEAMKTTDIVCSSINIGSTRAGINMDAVRLAGETIKRTAEITLEG
              130     140     150     160     170     180

              190     200     210     220     230
m312.pep    FGCAKIVVFCNAVEDNPF XAGAFHGS--DAVINVGVS GPGVKAALENS DATTLTEVAE
              |||
a312        FGCAKIVVFCNAVEDNPF MAGAFHGSGEADAVINVGVS GPGVKAALENS DATTLTEVAE
              190     200     210     220     230     240

              240     250     260     270     280     290
m312.pep    VVKKTAFKITRVGELIGREASKMLNIPFGILDLS--PTPPVGDSVARILEEMGLSVCETH
              |||
a312        VVKKTAFKITRVGELIGREASKMLNIPFGILDLSLAPTPAVGDSVARILEEMGLSVCETH

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	250	260	270	280	290	300
	300	310	320	330	340	350
m312.pep	GT	TAALALLND	AVKKGGMM	ASSAVGGL	S	GA
a312	GT	TAALALLND	AVKKGGMM	ASSAVGGL	S	GA
	310	320	330	340	350	360
	360	370	380	390	400	410
m312.pep	CS	VGLDMI	AVPGD	TPAHT	IS	GI
a312	CS	VGLDMI	AVPGD	TPAHT	IS	GI
	370	380	390	400	410	420
	420	430	440			
m312.pep	Y	AP	VP	V	K	E
a312	Y	AP	VP	V	K	E
	430	440	450			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1307>:

g313.seq
 1 atggacgacc cgcgcaccta cggatcgggc aatcccggcg cgaccaatgt
 51 tttagcgagc ggcaaaaaaa aggcggccgc gctgacgctc ttgggcatg
 101 ccgcaaaagg tttagttgcc gttttgcttg cagcggtgct tcaagaaccg
 151 ctccggtttat ccgacagcgc aatcgccgcc gtcgcactcg ccgcgctggt
 201 cgggcatatg tggccggtgt ttttcggatt taaggcgccg aaaggcgtgg
 251 caacggcatt gggcggtgct ctggcactct ctctgcaac tgccttggtc
 301 tgccggttga tttggcttgt gatggcattc ggcttcaaag tatcctccct
 351 tgccgcgctg gtcgccacaa ccgccgcccc ccttgccgca ctggttttta
 401 tgccgcatac ttcttggatt ttgcgaaccc tcgcaatcgc catattggtg
 451 ttgtccgcc ataagagcaa catcctcaac ctgattaaag gcaaaagaaag
 501 caaatcggc gaaaaacgct ga

This corresponds to the amino acid sequence <SEQ ID 1308; ORF 313.ng>:

g313.pep
 1 MDPRTYSG NPGATNVLRS GKKKAAALTL LGDAAKGLVA VLLARVLOEP
 51 LGLSDSAIAA VALAALVGHM WPVFFGFKGG KGVATALGVL LALSPATALV
 101 CALIWLVMFA GFKVSSLAAL VATTAPLAA LFFMPHTSWI FATLAIALLV
 151 LLRHKSNIILN LIKGESKIG EKR*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1309>:

m313.seq
 1 ATGGACGACC CGCGCACCTA CGGATCGGGC AATCCGGGGG CAACCAATGT
 51 TTTACGCAGC GGCAAAAAAA AGGCGGCCGC GCTGACGCTC TTGGGCSATG
 101 CCGCCAAAGG TTTAGTTGCC GTTTTGCTTG CACGCGTGCT TCAAGAACCG
 151 CTCGGTTTAT CCGACAGCGC AATCGCGGCC GTCGCACTCG CCGCGCTGGT
 201 CGGGCATATG TGGCCGGTGT TTTTCGGATT TAAAGGCGGC AAAGGCGTGG
 251 CAACGGCATT GGGCGTGCTT CTGGCACTCT CTCCCGCAAC TGCTTGCTC
 301 TGC CGTGA TTTGGCTTGT TATGGCATTC GGCTTCAAGG TGCTCTCCCT
 351 TGCCGCATTA ACCGCCACAA TCGCCGCACC GGTCCGCGCA TCCTTCTTTA
 401 TGCCGCACGT CTCGTGGGTT TGGGCGACCG TCGCCATTGC TTTGCTGGTG
 451 TTGTTCCGCC ACAAAGTAA TATCGTCAAG CTGCTCGAAG GCAGAGAAAG
 501 CAAATCGGC GGCAGCCGCT GA

This corresponds to the amino acid sequence <SEQ ID 1310; ORF 313>:

m313.pep
 1 MDPRTYSG NPGATNVLRS GKKKAAALTL LGDAAKGLVA VLLARVLOEP
 51 LGLSDSAIAA VALAALVGHM WPVFFGFKGG KGVATALGVL LALSPATALV
 101 CALIWLVMFA GFKVSSLAAL TATIAAPVAA SFFMPHVSWS WATVAIALLV
 151 LFRHKSNIIVK LEGRESKIG GSR*

Computer analysis of this amino acid sequence gave the following results:

m313/g313

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1311>:

This corresponds to the amino acid sequence <SEQ ID 1312; ORF 313.a>:

m313/a313 90.8% identity in 173 aa overlap

	10	20	30	40	50	60
m313.pep	MDDPRTYGSNGPGATNVLRS	GKKKAAALTLLG	DAAKGLVAVLLARVLQ	EPLGLSDSAIAA		
a313						
	10	20	30	40	50	60
	70	80	90	100	110	120
m313.pep	VALAALVGHMWPVFFGFKG	GKGVATALGVLLALS	PATALVCA	IWLVM	AFGFKVSS	LAL
a313						
	70	80	90	100	110	120
	130	140	150	160	170	
m313.pep	TATIAAPVAASFFMPHVS	WWATVAIA	LLVLF	RHKS	NI	VKLLEGRESKIGGSRX
a313						
	130	140	150	160	170	
	TATIAAPLAALFFMPHTS	WIFATL	AI	LVLL	RHKS	NI

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1313>:

```

g401.seq
1  atgaaattac aacaattggc tgaagaaaaa atcggcggtc tgattgtgtt
51  cagcgtgctt gtagtcagtg tcggtctgtt gattgaagtt gtgcccttgg
101 cctttaccac ggccggcaaca cagccggcgc cggcgctgaa gccttacaat
151 gccctgcagg ttgccggacg cgatatttac atccgtgagg gctgttacia
201 ctgccactct caaatgattc gtccgttccg tgcggaaacc gagegttacg
251 gtcattactc tgttgccgga gagtcgggtt acgaccatcc gttccaatgc
301 ggttccaaac gtaccgggtc tgatttgcca cgtgtggggc gccgctattc
351 cgacgaatgg caccgcatcc acctgctgaa tccccgtgat gtcgtgcctg
401 agtccaatat gccggcattc ccgtggcttg cagcaataa agtcgatgtc
451 gatgcaaccg ttgccaacat gaaggctttg cgtaaagtag gtactcctta
501 cagtgatgag gaaattgcga aagcgctga ggctttggca aacaaatccg
551 agctggatgc tgtagtgcgc tatctgcaag gattgggtct ggctttgaaa
601 aacgtaaggt aa

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This corresponds to the amino acid sequence <SEQ ID 1314; ORF 401.ng>:

```

g401.pep
1  MKLQQLAEEK IGVLIVFTLL VSVGLLIEV VPLAFTKAAT QPAPGVKPYN
51  ALQVAGRDIY IREGCYNCHS QMIRPFRAET ERYCHYSVAG ESYDHPFQW
101 GSKRTGPDLA RVGGRYSEW HRIHLLNPRD VVPESNMPAF PWLARNKVDV
151 DATVANMKAL RKVGTPYSDE EIAKAPEALA NKSELDVVA YLQGLGLALK
201 NVR*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1315>:

```

m401.seq
1  ATGAAATTAC AaCAATTGGC TGAAGAAAAA ATCGGCGTTC TGATTGTGTT
51  CACGCTGCTT GTAGTCAGTG TCGGTCTGTT GATTGAAGTT GTGCCCTTGG
101 CCTTTACCAA GGCGGCAACA CAGCCGGCGC CGGGCGTGAA GCCTTACAA
151 GCCCTGCAGG TTGCCGGACG CGATATTAC ATCCGTGAGG GCTGTTACAA
201 CTGCCACTCG CAAATGATTG GTCCGTTCG TCGGAAACC GAGCGTTACG
251 GTCATTACTC TGTGCGGGA GAGTCGGTTT ACGACCATCC GTTCCAATGG
301 GGTTCCAAAC GTACCGGTCC TGATTGGCA CGTGTGGGCG GTCGCTATTG
351 CGACGAATGG CACCGTATCC ACCTGCTGAA TCCCCGTGAT GTCGTGCCTG
401 AGTCCAATAT GCCGGCATTG CCGTGGCTTG CACGCAATAA AGTCGATGTC
451 GATGCAACCG TTGCCAACAT GAAGGCTTTG CGTAAAGTAG GTACTCCTTA
501 CAGTGATGAG GAAATTGCGA AAGCACCTGA GGCTTTGGCA AACAAATCCG
551 AGCTGATGTC TGTAGTCGCC TATCTGCAAG GATTGGGTCT GGCTTTGAAA
601 AACGTAAGGT AA

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This corresponds to the amino acid sequence <SEQ ID 1316; ORF 401>:

```

m401.pep
1  MKLQQLAEEK IGVLIVFTLL VSVGLLIEV VPLAFTKAAT QPAPGVKPYN
51  ALQVAGRDIY IREGCYNCHS QMIRPFRAET ERYCHYSVAG ESYDHPFQW
101 GSKRTGPDLA RVGGRYSEW HRIHLLNPRD VVPESNMPAF PWLARNKVDV
151 DATVANMKAL RKVGTPYSDE EIAKAPEALA NKSELDVVA YLQGLGLALK
201 NVR*

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Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 401 shows 100.0% identity over a 203 aa overlap with a predicted ORF (ORF 401.ng) from *N. gonorrhoeae*:

m401/g401

	10	20	30	40	50	60
m401.pep	MKLQQLAEEKIGVLIVFTLLVSVGLLIEVVPLAFTKAATQPAPGVKPYNALQVAGRDIY					
g401	MKLQQLAEEKIGVLIVFTLLVSVGLLIEVVPLAFTKAATQPAPGVKPYNALQVAGRDIY					
	10	20	30	40	50	60
	70	80	90	100	110	120
m401.pep	IREGCYNCHSQMIRPFRAETERYGHYSVAGESVYDHPFQWGSKRTGPDLARVGGRYSEW					

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      |||
g401  IREGCYNCHSQMIRPFRAETERYGHYSVAGESVYDHPFQWGSKRTGPDLARVGGRYSEW
      70      80      90      100     110     120

      130     140     150     160     170     180
m401.pep HRIHLLNPRDVPESNMPAFWFLARNKVDVDATVANMKALRKVGTPYSDEEIAKAPEALA
      |||
g401  HRIHLLNPRDVPESNMPAFWFLARNKVDVDATVANMKALRKVGTPYSDEEIAKAPEALA
      130     140     150     160     170     180

      190     200
m401.pep NKSELDVVAYLQGLGLALKNVRX
      |||
g401  NKSELDVVAYLQGLGLALKNVRX
      190     200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1317>:

```

a401.seq
  1  ATGAAATTAC  AACAAATTGGC  TGAAGAAAAA  ATCGGCGTTC  TGATTGTGTT
51  CACGCTGCTT  GTAGTCAGTG  TCGGTCTGTT  GATTGAAGTT  GTGCCCTTGG
101 CCTTTACCAA  GCGCGCAACA  CAGCCGGCGT  CGGGCGTGAA  GCCTTACAA
151 GCCCTGCAGG  TTGCCGGACG  CGATATTAC  ATCCGTGAGG  GCTGTTACAA
201 CTGCCACTCG  CAAATGATTC  GTCCGTTCGG  TCGGGAACCC  GAGCGTTACG
251 GTCATTACTC  TGTTCGCCGA  GAGTCGGTTT  ACGACCATCC  GTTCCAATGG
301 GGTTCCAAAC  GTACCGGTCC  TGATTGGCA  CGTGTGGCG  GTCGCTATTC
351 CGACGAATGG  CACCGTATCC  ACCTGCTGAA  TCCCCGTGAT  GTCGTGCTG
401 AGTCCAATAT  GCCGGCATT  CCGTGGCTTG  CACGCAATAA  AGTCGATGTC
451 GATGCAACCG  TTGCCAACAT  GAAGGCTTTG  CGTAAAGTAG  GTACTCCTTA
501 CAGTGATGAG  GAAATTGCGA  AAGCGCCTGA  GGCTTTGGCA  AACAAATCCG
551 AGCTGGATGC  TGTAGTCGCC  TATCTGCAAG  GATTGGGTCT  GGCTTTGAAA
601 AACGTAAGGT  AA

```

This corresponds to the amino acid sequence <SEQ ID 1318; ORF 401.a>:

```

a401.pep
  1  MKLQQLAEEK  IGVLLIVFTLL  VVSVGLLIEV  VPLAFTKAAT  QPASGVKPYN
51  ALQVAGRDIY  IREGCYNCHS  QMIRPFRAET  ERYGHYSVAG  ESVYDHPFQW
101 GSKRTGPDLA  RVGGRYSEW  HRIHLLNPRD  VVPESNMPAF  WFLARNKVDV
151 DATVANMKAL  RKVGTPYSDE  EIAKAPEALA  NKSELDVVA  YLQGLGLALK
201 NVR*

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m401/a401 99.5% identity in 203 aa overlap

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      10      20      30      40      50      60
m401.pep MKLQQLAEEKIGVLIVFTLLVSVGLLIEVVPLAFTKAATQPAPGVKPYNALQVAGRDIY
      |||
a401  MKLQQLAEEKIGVLIVFTLLVSVGLLIEVVPLAFTKAATQPASGVKPYNALQVAGRDIY
      10      20      30      40      50      60

      70      80      90      100     110     120
m401.pep IREGCYNCHSQMIRPFRAETERYGHYSVAGESVYDHPFQWGSKRTGPDLARVGGRYSEW
      |||
a401  IREGCYNCHSQMIRPFRAETERYGHYSVAGESVYDHPFQWGSKRTGPDLARVGGRYSEW
      70      80      90      100     110     120

      130     140     150     160     170     180
m401.pep HRIHLLNPRDVPESNMPAFWFLARNKVDVDATVANMKALRKVGTPYSDEEIAKAPEALA
      |||
a401  HRIHLLNPRDVPESNMPAFWFLARNKVDVDATVANMKALRKVGTPYSDEEIAKAPEALA
      130     140     150     160     170     180

      190     200
m401.pep NKSELDVVAYLQGLGLALKNVRX
      |||
a401  NKSELDVVAYLQGLGLALKNVRX
      190     200

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The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1319>:

g402.seq

```

1  ATGGATATGG TGAACACTAA Accgaatact agtgtgatta atatgctttc
51  tttcccttacc ggattATTGA GCTTGGGTat agaagtCtTg tGGGTAAGGA
101 TGtttttcgTT CGCagcAcag tccgtgcctc aggCATTtTC atttattcctt
151 gcctGttttc tgACCGgtat cgcctgcggc gCgTATTtTG GCAAACGGAT
201 TTGCCCGCAGC CGCTTTGTTG ATATTCCctT TATCGGGCAG TgcttcttgT
251 GGGCGGGTAT TgccgaTttt ttgatTTTGG GTGCTGCGTG GTTGTGACG
301 G3TTTTTccg gtttcGTCCA CCACGCCGGT AtttTCATTA CCCTgtctgc
351 C3tcGTCAGG GGGTTGATTT TCCCACtTGT ACACCATgtg GGTACGGATG
401 GCAACAAATC CGGACGACAG GTTTCCAATG TTTATTTCGC CAACGTGtCC
451 G3CAGTGCAT TGGGTCCGGT CCTTATCGGC TTTGTGATAC TTGATttgtt
501 gTCCACCCAA CAGATTtacc tgctcatCTG TTTGATTtCT CTGCTgtctc
551 cTTTGTtTTg tacaCTGtTC CAAAAAAGTC TCCGACTGAA TGCAGTGTcG
601 GTAGCAGTTT CCCTAATGTT CGGCATCCTC ATGTTCTTAC TGCCGGATTc
651 TGTCTTTCAA AATATTGCTG GCCGTCCGGA TAGGTTGATT GAAAACAAAC
701 ACGGCATTGT TGCGGTTTAC CATAGAGATG GTGATAAGGT TGTtTATGGG
751 GCGAATGTAT ACACGGCGC ATACAATACC GATATATTCA ATAGTGTCAA
801 CGGCATCGAA CGTGCTATC TGCTACCCTC CCTGAAGTCC GGCATACGCC
851 GCATTtTCGT CGTTGGATTG AGTACAGGTT CGTGGGCGCG CGTCTTGTCT
901 GCCATTCCGG AAATGCAGTC GATGATCGTT GCGGAAATCA ATCCGGCATA
951 CCGTAGCCTT ATCGCGGAcg agccgcAAAT CGCACCgCTT TTGCAGGACA
1001 AACGTGTTGA AATTGTATTG GATGACGGTA GGAATGGCT GCGTCGCCAT
1051 CCTGATGAAA AATTCGACCT GATTtTGATG AATTGCACTT GGTACTGGCG
1101 TGCCtATTTC ACTAACCTGT TGAGTGCGGA ATTTTtAAAA CAGGTGCAAA
1151 GCCACCTTAC CCCGGATGGT ATTGTAATGT TTAATACCAC GCACAGCCCG
1201 CATgctTTTG CTACCGCCGT ACACAGTATT CCCTATGCAT ACCGCTACGG
1251 GCATATGGTA GTCGGCTCGG CAACCCCGGT AGTTTTCcct AATAAAGAAC
1301 TGCTCaagca aCGCCTTtcc cgGTTGATTT GCGCGGAAAG CGGCAGgcac
1351 gTATTGACA GCAGCACCGT G3ATGCTGCA GCACAAAAGG TTGctctctCG
1401 TATGCTGATT CGGATGACGG AAcctTCGGC TGGGGCGGAA GTCATTACTG
1451 ACGATAATAT GATTGTAGAA TACAAATACG GCAGAGGGAT TTAA

```

This corresponds to the amino acid sequence <SEQ ID 1320; ORF 402.ng>:

g402.pep

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1  MDMVNTKPNT SVINMLSFLT GLLSLGIEVL WVRMFSFAAQ SVPQAFSFLI
51  ACFLTGIavg AYFGKRICRS RFVDIPFIGQ CFLWAGIADF LILGAAWLLT
101 GFSGFVHHAG IFITLSAVVR GLIFPLVHHV GTDGNKSGRQ VSNVYFANVA
151 GSALGPVLIG FVILDLLSTQ QIYLLICLIS AAVPLFCTLF QKSLRLNAVS
201 VAVSLMFGIL MFLLPDSVFO NIAGRPDRLI ENKHGIVAVY HRDGDKVYVG
251 ANVYDGAYNT DIFNSVNGIE RAYLLPSLKS GIRRIFVUGL STGSWARVLS
301 AIPEMQSMIV AEINPAYRSL IADEPQIAPL LQDKRVEIVL DDGRKWLRRH
351 PDEKFDLILM NSTWYWRAYS TNLLSAEFLK QVQSHLTPDG IVMFNTTHSP
401 HAFATAVHSI PYAYRYGHMV VGSATFVVFV NKELLKQRLS RLIWPESGRH
451 VFDSSSTVDA AOKVVSRLMI RMTEPSAGAE VITDDNMIVE YKYGRGI*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1321>:

m402.seq

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1  ATGGATATAG TGAACACTAA ACCGAATACT AGTTTGATTt ATATGCnTTC
51  TTTCCtTAGC GGCTTATTGA GCTTGGGTAT AGAAGTCTTG TGGGTGAGGA
101 TGTTTTTCGTT CGCAGCACAG TCCGTGCCTC AGGCATTtTC ATTTACCCTT
151 GCCTGTTTTc TGACCGGTAT CGCCGTGCGC GCGTATTtTG GCAAACGGAT
201 TTGCCCGCAGC CGCTTTGTTG ATATTCCCTT TATCGGGCAG TGCTTCTTGT
251 GGGCGGGTAT TGCCGACTTT TTGATTtTG GTGCTGCGTG GTTGTGACG
301 GGTTTTTCCG GCTTCGTCCA CCACGCCGGT ATCTTCATTA CCCTGTCTGC
351 CGTCGTCAsA sGGTTGATTT TCCCGCTCGT ACACCATGTG GGTACGGATG
401 GCAACAAATC CGGACGACAG GTTTCCAATG TTTATTTCGC CAACGTGtCC
451 GGCAGTGCAT TGGGTCCGGT CCTTATCGGC TTTGTGATAC TTGATTtCTT
501 GTCCACCCAA CAGATTtACC TGCTCATCTG TwTGATTtCT GCTGCTGTCC
551 CTTTGTtTTG TACACTGTTT CAAAAAAGTC TCCGACTGAA TGCAGTGTcG
601 GTAGCAGTTT CCCTAATGTT CGGCATCCTC ATGTTCTyTAC TGCCGGATTc

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651 TGTCTTTCAA AATATTGCTG ACCGTCCGGA TagGCTGATT GAAAACAAAC
701 ACGGCATTGT TGC GGTTTAC CATAGAGATG GTGATAAGGT TGTTTATGGG
751 GCGAATGTAT ACGACGCGC ATACAATACC GATGTATTCA ATAGTGTCAC
801 CGGCATCGAA CGTGCCATC TGCTACCCCT CCTGAAGTCT GGCAATACGCC
851 GCATTTTCGT CGTTGGACTG AGTACAGGTT CGTGGGCGCG CGTCTTGCTCT
901 GCCATTCCGG AAATGCAGTC GATGATCGTT GCGGAAATCA ATCCGGCATA
951 CCGTAGCCTT ATCGCGGACG AGCCGCAAAT CGCCCGCTT TTGCAGGACA
1001 AACGTGTTGA AATTGTATTG GATGACGGTA GGAAATGGCT GCGTCGCCAT
1051 CCTGATGAAA AATTCGACCT GATTTTGATG AATACGACTT GGTACTGGCG
1101 TGCCTATTCC ACCAACCTGT TGAGTGC GGA ATTTTAAAA CAGGTGCAAA
1151 GCCACCTTAC CCCGGATGGT ATTGTAATGT TTAATACCAC GCACAGCCCG
1201 CATGCTTTTG CTACCGCCGT ACACAGTATT CCCTATGCAT ACCGCTATGG
1251 GCATATGGTA GTCGGCTCGG CAACCCCGGT AGTTTTCCT AATAAAGAAC
1301 TGCTCAAGCA ACGTCTCTCC CGGTTGATTT GGCCGGAAAG CGGCAGGCAC
1351 GTATTTGACA GCAGCACCGT GGATGCTGCA GCACAAAAGG TTGTCTCTCG
1401 TATGCTGATT CAGATGACGG aAcCTTCGGC TGGGGCGGAA GTTATTACCG
1451 ACGATAATAT GATTGTAGAA TACAAATACG GCAGAGGGAT TTAA

```

This corresponds to the amino acid sequence <SEQ ID 1322; ORF 402>:

m402 . pep

```

1 MDIVNTKPNT SLIYMXSFLS GLLSLGLIEVL WVRMFSFAAQ SVPOAFSFTL
51 ACFLTGIAVG AYFGKRICRS RFVDIPFIGQ CFLWAGIADF LILGAAWLLT
101 GFSGFVHHAG IFITLSAVVX XLIFPLVHHV GTDGNKSGRQ VSNVYFAXVA
151 GSALGPVLIG FVILDFLSTQ QIYLLICXIS AAVPLFCTLF QKSLRLNAVS
201 VAVSLMFGIL MFLLPDSVFQ NIADRPDRLI ENKHGIVAVY HRDGDKVYVG
251 ANVYDGAYNT DVFN SVNGIE RAYLLPSLKS GIRRI FVVGL STGSGWARVLS
301 AIPMQSMIV AEINPAYRSL IADEPQIAPL LQDKRVEIVL DDGRKWLRRH
351 PDEKFDLILM NTTWYWRAYS TNLSSAEFLK QVQSHLTPDG IVMFNTTHSP
401 HAFATAVHSI PYAYRYGHMV VGSATPVVFP NKELLKQRLS RLIWPESGRH
451 VFDSSSTVDA A QKVVSRLI QMTEPSAGAE VITDDNMIVE YKYGRGI*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 402 shows 97.0% identity over a 497 aa overlap with a predicted ORF (ORF 402.ng) from *N. gonorrhoeae*:

m402/g402

	10	20	30	40	50	60
m402 . pep	MDIVNTKPNTSLIYMXSFLSGLLSLGLIEVLWVRMFSFAAQSVPOAFSFTLACFLTGIAVG					
g402	MDMVNTKPNTSVINMLSFLTGLLSLGLIEVLWVRMFSFAAQSVPOAFSFTLACFLTGIAVG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m402 . pep	AYFGKRICRSRFVDIPFIGQCFLWAGIADF LILGAAWLLTGFSGFVHHAGIFITLSAVVX					
g402	AYFGKRICRSRFVDIPFIGQCFLWAGIADF LILGAAWLLTGFSGFVHHAGIFITLSAVVR					
	70	80	90	100	110	120
	130	140	150	160	170	180
m402 . pep	XLIFPLVHHVGTGDNKSGRQVSNVYFAXVAGSALGPVLIGFVILDFLSTQQIYLLICXIS					
g402	GLIFPLVHHVGTGDNKSGRQVSNVYFANVAGSALGPVLIGFVILDLLSTQQIYLLICLIS					
	130	140	150	160	170	180
	190	200	210	220	230	240
m402 . pep	AAVPLFCTLFQKSLRLNAVS VAVSLMFGILMFLLPDSVFQNIADRPDRLIENKHGIVAVY					
g402	AAVPLFCTLFQKSLRLNAVS VAVSLMFGILMFLLPDSVFQNIAGRDPDRLIENKHGIVAVY					
	190	200	210	220	230	240
	250	260	270	280	290	300
m402 . pep	HRDGDKVYVGANVYDGAYNTDVFN SVNGIERAYLLPSLKS GIRRI FVVGLSTGSGWARVLS					

726

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g402      |||||:|||||
          HRDGDKVYGANVYDGAYNTDIFNSVNGIERAYLLPSLKS GIRRIFVVG LSTG SWARVLS
          250      260      270      280      290      300

m402 . pep      310      320      330      340      350      360
          A I P E M Q S M I V A E I N P A Y R S L I A D E P Q I A P L L Q D K R V E I V L D D G R K W L R R H P D E K F D L I L M
g402      |||||:|||||
          A I P E M Q S M I V A E I N P A Y R S L I A D E P Q I A P L L Q D K R V E I V L D D G R K W L R R H P D E K F D L I L M
          310      320      330      340      350      360

m402 . pep      370      380      390      400      410      420
          N T T W Y W R A Y S T N L L S A E F L K Q V Q S H L T P D G I V M F N T T H S P H A F A T A V H S I P Y A Y R Y G H M V
g402      |||||:|||||
          N T T W Y W R A Y S T N L L S A E F L K Q V Q S H L T P D G I V M F N T T H S P H A F A T A V H S I P Y A Y R Y G H M V
          370      380      390      400      410      420

m402 . pep      430      440      450      460      470      480
          V G S A T P V V F P N K E L L K Q R L S R L I W P E S G R H V F D S S T V D A A A Q K V V S R M L I Q M T E P S A G A E
g402      |||||:|||||
          V G S A T P V V F P N K E L L K Q R L S R L I W P E S G R H V F D S S T V D A A A Q K V V S R M L I R M T E P S A G A E
          430      440      450      460      470      480

m402 . pep      490
          V I T D D N M I V E Y K Y G R G I X
g402      |||||:|||||
          V I T D D N M I V E Y K Y G R G I
          490

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1323>:

```

a402 . seq
1  ATGGATATAG TGAACACTAA ACCGAATACT AGTTTGATTT ATATGCTTTT
51  TTTCCTTAGC GGCTTATTGA GCTTGGGTAT AGAAGTCTTG TGGGTAAGGA
101 TGTTCCTCGT CGCAGCACAG TCCGTGCCTC AGGCATTTTC ATTTACTCTT
151 GCCTGTTTTC TGACCGGTAT CGCCGTCGGC GCGTATTTTG GCAAACGGAT
201 TTGCCGCAGC CGCTTTGTTG ATATCCCTT TATCGGGCAG TGCTTCTTGT
251 GGGCGGGTAT TGCCGACTTT TTGATTTTGG GTGCTGCGTG GTTGTGACG
301 GGTTCCTCCG GCTTCGTCCA CCACGCCGGT ATCTTCATTA CCCTGTCTGC
351 CGTCGTCAGA GGGTTGATTT TCCCGCTCGT ACACCATGTG GGTACGGATG
401 GCAACAAATC CGGACGACAG GTTTCCAATG TTTATTTCGC CAACGTTGCC
451 GGCAGTG CAT TGGGTCCGGT CCTTATCGGC TTTGTGATAC TTGATTTCTT
501 GTCACCCAA CAGATTACC TGCTCATCTG TTTGATTTCT GCTGCTGTCC
551 CTTTGTTCG TACACTGTTT CAAAAAGTC TCCGACTGAA TGCAGTGTCT
601 GTAGCAGTTT CCCTAATGTT CGGCATCCTC ATGTTCTTAC TGCCGGATTC
651 TGTCTTTCAA AATATTGCTG ACCGTCCGGA TAGGCTGATT GAAACAAAC
701 ACGGCATTGT TGCGGTTTAC CATAGAGATG GTGATAAGGT TGTTCATGGG
751 GCGAATGTAT ACGACGGCGC ATACAATACC GATGTATTCA ATAGTGTCAG
801 CGGCATCGAA CGTGCCATAT TGCTACCTCT CCTGAAGTCT GGCATACGCC
851 GCATTTTCGT CGTTGGATTG AGTACAGGTT CGTGGGCGCG CGTCTTGTCT
901 GCCATTCCGG AAATGCAGTC GATGATCGTT GCGGAAATCA ATCCGGCATA
951 CCGTAGCCTT ATCGCGGACG AGCCGCAAAT CGCCCGCTT TTGCAGGACA
1001 AACGTGTGTA AATTGTATTG GATGACGGTA GGAAATGGCT GCGTCGCCAT
1051 CCTGATGAAA AATTCGACCT GATTTTGATG AATACGACTT GGTACTGGCG
1101 TGCCTATTCC ACCAACCTGT TGAGTGCGGA ATTTTAAAA CAGGTGCAAA
1151 GCCACCTTAC CCCGGATGGT ATTGTAATGT TTAATACCAC GCACAGCCCG
1201 CATGCTTTTG CTACCGCCGT ACACAGTATT CCCTATGCAT ACCGCTATGG
1251 GCATATGGTA GTCGGCTCGG CAACCCCGGT AGTTTTCCTT AATAAAGAAC
1301 TGCTCAAGCA ACGTCTCTCC CGGTTGATTT GGCCGGAAG CCGCAGGCAC
1351 GTATTGACA GCAGACCGT GGATGCTGCA GCACAAAAGG TTGTCTCTCG
1401 TATGCTGATT CAGATGACGG AACCTTCGGC TGGTGCGGAA GTCATTACCG
1451 ACGATAATAT GATTGTAGAA TACAAATACG GCAGAGGGAT TTAA

```

This corresponds to the amino acid sequence <SEQ ID 1324; ORF 402.a>:

```

a402 . pep
1  MDIVNTKPNT SLIYMLSFLS GLLSLGIEVL WVRMFSFAAQ SVPQAFSEFL

```

m402.pep	MDIVNTKPNTSLIYMXSFLSGLLSLGLIEVLWVRMFSAFAQSVPAQAFSFTLACFLTGI	10	20	30	40	50	60
a402	MDIVNTKPNTSLIYMLSFLSGLLSLGLIEVLWVRMFSAFAQSVPAQAFSFTLACFLTGI	10	20	30	40	50	60
m402.pep	AYFGKRICRSRFDIPFIGQCFLWAGIADFLILGAAWLLTGFSGFVHHAGIFITLSAVVX	70	80	90	100	110	120
a402	AYFGKRICRSRFDIPFIGQCFLWAGIADFLILGAAWLLTGFSGFVHHAGIFITLSAVVR	70	80	90	100	110	120
m402.pep	XLIFPLVHHVGTGDNKSGRQVSNVYFAXVAGSALGPVLIGFVILDFLSTQQIYLLICXIS	130	140	150	160	170	180
a402	GLIFPLVHHVGTGDNKSGRQVSNVYFANVAGSALGPVLIGFVILDFLSTQQIYLLICLIS	130	140	150	160	170	180
m402.pep	AAVPLFCTLFQKSLRLNAVSVAVSLMFGILMFLLPDSVVFQNIADRPDRLIENKHGIVAVY	190	200	210	220	230	240
a402	AAVPLFCTLFQKSLRLNAVSVAVSLMFGILMFLLPDSVVFQNIADRPDRLIENKHGIVAVY	190	200	210	220	230	240
m402.pep	HRDGDQKVYGANVYDGAYNTDVFNVSNGIERAYLLPSLKSIGIRRIFFVGLSTGSGWARVLS	250	260	270	280	290	300
a402	HRDGDQKVYGANVYDGAYNTDVFNVSNGIERAYLLPSLKSIGIRRIFFVGLSTGSGWARVLS	250	260	270	280	290	300
m402.pep	AIPEMQSMIVAEINPAYRSLIADEPQIAPLLQDKRVEIVLDDGRKWLRRHPDEKFDLILM	310	320	330	340	350	360
a402	AIPEMQSMIVAEINPAYRSLIADEPQIAPLLQDKRVEIVLDDGRKWLRRHPDEKFDLILM	310	320	330	340	350	360
m402.pep	NTTWYWRAYSTNLLSAEFLKQVQSHLTPDGIVMFNTTHSPHAFATAVHSIPYARYGHMV	370	380	390	400	410	420
a402	NTTWYWRAYSTNLLSAEFLKQVQSHLTPDGIVMFNTTHSPHAFATAVHSIPYARYGHMV	370	380	390	400	410	420
m402.pep	VGSATPVVFPNKELLKQRLSRLIWPESGRHVFDSSSTVDAAAQKVVSRLIQMTEPSAGAE	430	440	450	460	470	480
a402	VGSATPVVFPNKELLKQRLSRLIWPESGRHVFDSSSTVDAAAQKVVSRLIQMTEPSAGAE	430	440	450	460	470	480
m402.pep	VITDDNMIVEYKYGRGIX	490					
a402	VITDDNMIVEYKYGRGIX	490					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1325>:

g406.seq

```

1  ATGCGGGCAC GGCTGCTGAT ACCTATTCTT TTTTCAGTTT TTATTTTATC
51  CGCCTGCGGG AACTGACAG GTATTCCATC GCATGGCGGA GGCAAACGCT
101 TC GCGGT CGA ACAAGAACTT GTGGCGGCTT CTGCCAGAGC TGCCGTAAAA
151 GACATGGATT TACAGGCATT ACACGGACGA AAAGTTGCAT TGTACATTGC
201 AACTATGGGC GACCAAGGTT CAGGCAGTTT GACAGGGGGT CGCTACTCCA
251 TTGATGCACT GATTCGCGGC GAATACATAA ACAGCCCTGC CGTCCGCACC
301 GATTACACCT ATCCGCGTTA CGAAACCACC GCTGAAACAA CATCAGGCGG
351 TTTGACGGGT TTAACCACTT CTTTATCTAC ACTTAATGCC CCTGCACTCT
401 CGCGCACCCA ATCAGACGGT AGCGGAAGTA GGAGCAGTCT GGGCTTAAAT
451 ATTGGCGGGA TGGGGGATTA TCGAAATGAA ACCTTGACGA CCAACCCGCG
501 CGACACTGCC TTTCTTTCCC ACTTGGTGCA GACCGTATTT TTCTGCGCG
551 GCATAGACGT TGTTTCTCCT GCCAATGCCG ATACAGATGT GTTTATTAAC
601 ATCGACGTAT TCGGAACGAT ACGCAACAGA ACCGAAATGC ACCTATACAA
651 TGCCGAAACA CTGAAAGCCC AAACAAAACCT GGAATATTTT GCAGTAGACA
701 GAACCAATAA AAAATTGCTC ATCAAACCCA AAACCAATGC GTTTGAAGCT
751 GCCTATAAAG AAAATTACGC ATTGTGGATG GGGCCGTATA AAGTAAGCAA
801 AGGAATCAAA CCGACGGAAG GATTGATGGT CGATTTCTCC GATATCCAAC
851 CATACGGCAA TCATACGGGT AACTCCGCCC CATCCGTAGA GGCTGATAAC
901 AGTCATGAGG GGTATGGATA CAGCGATGAA GCAGTGCAC AACATAGACA
951 AGGGCAACCT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1326; ORF 406>:

g406.pep

```

1  MRARLLIPIL FSVFILSACG TLTGIPSHGG GKRFAVEQEL VAASARAAVK
51  DMDLQALHGR KVALYIATMG DQSGSLTGG RYSIDALIRG EYINSPAVRT
101 DYTYPREYET AETTSGLLTG LTSSLSTLNA PALSRQSDG SGRSSSLGLN
151 IGGMGDYRNE TLTINPRDTA FLSHLVQTVF FLRGIDVVSP ANADTDVFIN
201 IDVFGTIRNR TEMHLYNAET LKAQTKLEYF AVDRTNKKLL IKPKTNAFEA
251 AYKENYALWM GPYKVSIGIK FTEGLMVDFFS DIQPYGNHTG NSAPSVEADN
301 SHEGYGYSDE AVRQHRQQP *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1327>:

m406.seq

```

1  ATGCAAGCAC GGCTGCTGAT ACCTATTCTT TTTTCAGTTT TTATTTTATC
51  CGCCTGCGGG AACTGACAG GTATTCCATC GCATGGCGGA CGTAAACGCT
101 TTGCGGT CGA ACAAGAACTT GTGGCGGCTT CTGCCAGAGC TGCCGTAAAA
151 GACATGGATT TACAGGCATT ACACGGACGA AAAGTTGCAT TGTACATTGC
201 CACTATGGGC GACCAAGGTT CAGGCAGTTT GACAGGGGGT CGCTACTCCA
251 TTGATGCACT GATTCGTGGC GAATACATAA ACAGCCCTGC CGTCCGTACC
301 GATTACACCT ATCCACGTTA CGAAACCACC GCTGAAACAA CATCAGGCGG
351 TTTGACAGGT TTAACCACTT CTTTATCTAC ACTTAATGCC CCTGCACTCT
401 CTCGCACCCA ATCAGACGGT AGCGGAAGTA AAAGCAGTCT GGGCTTAAAT
451 ATTGGCGGGA TGGGGGATTA TCGAAATGAA ACCTTGACGA CTAACCCGCG
501 CGACACTGCC TTTCTTTCCC ACTTGGTACA GACCGTATTT TTCCTGCGCG
551 GCATAGACGT TGTTTCTCCT GCCAATGCCG ATACAGATGT GTTTATTAAC
601 ATCGACGTAT TCGGAACGAT ACGCAACAGA ACCGAAATGC ACCTATACAA
651 TGCCGAAACA CTGAAAGCCC AAACAAAACCT GGAATATTTT GCAGTAGACA
701 GAACCAATAA AAAATTGCTC ATCAAACCAA AAACCAATGC GTTTGAAGCT
751 GCCTATAAAG AAAATTACGC ATTGTGGATG GGGCCGTATA AAGTAAGCAA
801 AGGAATTAAG CCGACGGAAG GATTAAATGGT CGATTTCTCC GATATCCGAC
851 CATACGGCAA TCATACGGGT AACTCCGCCC CATCCGTAGA GGCTGATAAC
901 AGTCATGAGG GGTATGGATA CAGCGATGAA GTAGTGCAC AACATAGACA
951 AGGACAACCT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1328; ORF 406>:

m406.pep

```

1  MQARLLIPIL FSVFILSACG TLTGIFSHGG GKRFAVEQEL VAASARAAVK

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729

```

51  DMDLQALHGR KVALYIATMG DQSGSLTGG RYSIDALIRG EYINSPAVRT
101 DYTYPREYETT AETTSCGLTG LTSLSTLNA PALSRQSDG SGSKSSLGLN
151 IGGMGDYRNE TLTTNPRDTA FLSHLVQTVF FLRGIDVVSF ANADTDVFIN
201 IDVFGTIRNR TEMHLYNAET LKAQTKLEYF AVDRTNKKLL IKPKTNAFEA
251 AYKENYALWM GPYKVSIGIK PTEGLMVDFS DIRPYGNHTG NSAPSVEADN
301 SHEGYGYSDE VVRQHRQGP *

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 406 shows 98.8% identity over a 320 aa overlap with a predicted ORF (ORF406.a) from *N. gonorrhoeae*:

g406/m406

	10	20	30	40	50	60
g406 .pep	MRARLLIPILFSVFILSACGTLTGIPSHGGGKRFAVEQELVAASARA AVKMDLQALHGR					
	:					
m406	MQARLLIPILFSVFILSACGTLTGIPSHGGGKRFAVEQELVAASARA AVKMDLQALHGR					
	10	20	30	40	50	60
	70	80	90	100	110	120
g406 .pep	KVALYIATMGDQSGSLTGG RYSIDALIRGEYINSPAVRTDYTYPRYETTAETTSGGLTG					
	:					
m406	KVALYIATMGDQSGSLTGG RYSIDALIRGEYINSPAVRTDYTYPRYETTAETTSGGLTG					
	70	80	90	100	110	120
	130	140	150	160	170	180
g406 .pep	LTSLSTLNAPALSRQSDGSGSRSSGLNIGGMGDYRNETLTNPRDTAFLSHLVQTVF					
	: :					
m406	LTSLSTLNAPALSRQSDGSGSKSSLNIGGMGDYRNETLTNPRDTAFLSHLVQTVF					
	130	140	150	160	170	180
	190	200	210	220	230	240
g406 .pep	FLRGIDVVS PANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL					
	: :					
m406	FLRGIDVVS PANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL					
	190	200	210	220	230	240
	250	260	270	280	290	300
g406 .pep	IKPKTNAFEAAYKENYALWMGPYKVSIGIKPTEGLMVDFS DIRPYGNHTGNSAPSVEADN					
	: :					
m406	IKPKTNAFEAAYKENYALWMGPYKVSIGIKPTEGLMVDFS DIRPYGNHTGNSAPSVEADN					
	250	260	270	280	290	300
	310	320				
g406 .pep	SHEGYGYSDEAVRQHRQGPX					
	:					
m406	SHEGYGYSDEVVRQHRQGPX					
	310	320				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1329>:

```

a406 .seq
1  ATGCAAGCAC GGCTGCTGAT ACCTATTCTT TTTTCAGTTT TTATTTTATC
51  CGCCTGCGGG AACTGACAG GTATTCCATC GCATGGCGGA GGTAAACGCT
101 TCGCGGTCGA ACAAGAACTT GTGGCCGCTT CTGCCAGAGC TGCCGTTAAA
151 GACATGGATT TACAGGCATT ACACGGACGA AAAGTTGCAT TGTACATTGC
201 AACTATGGGC GACCAAG3TT CAGGCAGTTT GACAGGGGGT CGTACTCCA
251 TTGATGCACT GATTCGTGGC GAATACATAA ACAGCCCTGC CGTCCGTACC
301 GATTACACCT ATCCACGTTA CGAAACCACC GCTGAAACAA CATCAGGCGG
351 TTTGACAGGT TTAACCACTT CTTTATCTAC ACTTAATGCC CCTGCACTCT
401 CGCGCACCCA ATCAGACGGT AGCGGAAGTA AAAGCAGTCT GGGCTTAAAT
451 ATTGGCGGGA TGGGGGATTA TCGAAATGAA ACCTTGACGA CTAACCCGCG

```

730

```

501 CGACACTGCC TTTCTTTCCC ACTTGGTACA GACCGTATTT TTCCTGCGCG
551 GCATAGACGT TGTTTCTCCT GCCAATGCCG ATACGGATGT GTTTATTAAC
601 ATCGACGTAT TCGGAACGAT ACGCAACAGA ACCGAAATGC ACCTATACAA
651 TGCCGAAACA CTGAAAGCCC AAACAAAAC GGAATATTTC GCAGTAGACA
701 GAACCAATAA AAAATTGCTC ATCAAACCAA AAACCAATGC GTTGAAGCT
751 GCCTATAAAG AAAATTACGC ATTGTGGATG GGACCGTATA AAGTAAGCAA
801 AGGAATTAAA CCGACASAAG GATTAATGGT CGATTTCTCC GATATCCAAC
851 CATACGGCAA TCATATGGGT AACTCTGCCC CATCCGTAGA GGCTGATAAC
901 AGTCATGAGG GGTATGGATA CAGCGATGAA GCAGTGCAC GACATAGACA
951 AGGGCAACCT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1330; ORF 406.a>:

```

a406.pep
  1 MQARLLIPIL FSVFILSACG TLTGIPSHGG GKREFAVEQEL VAASARAAVK
  51 DMDLQALHGR KVALYIATMG DQSGSLTGG RYSIDALIRG EYINSPAVRT
 101 DYTYPRIYET AETTSGLTGT LTSLSTLNA PALSRQSDG SGSKSSLGLN
 151 IGGMGDYRNE TLTTNPRDTA FLSHLVQTVF FLRGIDVVSF ANADTDVFIN
 201 IDVFGTIRNR TEMHLYNAET LKAQTKLEYF AVDRTNKKLL IKPKTNAFEA
 251 AYKENYALWM GPYKVSIGIK PTEGLMVDFS DIQPYGNHMG NSAPSVEADN
 301 SHEGYGYSDE AVRRHRQGQP *

m406/a406 98.8% identity in 320 aa overlap

      10      20      30      40      50      60
m406.pep MQARLLIPILFSVFILSACGTLTGIPSHGGGKREFAVEQELVAASARAAVKMDLQALHGR
      |||
a406      MQARLLIPILFSVFILSACGTLTGIPSHGGGKREFAVEQELVAASARAAVKMDLQALHGR
      10      20      30      40      50      60

      70      80      90      100     110     120
m406.pep KVALYIATMGDQSGSLTGGRYSIDALIRGEYINSPAVRTDYTYPRIYETTAETTSGLTGT
      |||
a406      KVALYIATMGDQSGSLTGGRYSIDALIRGEYINSPAVRTDYTYPRIYETTAETTSGLTGT
      70      80      90      100     110     120

      130     140     150     160     170     180
m406.pep LTSLSTLNAPALSRQSDGSGSKSSLGLNIGMGDYRNETLTNPRDTAFLSHLVQTVF
      |||
a406      LTSLSTLNAPALSRQSDGSGSKSSLGLNIGMGDYRNETLTNPRDTAFLSHLVQTVF
      130     140     150     160     170     180

      190     200     210     220     230     240
m406.pep FLRGIDVVSPANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL
      |||
a406      FLRGIDVVSPANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL
      190     200     210     220     230     240

      250     260     270     280     290     300
m406.pep IKPKTNAFEAAAYKENYALWMGPYKVSIGIKPTEGLMVDFS DIRPYGNHTGNSAPSVEADN
      |||
a406      IKPKTNAFEAAAYKENYALWMGPYKVSIGIKPTEGLMVDFS DIQPYGNHMGNSAPSVEADN
      250     260     270     280     290     300

      310     320
m406.pep SHEGYGYSDEVVRQHRQGQPX
      |||
a406      SHEGYGYSDEAVRRHRQGQPX
      310     320

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1331>:

```

g501.seq
  1 atggtcggac ggaccttgac cgcagatacc gacatatttg ttctgcttgc,
  51 ggcaggcgga gatggcaaga tgcagcatca ctttgacggc aggggtgcgt

```

731

```

101 tcgtcaaacg attcggacac caagccgctg tctcggtcga ggccgagggg
151 cagctgggtc atgtcgctcg agccgatgga gaagccgtcg aagtattgca
201 ggaattgttc cgccaataacc gcgttgctcg gcagctcgca catcataatc
251 aggcgcaggc cgtttttgcc gcgttccaag ccgttttctt tcaatgcctt
301 aaccactgct tcggcttcgc ccaaagtgcg gacgaacgga atcatgattt
351 cgacgttggt cagacccatt tcgtcacgaa cgcgtttcaa ggctttgcat
401 tccaaggcga aacagtcttt gaagctctcg gcaacataac gcgccgcacc
451 acggaagccc aacatcgggt tttcttcatt cggttcgtat acgctgccgc
501 cgaccaggtt ggcgtattcg ttggatttga agtcggacat acggacgatg
551 gttttacgcy gataaaccga tgcggcaagc gttgccacgc cttcggcgat
601 tttatcgacy tagaagtcga caggggatgc gtaaccggcg atcggcgcgga
651 taatttccgc tttcagttcg tcgtcttgtt tgtcaaattc caacaaggct
701 ttcgggtgga tgccgatttg gcggttgatg ataaattcca tacgcgcaa
751 gccgatgcct tcgctgggca gattggcgaa gctgaatgcy agttcgggat
801 tgccgacgtt catcatgact ttgacgggtg cttttggcat attgtccaag
851 gcgacatcgg taatttgtac gtccagcagg ccggcataga taaagccggt
901 atcgcttcg gcacaggata cggtaacttc ctgaccgttt tccaagagtt
951 cggctcgatt gccgcagccg acgacggcag gaatacccg ttcgcgcgcg
1001 atgatggcgg cgtggcaggt gcgtccgcgg cggttggtca cgtatggcga
1051 agcacgtttc atcacgggtt cccaatccgg atcggtcatg tcggtaacca
1101 gtacgtcgcc ggcttcgacg gaatccatct cgggaagcat tttaatcagg
1151 cgcaccttgc cctgaccgac tttttgaccg atggcacgac cttcgacaa
1201 gacggttttt tcgccgttga tggcgtagcg gcgcaggttg cggtgcctt
1251 cttcttggga tttgacgggt tcggggcggg cttgcaggat gtatagtttg
1301 ccgtccaggc cgtcgcgtcc ccattcgata tccatcgggc ggccgtagtg
1351 tttttcgatg gtcagcgctg agtgtgcaa ctcggtgatt tcttcgtcgg
1401 taatggagaa gcggttgcyg tcttcttcgg ggacttcgac gttggttacc
1451 gatttgccgg cttcggcttt gtcggtgaaa atcattttga tgtgtttcga
1501 acccatgggtc ttgcgcagga tggcggttt gcctgctttg agcgtgggtt
1551 tgaacacata aaattcgtcc ggggtgaccg cgccttgatc gacgttttcg
1601 cccagaccgt aagaggaggt aacaaagacg acttggttgt agccggattc
1651 ggtgtcgagg gtgaacatca cacctga

```

This corresponds to the amino acid sequence <SEQ ID 1332; ORF 501.ng>:

```

g501.pep
1  MVGRITLTADT DIFVLLAAGG DGKMQHFDG RFAVKRFGH QAAVSVEAEG
51  QLGHVVRADG EAVEVLQELF RQYRVARQLA HHNQAQAVFA AFQAVFFQCL
101 NHCFGFAQSA DERNHDFDVG QTHFVINAFO GFAFQGETVF EALGNITRRT
151 TEAQHRVFFM RFVYAAADQV GVFGFVEVGH TDDGFTRINR CGKRCHAFGD
201 FIDVEVDRGC VTGDAADNFR FQFVVLVVKF QQGFVRDADL AVDDKFHTRQ
251 ADAFAGQIGE AECEFGIADV HHDFDGCFWH IVQGDIGNLY VQQAGIDKAG
301 IAFGTGYGNF LTVFQEFGR I AAADDGRNTQ FARDDGGVAG ASAAVGHDDG
351 STFHHGFPIR IGHVGNQYVA GFDGIHLGSI FNQAHALTD FLTDGTTFAQ
401 DGFFAVDQVA AQVAAFFFLG FDGFGAGLQD VEFVAVQAVS PFDIHRAAVV
451 PFDGQRVVCQ LGDFFVGNCE AVAVFPGDFD VGYRFAGGFG VGENHFDVFR
501 THGLAQDGGF ACFERGF EHI KFVRVLRALY DVFAQTVRGG NKDDLVLVAGF
551 GVEGEHHT*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1333>:

```

m501.seq
1  atggctcgac sggccttgac cgcagatgcc gacatatttg tctgcttgcc
51  ggcaggcgga gatggcaagg tgcagcatca ctttgacggc aggggttcgt
101 tcgtcaaacg attcggatac caagccgctg tcgcggtcga gaccgagggg
151 cagttgggtc atgtcgctcg agccgatgga gaagccgtcg aagtattgca
201 ggaattgttc cgccaataacc gcgttgctcg gcagctcgca catcataatc
251 aggcgcaggc cgtttttgcc gcgttccaag ccgttttctt tcagggtttt
301 gacaacggmt tcggcttcgc ccaaagtgcg gacgaacgga atcatgattt
351 caacgttggc caacccatt tcatcgcgga cgcgtttcaa ggctttgcat
401 tccaaggcga aacagtcttt gaagttgtcg gcgacataac gcgccgcacc
451 acggaagccc aacatcgggt tttcttcatt cggttcgtat acgttgccgc
501 cgaccaggtt ggcgtattcg ttgatttga agtcggacat acggacgatg
551 gttttacgcy gataaaccga tgcggcaaat gtcgccacgc cttcggcgat
601 tttatcgacy tagaagtcga caggggacgc gtaaccggcg atacggcggg
651 taatttccgc ttttaattcg tcgtcttgtt tgtcaaaatc caacaargct

```

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```

701 ttgggggtgga taccgatttg gcggttgatg ataaattcca tacgcgccaa
751 gccgatgcct tcgctgggca ggttggcgaa gctgaatgcg agttcgggat
801 tgccgacggt catcatgact tttacagtg ctttaggcat attgtctaag
851 gcgacatcgg taatctgtac gtccaacaga ccggcataga taaagccggt
901 atcgcccttcg gcacaggata cggttaacttc ttgaccgttt ttcagcaatt
951 cgggtgcatt gccgcagccg acaacggcag gaatgcccaa ttcacgcgcg
1001 atgatggcgg cgtggcaggt acggccgcgg cggttggtaa cgatggcaga
1051 agcacgtttc atcacggggt cccaatccgg atcggtcatg tcggtaacga
1101 gtacgtcgcc ggcttcgacg gaatccatct cgaagcatc ttaatacagg
1151 cgcaccttgc cctgaccgac tttctgaccg atggcgcgcc cttcgcataa
1201 tacgggttttg tcgccgttga tggcgaagcg gcgcagggtt cggttgccct
1251 cttcttggga ttttacgggt tcgggacggg cttgcaggat gtagagtttg
1301 ccgtccaagc cgtcgcgctc ccattcgata tccatcgggc gcccgtagtg
1351 tttttcgatg gtcagtgcgt aatgcgccaa ctcagtaatt tcttcgctcg
1401 taatggagaa gcggttgccg tcttcctcgg ggacatcgac gttggttacg
1451 gatttacgg cttctgcttt gtcggtaaaa atcattttga tctgttttga
1501 acccatggtt ttacgcagga tggcgggcgt gcccggtttg agcgtgggtt
1551 tgaacacatr aaattcgtcc gggttgaccg caccctgtac gacgttttcg
1601 cccagaccgt aagaggaggt aacaaagacg acytgatcgt akccggattc
1651 ggtgtcgagg gtgaacatca cacctga

```

This corresponds to the amino acid sequence <SEQ ID 1334; ORF 501>:

```

m501.pep
1  MVGXALTADA DIFVLLAAGG DGKVQHFFDG RFAFVKRFGY QAAVAVETEG
51  QLGHVVRADG EAVEVLQELF RQYRVARQLA HHNQAQAVFA AFQAVFFQGF
101 DNGFGFAQSA DERNHDFNVG QPHFIADAFQ GFAFQGETVF EVVGDITRRT
151 TEAQHRVFFM RFVYVAADQV GVFGFVEVGH TDDGFTRINR CGQCRHAFGD
201 FIDVEVDRGR VTGDTAGNFR FXFVVLVFKF QXFGVDTDL AVDDKFHTRQ
251 ADAFAGQVGE ABCEFGIADV HHDFYRCFRH IVXGDIENLY VQQTGIDKAG
301 IAFGTGYGNF LTVFQQFGCI AAADNGRNAQ FTRDDGGVAG TAAAVGNDGR
351 STFHHGFPIR IGHVGNFYVA GFDGIHLGSI FNQAHALALD FLTDGAFAFX
401 YGFVAVDGEA AQVAVALFLG FYFGFTGLQD VEFVQAVAS PFDIHHAAVV
451 FFDGQCVMRQ LSNFFVNGE AVAVFLGDI D VGYGTGFCF VGKNHFDVFX
501 THGFTQDGLL ARFERGFEXH KFVRVDRITLY DVFAQTVRGG NKDDLIVXGF
551 GVEGEHHT*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 501 shows 86.2% identity over a 558 aa overlap with a predicted ORF (ORF 501.ng) from *N. gonorrhoeae*:

m501/g501

	10	20	30	40	50	60
m501.pep	MVGXALTADADI FVLLAAGGDGKVQHFFDGRVAFVKRFGYQAAVAVETEGQLGHVVRADG					
	: : : : : : :					
g501	MVGRLTADTDI FVLLAAGGDGKMQHFFDGRVAFVKRFGHQAAVSVEAEGQLGHVVRADG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m501.pep	EAVEVLQELFRQYRVARQLAHHNQAQAVFAAFQAVFFQGFNDNGFGFAQSADERNHDFNVG					
	: : :					
g501	EAVEVLQELFRQYRVARQLAHHNQAQAVFAAFQAVFFQCLNHCFGFAQSADERNHDFDVG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m501.pep	QPHFIADAFQGFQGETVFEVVDITRRTTEAQHRVFFMRVYVAADQVGVFGFVEVGH					
	: : : : : : : : :					
g501	QTHFVTNAFCGFAFQGETVFEALGNI TRRTTEAQHRVFFMRVYVAADQVGVFGFVEVGH					
	130	140	150	160	170	180
	190	200	210	220	230	240
m501.pep	TDDGFTRINRCGQCRHAFGDFIDVEVDRGRVTGDTAGNFRFXFVVLVFKFQXFGVDTDL					
	: : : :					

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g501	TDDGFTRINRCGKRCHAFGDFIDVEVDRGCVTGDAADNFRFQFVVLFVKFQOQGFVRVDADL
	190 200 210 220 230 240
m501.pep	AVDDKFHTRQADAFAGQVGEAECEFGIADVHHDFYRCFRHIVXGDI GNLYVQQTGIDKAG
g501	AVDDKFHTRQADAFAGQVGEAECEFGIADVHHDFDGCFWHIVQDIGNLYVQQAGIDKAG
	250 260 270 280 290 300
m501.pep	IAFGTGYGNFLTVFQQFGCIAAADNGRNAQFTRDDGGVAGTAAAVGNDGRSTFHHGFPPIR
g501	IAFGTGYGNFLTVFQEFGRIAAADNGRNTQFARDDGGVAGASAAVGHGSGSTFHHGFPPIR
	310 320 330 340 350 360
m501.pep	IGHVGNQYVAGFDGIHLGSI FNQAH LALTDFLTDGAAFAXYGFVAVDGEAAQVAVALFLG
g501	IGHVGNQYVAGFDGIHLGSI FNQAH LALTDFLTDGTTFAQDGFFAVDGVAAQVA AAFVLG
	370 380 390 400 410 420
m501.pep	FYGFGLQDVEFAVQAVASPFDIHRAAVVFFDQCVMRQLSNFFVNGEAVAVFLGDID
g501	FDGFGAGLQDVEFAVQAVASPFDIHRAAVVFFDQQRVVCQLGDFVNGEAVAVFFGDFD
	430 440 450 460 470 480
m501.pep	VGYGFTGFVFGKNHFDVFXTHGFTQDGLARFERGFHXXFVRVDRTLVDVFAQTVRGG
g501	VGYRFAGFGFVGENHFDVFRTHGLAQDGGFACFERGFHIXFVRVDRALYDVFAQTVRGG
	490 500 510 520 530 540
m501.pep	NKDDLIVXGFGVEGEHHT
g501	NKDDLIVVAGFGVEGBHHT
	550

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1335>:

a501.seq (partial)

1	ATGGTCGGAC	GGGCCTTGAC	CGCAGATGCC	GACATATTTG	TTCTGCTTGC
51	GGCAGGCGGA	GATGGCAAGG	TGCAGCATCA	CTTTGACGGC	AGGGTTGCGT
101	TCGTCAAACG	ATTCCGATAC	CAAGCCGCTG	TCGCGGTCGA	GACCGAGGGT
151	CAGTTGGGTC	ATGTCGTTCC	AGCCGATGGA	GAAGCCGTCG	AAGTATTGCA
201	GGAAATTGTT	CGCCAATACC	GCGTTGCTCG	GCAGCTCGCA	CATCATAATC
251	AGGCGCAGGC	CGTTTTTGCC	GCGTTCCAAG	CCGTTTCTCT	TCAGGGCTTT
301	GACAACGGCT	TCGGCTTCGC	CCAAAGTGCG	GACGAACGGA	ATCATGATTT
351	CAACGTTGGT	CAACCCATT	TCATCGCGGA	CGCGTTTCAA	GGCTTTGCAT
401	TCCAAGGCGA	AACAGTCTTT	GAAGTTGTCG	GCGACATAAC	GCGCCGCACC
451	ACGGAAGCCC	AACATCGGGT	TTCTTTCATG	CGGTTTCGTAT	ACGTTGCCCG
501	CGACCAGGTT	GGCGTATTCG	TTGGATTTGA	AGTCGGACAT	ACGGACGATG
551	GTTTTACCGG	GATAAACCGA	TGCGGCCAAT	GTCGCCACGC	CTTCGGCGAT
601	TTTATCGACG	TAGAAGTCGA	CAGGGGACGC	GTAACCGGCG	ATACGGCGGG
651	TAATTTCCGC	TTTAAATTCG	TCGTCTTGTT	TGTCAAATTC	CAACAAGGCT
701	TTGGGGTGGA	TACCGATTTC	GCGGTTGATG	ATAAATTCCA	TACGCGCCAA
751	CCGATGCCT	TCGCTGGGCA	GGTTGGCGAA	GCTGAATGCG	AGTTCGGGAT
801	TGCCGACGTT	CATCATGACT	TTACAGGTG	CTTTAGSCAT	GTTGTCCAAA
851	GCAACATCGG	TAATTTGTAC	GTCCAGCAGG	CCGGAGTAGA	TGAAGCCGGT
901	ATCGCCTTCG	GCACAGGATA	CGGTAAC TTC	TTGACCGTTT	TTCAGCAATT
951	CGGTTGCATT	GCCGCAGCCG	ACAACGGCAG	GAATACCCAG	TTCGCGCGCG

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1001 ATGATGGCGG CGTGGCAGGT ACGTCCGCCC CTGTGGTCA CGATGGCGGA
1051 AGCGCGTTTC ATCACCAGTT CCCAATCTGG GTCGGTCATG TCGGTAACCA
1101 GTACGTCGCC GGCTTCGACG GAATCCATCT CGGAAGCATC TTTAATCAGG
1151 CGTACCTTGC CCTGACCGAC TTTCTGACCG ATGGCGCGGC CTTCGCACAA
1201 GACGGTTTTT TCGCCGTTGA TAGAAAAGCG GCGCAGGTTG CGGCTGCCTT
1251 CTTCTGGGGA TTTGACGGTT TCGGGACGGG CTTGCAGGAT GTAGAGTTTG
1301 CCGTCCAAGC CGTCGCGTCC CCATTCGATG TCCATCGGGC GGCCGTAAGT
1351 TTTTTCGATG GTCAGTGCCT AATGCGCCAA CTCGGTGATT TCTTCGTCGG
1401 TAATGGAGAA GCGGTTGCGG TCTTCTTCGG GGACATCGAC GTTGGTTACC
1451 GATTTGCCGG CTTCTGCTTT GTCGGTAAAA ATCATTTTGA TGTGTTTTGA
1501 GCCCATGGTT TTGCGCAGGA TGGCAGGTTT GCCTGCTTTC AGCGTGGGTT
1551 TGAACACATA GAATTCGTCG GGATTGACTG CGCCTTGATC GACGTTTTCG
1601 CCCAGACCGT AGGATGAAGT GACAAAGACG ACTTGGTCGT AACCGGATTG
1651 GGTATCGAGG GTGAACATCA C

```

This corresponds to the amino acid sequence <SEQ ID 1336; ORF 501.a>:

a501.pep

```

1  MVGRALTADA DIFVLLAAGG DGKVQHFDG RVAFVKRFGY QAAVAVETEG
51  QLGHVVRADG EAVEVLQELF RQYRVAROLA HHNQAQAVFA AFQAVFFQGF
101 DNGFGFAQSA DERNHDFNVG QPHFIADAFQ GFAFQGETVF EVVGDITRRT
151 TEAQHRVFFM RFVYVAADQV GVFGFVGVGH TDDGFTRINR CGQCRHAFGD
201 FIDVEVDRGR VTGDTAGNFR F*FVVLVFKF QQGFGVDTDL AVDDKFHTRQ
251 ADAFAGQVGE AECEFGIADV HHDFYRCFRH VVQSNIGNLY VQAGVDEAG
301 IAFGTGYGNF LTVFQQFGCI AAADNGRNTQ FARDDGGVAG TSAPVGHGDDG
351 SAFHHRFPIW VGHVGNQYVA GFDGIHLGSI FNQAYLALTD FLTDGAFAAQ
401 DGFFAVDRKA AQVAAAFFLG FDGFGTGLQD VEFVAVAVAS PFDVHRAAVV
451 FFDGQCVMRQ LGDFFVGNGE AVAVFFGDDID VGYRFAGFCF VGKNHFDVF*
501 AHGFAQDGRF ACFQRGFEHI EFVGIDCALY DVEAQTVG*S DKDDLVTGTF
551 GIEGEHH

```

m501/a501 90.3% identity in 557 aa overlap

	10	20	30	40	50	60
m501.pep	MVGXALTADADIFVLLAAGGDGKVQHFDGRVAFVKRFGYQAAVAVETEGQLGHVVRADG					
a501	MVGRALTADADIFVLLAAGGDGKVQHFDGRVAFVKRFGYQAAVAVETEGQLGHVVRADG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m501.pep	EAVEVLQELFRQYRVARQLAHNQAQAVFAAFQAVFFQGFQDNGFGFAQSADERNHDFNVG					
a501	EAVEVLQELFRQYRVARQLAHNQAQAVFAAFQAVFFQGFQDNGFGFAQSADERNHDFNVG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m501.pep	QPHFIADAFQGFQGETVFEVVDITRRTTEAQHRVFFMRVYVAADQVGVFGFVGVGH					
a501	QPHFIADAFQGFQGETVFEVVDITRRTTEAQHRVFFMRVYVAADQVGVFGFVGVGH					
	130	140	150	160	170	180
	190	200	210	220	230	240
m501.pep	TDDGFTRINRCGQCRHAFGDFIDVEVDRGRVTGDTAGNFRFXFVVLVFKFQQXFGVDTEL					
a501	TDDGFTRINRCGQCRHAFGDFIDVEVDRGRVTGDTAGNFRFXFVVLVFKFQQXFGVDTEL					
	190	200	210	220	230	240
	250	260	270	280	290	300
m501.pep	AVDDKFHTRQADAFAGQVGEAECEFGIADVHHDFYRCFRHIVXGDIIGNLYVQQTGIDKAG					
a501	AVDDKFHTRQADAFAGQVGEAECEFGIADVHHDFYRCFRHVVQSNIGNLYVQAGVDEAG					
	250	260	270	280	290	300
	310	320	330	340	350	360
m501.pep	IAFGTGYGNFLTVFQQFGCIAAADNGRNAQFTRDDGGVAGTAAAVGNDGRSTFHHGFPIR					
a501	IAFGTGYGNFLTVFQQFGCIAAADNGRNTQFARDDGGVAGTAAAVGNDGGSAFHHRFPIW					
	310	320	330	340	350	360

g502.seq

1	atgatgaaac	cgcacaacct	gttccaattc	ctcgccggtt	gtccccctgac
51	cgtcgccgtc	gcttcgcgac	aggcggggcg	ggtggacgcg	ctcaagcaat
101	tcaacaacga	tgccgacggt	atcagcggca	gcttcaccca	aaccgtccaa
151	agcaaaaaga	aaacccaaac	cgcgcacggc	acgttcaaaa	tccttcgcccc
201	gggcctcttc	aaatgggaat	acacttggc	ctacagacag	actattgtgc
251	gcgacggtca	aaccggttgg	ctctacgat	ttgatttggc	acaagtgacc
301	aagtcgtccc	aagaccaggc	catcggcggc	agccccgcgc	ccatcctgtc
351	gaacaaaacc	gccctcgaaa	gcagttacac	gctgaaagag	gacggttcgt
401	ccaacggcat	cgattatgtg	cggggcaacg	ccaaacgca	acaacgcggg
451	ctaccaatac	atccgcacgc	gcttcaaagg	cggcaacctc	gccgccatgc
501	acgttaa				

g502.ppt

1 MMKPHNLQFQ LAVCSLTVAV ASAQAGAVDA LKQFNNDADG IGSFTQTQVQ
51 SKKKTTQTAHG TFKILRPGLF KWEYTLPYRQ TIVGDGQTVW LYDVDLAQVT
101 KSSQDQAIGG SPAAILSNKT ALESSYTLKE DGSSNGIDYV RGNAQTQQR
151 LPIHPHRLOR ROPRRHAA*

m502.seq

1	atgatgaaac	cgcacaacct	gttccaattc	ctcgccgttt	gtcccttgac
51	cgtcgccgtc	gttccgcac	aggcgggcgc	ggtagacgcg	cttaagcaat
101	tcaacaacga	tgccgacggt	atcagcggca	gcttcacca	amccgtccaa
151	wgcaaaaaag	aaacccaaac	cgcgcaacct	acgttcaaaa	tccctgcgacc
201	gggccttttc	aaatgggaat	acaccaaagt	t.acaggcaa	accatcgctg
251	gcgacggtca	aacyygtttg	ctmtacgatg	tyagatctggc	acaagtgacc
301	aagtcgtccc	aagaccaggc	cataggcgsc	agccccgccg	ccatcctgtc
351	gaacaaarcc	gccctcgaaa	gcagctacac	gctgaaagag	gacggttcgt
401	ccaacggcat	cgattatgtg	ggcaacgccc	aaacgcaaca	acgccggcta
451	ccaatacatc	cgcaticggt	tcaaaggcgg	caacctcgcc	gccatgcagc
501	ttaa				

m502 . pep

```

1  MMKPHNLFQF LAVCSLTVAV ASAQAGAVDA LKQFNNDADG IGSFTQXVQ
51  XKKKTQTAHG TFKILRPLGF KWEYTKLYRQ TIIGDGGQTVW LYDVDLAQVT
101 KSSQDQAIGX SPAAILSNXX ALESSYTLKE DGSSNGIDYV GNAQTQRRRL
151 PIHPHRLORR OPRRHAAX

```


Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 502 shows 95.8% identity over a 168 aa overlap with a predicted ORF (ORF 502.ng) from *N. gonorrhoeae*:

m502/g502

	10	20	30	40	50	60
m502.pep	MMKPHNLFQFLAVCSLTVAVASAQAGAVDALKQFNNDADGISGSFTQXVQXKKKTQTAHG					
g502	MMKPHNLFQFLAVCSLTVAVASAQAGAVDALKQFNNDADGISGSFTQTVQSKKKTQTAHG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m502.pep	TFKILRPGLFKWEYTKLYRQTIVGDGQTVWLYDVLDAQVTKSSQDQAIGXSPAAILSNKX					
g502	TFKILRPGLFKWEYTLPRYRQTIVGDGQTVWLYDVLDAQVTKSSQDQAIGGSPAAILSNKT					
	70	80	90	100	110	120
	130	140	150	160		
m502.pep	ALESSYTLKEDGSSNGIDYV-GNAQTQORRLPIHPHRLQRRQPRRHAA					
g502	ALESSYTLKEDGSSNGIDYVRGNAQTQORRLPIHPHRLQRRQPRRHAA					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1341>:

a502.seq

1	ATGATGAAC	CGCACAACCT	GTTCCAATTC	CTCGCCGTTT	GCTCCCTGAC
51	CGTCTCCGTC	GCTTCCGCAC	AGGCGGGCGC	GGTGGACGCG	CTCAAGCAAT
101	TCAACAACGA	TGCCGACGGT	ATCAGCGGCA	GCTTCACCCA	AACCGTCCAA
151	AGCAAAAAGA	AAACCCAAAC	CGCGCACGGC	ACGTTCAAAA	TCCTGCGCCC
201	GGGCTCTTT	AAATGGGAAT	ACACTTCGCC	TTACAAACAG	ACTATTGTCG
251	GCGACGGTCA	AACCGTTTGG	CTCTACGATG	TCGATTGGC	ACAAGTGACC
301	AAGTCGTCCC	AAGACCAGGC	CATAGGCGGC	AGCCCCGCCG	CCATCTGTG
351	GAACAAAACC	GCCCTCGAAA	GCAGCTACAC	GCTGAAAGAG	GACGGTTCGT
401	CCAACGGCAT	CGATTATGTG	GGCAACGCC	AAACGCAACA	ACGCCGGCTA
451	CCAATACATC	CGCATCGGCT	TCAAAGGCGG	CAACCTCGCC	GCCATGCAGC
501	TTAA				

This corresponds to the amino acid sequence <SEQ ID 1342; 502 217.a>:

a502.pep

1	MMKPHNLFQF	LAVCSLTVS	ASAQAGAVDA	LKQFNNDADG	ISGSFTQTVQ
51	SKKKTQTAHG	TFKILRPGLF	KWEYTSYKQ	TIVGDGQTVW	LYDVLDAQVT
101	KSSQDQAIGG	SPAAILSNKT	ALESSYTLKE	DGSSNGIDYV	GNAQTQORRL
151	PIHPHRLQRR	QPRRHAA*			

m502/a502 95.2% identity in 167 aa overlap

	10	20	30	40	50	60
m502.pep	MMKPHNLFQFLAVCSLTVAVASAQAGAVDALKQFNNDADGISGSFTQXVQXKKKTQTAHG					
a502	MMKPHNLFQFLAVCSLTVSVAASQAGAVDALKQFNNDADGISGSFTQTVQSKKKTQTAHG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m502.pep	TFKILRPGLFKWEYTKLYRQTIVGDGQTVWLYDVLDAQVTKSSQDQAIGXSPAAILSNKX					
a502	TFKILRPGLFKWEYTSYKQTIVGDGQTVWLYDVLDAQVTKSSQDQAIGGSPAAILSNKT					
	70	80	90	100	110	120
	130	140	150	160		
m502.pep	ALESSYTLKEDGSSNGIDYVGNAQTQORRLPIHPHRLQRRQPRRHAA					
a502	ALESSYTLKEDGSSNGIDYVGNAQTQORRLPIHPHRLQRRQPRRHAA					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1343>:

g502-1.seq

```

1  ATGatGAAAc cgcaCaacct gttccaaTtC CTCGCCGTTT GCTCCCTGAC
51  CGTCGCCGTC GCTTCCGCAC AGGCGGGCGC GGTGGACGCG CTCAGCAAT
101 TCAACAACGA TGCCGACGGT ATCAGCGGCA GCTTCACCCA AACCGTCAA
151 AGCAAAAAGA AAACCCAAAC CGCGCACGGC ACGTTCAAAA TCCTGCGCCC
201 GGGCCTCTTC AAATGGGAAT ACACTTGCC CTACAGACAG ACTATTGTCG
251 GCGACGGTCA AACCGTTTGG CTCTACGATG TTGATTGGC ACAAGTGACC
301 AAGTCGTCCC AAGACCAGGC CATCGGCGGC AGCCCCGCCG CCATCCTGTC
351 GAACAAAACC GCCCTCGAAA GCAGTTACAC GCTGAAAGAG GACGGTTCGT
401 CCAACGGCAT CGATTATGTG CGGGCAACGC CCAAACGCAA CAACGCCGGC
451 TACCAATACA TCCGCATCGG CTTCAAAGGC GGCAACCTCG CCGCCATGCA
501 GCTTAAAGAC AGCTTCGGCA ACCAAACCTC CATCAGTTTC GCGGGTTTGA
551 ATACCAATCC CCAACTCTCG CGCGGCGCGT TCAAGTTTAC CCCGCCAAA
601 GCGGTGGACG TGTGAGCAA CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1344; ORF 502-1.ng>:

g502-1.pep

```

1  MMKPHNLFQF LAVCSLTAV ASAQAGAVDA LKQFNNDADG ISGSFTQTVO
51  SKKKTQTAFH TFKILRPLGF KWEYTLPRQ TIVGDGQTVW LYDVLDAQVT
101 KSSQDQAIAG SPAAILSNKT ALESSYTLKE DGSSNGIDYV RATPKRNNAG
151 YQYIRIGFKG GNLAAMQLKD SFGNQTSSIF GGLTNPQLS RGAFFKTPPK
201 GVDVLSN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1345>:

m502-1.seq

```

1  ATGATGAAAC CGCACAACT GTTCCAATC CTCGCCGTTT GCTCCCTGAC
51  CGTCGCCGTC GCTTCCGCAC AGGCGGGCGC GGTAGACGCG CTTAAGCAAT
101 TCAACAACGA TGCCGACGGT ATCAGCGGCA GCTTCACCCA AACCGTCAA
151 AGCAAAAAGA AAACCCAAAC CGCGCACGGC ACGTTCAAAA TCCTGCGACC
201 GGGCCTTTTC AAATGGGAAT ACACCAAACC TTACAGGCAA ACCATCGTCG
251 GCGACGGTCA AACCGTTTGG CTCTACGATG TTGATCTGGC ACAAGTGACC
301 AAGTCGTCCC AAGACCAGGC CATAGGCGGC AGCCCCGCCG CCATCCTGTC
351 GAACAAAACC GCCCTCGAAA GCAGCTACAC GCTGAAAGAG GACGGTTCGT
401 CCAACGGCAT CGATTATGTG CTGGCAACGC CCAAACGCAA CAACGCCGGC
451 TACCAATACA TCCGCATCGG CTTCAAAGGC GGCAACCTCG CCGCCATGCA
501 GCTTAAAGAC AGCTTCGGCA ACCAAACCTC CATCAGTTTC GCGGGTTTGA
551 ATACCAATCC CCAACTCTCG CGCGGCGCGT TCAAGTTTAC CCCGCCAAA
601 GCGGTGGACG TGTGAGCAA CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1346; ORF 502-1>:

m502-1.pep

```

1  MMKPHNLFQF LAVCSLTAV ASAQAGAVDA LKQFNNDADG ISGSFTQTVO
51  SKKKTQTAFH TFKILRPLGF KWEYTKPYRQ TIVGDGQTVW LYDVLDAQVT
101 KSSQDQAIAG SPAAILSNKT ALESSYTLKE DGSSNGIDYV LATPKRNNAG
151 YQYIRIGFKG GNLAAMQLKD SFGNQTSSIF GGLTNPQLS RGAFFKTPPK
201 GVDVLSN*

```

m502-1/g502-1 99.0% identity in 207 aa overlap

	10	20	30	40	50	60
m502-1.pep	MMKPHNLFQFLAVCSLTAVASAQAGAVDAL	KQFNNDADGISGSFTQT	VQSKKKTQTAFH			
g502-1	MMKPHNLFQFLAVCSLTAVASAQAGAVDAL	KQFNNDADGISGSFTQT	VQSKKKTQTAFH			
	10	20	30	40	50	60
m502-1.pep	TFKILRPLGFKWEYTKPYRQTIVGDGQTVW	LYDVLDAQVTKSSQDQAI	GGSPAAILSNKT			
g502-1	TFKILRPLGFKWEYTLPRQTIVGDGQTVW	LYDVLDAQVTKSSQDQAI	GGSPAAILSNKT			
	70	80	90	100	110	120
m502-1.pep	ALESSYTLKEDGSSNGIDYVLRATPKRNNAG	YQYIRIGFKGNLAAMQLKDSFGNQTSSIF				
g502-1	ALESSYTLKEDGSSNGIDYVRATPKRNNAG	YQYIRIGFKGNLAAMQLKDSFGNQTSSIF				
	130	140	150	160	170	180
m502-1.pep	ALESSYTLKEDGSSNGIDYVRATPKRNNAG	YQYIRIGFKGNLAAMQLKDSFGNQTSSIF				
g502-1	ALESSYTLKEDGSSNGIDYVRATPKRNNAG	YQYIRIGFKGNLAAMQLKDSFGNQTSSIF				
	130	140	150	160	170	180

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```

                190      200
m502-1.pep    GGLNTNPQLSRGAFKFTPPKGV DVL SNX
                |||
g502-1        GGLNTNPQLSRGAFKFTPPKGV DVL SNX
                190      200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1347>:

```

a502-1.seq
1  ATGATGAAAC CGCACAACT GTTCCAATTC CTCGCCGTTT GCTCCCTGAC
51 CGTCTCCGTC GCTTCCGCAC AGGCGGGCGC GGTGGACGCG CTCAAGCAAT
101 TCAACAACGA TGCCGACGGT ATCAGCGGCA GCTTCACCCA AACCGTCCAA
151 AGCAAAAAGA AAACCCAAAC CGCGCACGGC ACGTTCAAAA TCCTGCGCCC
201 GGGCCTCTTT AAATGGGAAT ACACTTCGCC TTACAAACAG ACTATTGTCG
251 GCGACGGTCA AACCGTTTGG CTCTACGATG TCGATTGGC ACAAGTGACC
301 AAGTCGTCCC AAGACCAGGC CATAGGCGGC AGCCCCGCG CCATCCTGTC
351 GAACAAAACC GCCCTCGAAA GCAGCTACAC GCTGAAAGAG GACGGTTCGT
401 CCAACGGCAT CGATTATGTG CTGGCAACGC CCAACGCAA CAACGCGGC
451 TACCAATACA TCCGCATCGG CTTCAAAGGC GGCAACCTCG CCGCCATGCA
501 GCTTAAAGAC AGCTTCGGCA ATCAAACCTC CATCAGTTTC GCGGTTTGA
551 ATACCAATCC CCAACTCTCG CGCGGCGCGT TCAAGTTAC CCCGCCAAA
601 GGCSTGGACG TGTGAGCAA CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1348; ORF 502-1.a>:

```

a502-1.pep
1  MMKPHNLFQF LAVCSLTVSV ASAQAGAVDA LKQFNNDADG ISGSFTQTQVQ
51 SKKKTQTAHG TFKILRPGLF KWEYTSPLYKQ TIVGDGQTVW LYDVLDAQVT
101 KSSQDQAIGG SPAAILSNKT ALESSYLKE DGSSNGIDYV LATPKRNNAG
151 YQYIRIGFKG GNLAAMQLKD SFGNQTSISF GGLNTNPQLS RGAFTKTPPK
201 GVDVLSN*

```

a502-1/m502-1 98.6% identity in 207 aa overlap

```

                10      20      30      40      50      60
a502-1.pep    MMKPHNLFQFLAVCSLTVSVASQAQAVDALKQFNNDADGISGSFTQTQVQSKKKTQTAHG
                |||
m502-1        MMKPHNLFQFLAVCSLTVAVASQAQAVDALKQFNNDADGISGSFTQTQVQSKKKTQTAHG
                10      20      30      40      50      60

                70      80      90      100     110     120
a502-1.pep    TFKILRPGLFKWEYTSPLYKQTIVGDGQTVWLYDVLDAQVTKSSQDQAIGGSPAAILSNKT
                |||
m502-1        TFKILRPGLFKWEYTKPYRQTIVGDGQTVWLYDVLDAQVTKSSQDQAIGGSPAAILSNKT
                70      80      90      100     110     120

                130     140     150     160     170     180
a502-1.pep    ALESSYLKEDGSSNGIDYVLATPKRNNAGYQYIRIGFKGGNLAAMQLKDSFGNQTSISF
                |||
m502-1        ALESSYLKEDGSSNGIDYVLATPKRNNAGYQYIRIGFKGGNLAAMQLKDSFGNQTSISF
                130     140     150     160     170     180

                190     200
a502-1.pep    GGLNTNPQLSRGAFKFTPPKGV DVL SNX
                |||
m502-1        GGLNTNPQLSRGAFKFTPPKGV DVL SNX
                190     200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1349>:

```

g503.seq
1  atgtccgcgc cgtcggcadc ggtaatcatt ttgttccatg ccgcttcgat
51 ttcggcatcg agctgttcgg ggaagggcgt gtccaaaatc cattggcgga
101 tttctttgcc gacgcgtgcc agttcgaaa cgtcttcgac atccaatttt
151 gccagagcgg cggaaatgcg ttcgttcaga ccgttgtgtg cgagaaatgc
201 gcggttag

```

This corresponds to the amino acid sequence <SEQ ID 1350; ORF 503.ng>:

```

g503.pep
1  MSAPSASVII LFHAASISAS SCSGKGVSKI HWRISLPTRA SSETSSSTNF
51 ARAAEMRSFR PLCARNAR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1351>:

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```

m503.seq
1  atgtccgcac cgcgggcac ggcaaccatt ttgttccatg ccgcttcgat
51  ttcggcatcg agctgttcgg ggaaggcgt atccaaaatc cattggcgga
101 tttctttgcc gacgcgtgcc agttcggcaa cgtcttcgac atccaatttt
151 gccagtgcgg cggaaatgcg ttcgctcaga ccgttggtgt cgaggaatgc
201 gcggtag

```

This corresponds to the amino acid sequence <SEQ ID 1352; ORF 503>:

```

m503.pep
1  MSAPPASATI LFHAASISAS SCSGKGVSKI HWRISLPTRA SSATSSTSNF
51  ASAAEMRSLR PLCARNAR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 503 shows 91.2% identity over a 68 aa overlap with a predicted ORF (ORF 503.ng) from *N. gonorrhoeae*:

```

m503/g503
          10      20      30      40      50      60
m503.pep  MSAPPASATILFHAASISASSCSGKGVSKIHWRIPLTRASSATSSTSNFASAAEMRSLR
          ||| ||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g503      MSAPSASVILFHAASISASSCSGKGVSKIHWRIPLTRASSETSSTSNFARAAEMRSFR
          10      20      30      40      50      60

          69
m503.pep  PLCARNAR
          |||||
g503      PLCARNAR

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1353>:

```

a503.seq
1  ATGTCCGCGC CGCCGGCATC GGCAACCATT TTGTTCATG CCGCTTCGAT
51  TTCGGCATCG AGCTGTTCGG GGAAGGGCGT GTCCAAAATC CATTGGCGGA
101 TTTCTTTGCC GACGCGTGCC AGTTCGGCAA CGTCTTCGAC ATCTAATTTT
151 GCCAGTGCGG CGGAAATGCG TTCGCTCAGA CCGTTGTGTG CGAGGAATGC
201 GCGGTAG

```

This corresponds to the amino acid sequence <SEQ ID 1354; ORF 503.a>:

```

a503.pep
1  MSAPPASATI LFHAASISAS SCSGKGVSKI HWRISLPTRA SSATSSTSNF
51  ASAAEMRSLR PLCARNAR*

```

m503/a503 100.0% identity in 68 aa overlap

```

          10      20      30      40      50      60
m503.pep  MSAPPASATILFHAASISASSCSGKGVSKIHWRIPLTRASSATSSTSNFASAAEMRSLR
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a503      MSAPPASATILFHAASISASSCSGKGVSKIHWRIPLTRASSATSSTSNFASAAEMRSLR
          10      20      30      40      50      60

          69
m503.pep  PLCARNARX
          |||||
a503      PLCARNARX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1355>:

```

g503-1.seq
1  ATGGCGCGGT CGTTGTACAG GGAGGCGAAA ACGTGGCGCA TCGCTTTTTT
51  AACGTTATCC AAGCCATTGA TATTCAGGAA GGTTCCTGT TGGCCGGCAA
101 ATGATGCGTC GGCAGGTCT TCGCGGTTG CGGAAGAGCG TACGGCAACG
151 GAAATGTCCG CGCCGTCGGC ATCGGTAATC ATTTGTTC ATGCCGCTTC
201 GATTCGGCA TCGAGCTGTT CGGGGAAGGG CGTGCCAAA ATCCATTGGC
251 GGATTTCTTT GCCGACGCGT GCCAGTTCGG AAACGTCTTC GACATCCAAT
301 TTGCCCAGAG CGGCGGAAAT GCGTTCGTT AGACCGTTGT GTGCGAGAAA
351 TCGCGGTAG

```

This corresponds to the amino acid sequence <SEQ ID 1356; ORF 214.ng>:

g503-1.pep
 1 MARSLYREAK TWRIAFITLS KPLIFRKVSC WPANDASGRS SAVAEERTAT
 51 EMSAPSASVI ILFHAASISA SSCSGKGVSK IHWRI SLPTR ASSETSSTSN
 101 FARAAEMRSF RPLCARNAR*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1357>:

m503-1.seq
 1 ATGGCAGCGT CGTTATACAG GGAAGCGAAT ACATGGTGCA TCGCTTCTTT
 51 AACGTATACC AAGCCGTTGA TGTTCAGAA GGTTCCTGT TGTCCAGCGA
 101 ATGATGCGTC CGGCAGGTCT TCGGCAGTTG CGGAAGAAGC TACGGCAACG
 151 GAAATGTCCG CACCGCCGGC ATCGGCAACC ATTTGTTC TCGCCGCTTC
 201 GATTTCGGCA TCGAGCTGTT CGGGGAAAGG CGTATCCAAA ATCCATTGGC
 251 GGATTTCITT GCCGACGCGT GCCAGTTCGG CAACGTCTTC GACATCCAAT
 301 TTTGCCAGTG CGGCGGAAAT GCGTTCGCTC AGACCGTTGT GTGCGAGGAA
 351 TGC GCGGTAG

This corresponds to the amino acid sequence <SEQ ID 1358; ORF 503-1>:

m503-1.pep
 1 MARSLYREAN TWCIALTSL KPLMFKKVSC CPANDASGRS SAVAEERTAT
 51 EMSAPPASAT ILFHAASISA SSCSGKGVSK IHWRI SLPTR ASSATSSTSN
 101 FASAAEMRSL RPLCARNAR*

g503-1 / m503-1 89.9% identity in 119 aa overlap

	10	20	30	40	50	60
g503-1.pep	MARSLYREAKTWRIAFITLSKPLIFRKVSCWPANDASGRSSAVAEERTATEMSAPSASVI					
m503-1	MARSLYREANTWCIALTSLKPLMFKKVSCCPANDASGRSSAVAEERTATEMSAPPASAT					
	10	20	30	40	50	60
	70	80	90	100	110	120
g503-1.pep	ILFHAASISASSCSGKGVSKIHWRI SLPTRASSETSSTSNFARAAEMRSFRPLCARNARX					
m503-1	ILFHAASISASSCSGKGVSKIHWRI SLPTRASSATSSTSNFASAAEMRSLRPLCARNARX					
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1359>:

a503-1.seq
 1 ATGGCGCGGT CGTTGTACAG GGAGGCGAAT ACATGGCGCA TCGCTTCTTT
 51 AACGTTTTCC AAGCCGTTGA TATTCAGGAA GGTTCCTGT TGGCCGGCAA
 101 ATGATGCGTC GGGCAGGTCT TCGGCGGTTG CGGAAGAGCG TACGGCAACG
 151 GAAATGTCCG CGCGCCGGC ATCGGCAACC ATTTGTTC TCGCCGCTTC
 201 GATTTCGGCA TCGAGCTGTT CGGGGAAGGG CGTGTCCAAA ATCCATTGGC
 251 GGATTTCITT GCCGACGCGT GCCAGTTCGG CAACGTCTTC GACATCTAAT
 301 TTTGCCAGTG CGGCGGAAAT GCGTTCGCTC AGACCGTTGT GTGCGAGGAA
 351 TGC GCGGTAG

This corresponds to the amino acid sequence <SEQ ID 1360; ORF 503-1.a>:

a503-1.pep
 1 MARSLYREAN TWRIASLTFS KPLIFRKVSC WPANDASGRS SAVAEERTAT
 51 EMSAPPASAT ILFHAASISA SSCSGKGVSK IHWRI SLPTR ASSATSSTSN
 101 FASAAEMRSL RPLCARNAR*

a503-1 / m503-1 95.8% identity in 119 aa overlap

	10	20	30	40	50	60
a503-1.pep	MARSLYREANTWRIASLTFSKPLIFRKVSCWPANDASGRSSAVAEERTATEMSAPPASAT					
m503-1	MARSLYREANTWCIALTSLKPLMFKKVSCCPANDASGRSSAVAEERTATEMSAPPASAT					
	10	20	30	40	50	60
	70	80	90	100	110	120
a503-1.pep	ILFHAASISASSCSGKGVSKIHWRI SLPTRASSATSSTSNFASAAEMRSLRPLCARNARX					
m503-1	ILFHAASISASSCSGKGVSKIHWRI SLPTRASSATSSTSNFASAAEMRSLRPLCARNARX					
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1361>:

g504.seq

```

1   atgttggttc aggacttgcc ttttgaagtc aaactgaaaa aattccatat
51  cgatttttac aatacgggta tgccgcgcga ttttgccagc gatattgaag
101 taacggacaa ggcaaccggt gagaaactcg agcgaccat ccgcgtgaac
151 catcctttga ccttgacagg catcacgatt tatcaggcga gttttgccga
201 cggcggttcg gatttgacat tcaaggcgtg gaatttgagg gatgcttcgc
251 gcgaacctgt cgtgttgaag gcaacctcca tacaccagtt tccgttgga
301 atcggcaaac acaaatatcg tcttgagttc gatcagttca cttctatgaa
351 tgtggaggac atgagcgagg gtgcggaacg ggaaaaaagc ctgaaatcca
401 ctctgaacga tgtccgcgcc gttactcagg aaggtaaaaa atacaccaat
451 atcggccctt ccattcggtg cgcacatcgt gatgcggcag ggcaggcggg
501 cgaatataaa aactatatgc tgccggtttt gcaggacaaa gattattttt
551 ggctgaccgg cacgcgcagc ggcttgacgc agcaataacc ctggctgcgt
601 atcccccttg acaagcagtt gaaagcggac acctttatgg cattgctgta
651 gtttttgaaa gatggggaag ggcgcaaacg tctggttgcc gacgcaacca
701 aagagcgacc tgccgaaatc cgcgaacaat tcatgctggc tgcggaaaaa
751 acgtgaata tctttgcgca aaaaggctat ttgggattgg acgaatttat
801 tacgtccaat atcccgaag ggcagcagga taagatgcag ggctatttct
851 acgaaatgct ttacggcgtg atgaacgctg ctttggatga aaccatacgc
901 cggtagcgct tgcccgaatg gcagcaggat gaagcgcgga accgtttcct
951 gctgcacagt atggatgcct atacggggct gacggaatat cccgcgccta
1001 tgctgctcca gcttgacggg ttttccgagg tgcgttcctc aggtttgcag
1051 atgacccggt cgcggggtgc gcttttggtc tatctcggct cggatttgtt
1101 ggttttggtt acagtattta tgttttatgt gcccaaaaaa cgggcgtggg
1151 tattgttttc aaacdgc aaa atccgttttg ctatgtcttc ggcccgcagc
1201 gaacgggatt tgcagaagga atttccaaaa cagctcgaga gcctgcaacg
1251 gctcggcaag gacttgaatc atgactga

```

This corresponds to the amino acid sequence <SEQ ID 1362; ORF 504.ng>:

g504.pep

```

1   MLVQDLPEFV KLKPFHIDFY NTGMPRDFAS DIEVTDKATG EKLERTIRVN
51  HPLTLHGITI YQASFADGGS DLTFKAWNLR DASREPVVLK ATSIHQFPLE
101 IGKHKYRLEF DQFTSMNVED MSEGAREKS LKSTLNDVRA VTQEGKKYTN
151 IGPSIVYRIR DAAGQAVEYK NYMLPILQDK DYFWLTGTRS GLQQQYRWLR
201 IPLDKQLKAD TFMALREFLK DGEGRKRLVA DATKDAPAEI REQFMLAAEN
251 TLNIFAQKGY LGLDEFITSN IPKGQDKMQ GYFYEMLYGV MNAALDETIR
301 RYGLPEWQDD EARNRFLHS MDAYTGLTEY PAPMLQLDQG FSEVRSSGLQ
351 MTRSPGALLV YLGSVLLVLG TVFMFYVPKK RAWVLFNKKI RFAMSSARSE
401 RDLQKEFPKH VESLQRLGKD LNHD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1363>:

m504.seq..

```

1   atattggttc aggacttgcc ttttgaagtc aaactgaaaa aattccatat
51  cgatttttac aatacgggta tgccgcgcga ttttgccagc gatattgaag
101 tgacggacaa ggcaaccggt gagaaactcg agcgaccat ccgcgtgaac
151 catcctttga ccttgacagg catcacgatt tatcaggcga gttttgccga
201 cggcggttcg gatttgacat tcaaggcgtg gaatttgagg gatgcttcgc
251 gcgagcctgt cgtgttgaag gcaacatcca tacaccagtt tccgttgga
301 attggcaaac acaaatatcg tcttgagttc gatcagttca cttctatgaa
351 tgtggaggac atgagcgagg gcgcggaacg ggaaaaaagc ctgaaatcca
401 cgctgmmcga tgtccgcgcc gttactcagg aaggtaaaaa atacaccaat
451 atcggccctt ccattgttta ccgtatcgtg gatgcggcag ggcaggcggg
501 cgaatataaa aactatatgc tgccggtttt gcaggacaa gattattttt
551 ggattaccgg cacgcgcagc ggcttgacgc agcaataacc ctggctgcgt
601 atcccccttg acaagcagtt gaaagcggac acctttatgg cattgctgta
651 gtttttgaaa gatggggaag ggcgcaaacg tctggttgcc gacgcaacca
701 aaggcgacc tgccgaaatc cgcgaacaat tcatgctggc tgcggaaaaa
751 acgtgaaca tctttgcaca aaaaggctat ttgggattgg acgaatttat
801 tacgtccaat atcccgaag agcagcagga taagatgcag ggctatttct
851 acgaaatgct ttacggcgtg atgaacgctg ctttggatga aaccatacgc
901 cggtagcgct tgcccgaatg gcagcaggat gaagcgcgga atcgtttcct
951 gctgcacagt atggatgcgt acacgggttt gaccgaatat cccgcgccta
1001 tgctgctgca acttgatggg ttttccgagg tgcgttcgctc gggtttgcag

```

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```

1051 atgaccggtt ccccggtg cgttttggtc tatctcggt cgggtctggt
1101 ggtattgggt acggtattga tgttttatgt gcgcgaaaaa cgggcgtggg
1151 tattgttttc agacggcaaa atccggtttg ccatgtcttc ggcccgagc
1201 gaacgggatt tgcagaagga atttccaaaa cacgtcgaga gtctgcaacg
1251 gctcggcaag gacttgaatc atga

```

This corresponds to the amino acid sequence <SEQ ID 1364; ORF 504>:

m504.pep..

```

1 ILVQDLPEFEV KLKKFHIDFY NTGMPRDFAS DIEVTDKATG EKLERTIRVN
51 HPLTLHGITI YQASFADGGS DLTFKAWNLG DASREPVVLK ATSIHQFPLE
101 IGKHKYRLEF DQFTSMNVED MSEGAREKS LKSTLXDVRA VTQEGKKYTN
151 IGPSIVYRIR DAAGQAVEYK NYMLPVLQEQ DYFWITGTRS GLQQQYRWLR
201 IPLDKQLKAD TFMALREFLK DGEGRKRLVA DATKGAPAEI REQFMLAAEN
251 TLNIFAQKGY LGLDEFITSN IPKEQDDKMQ GYFYEMLYGV MNAALDETIR
301 RYGLPEWQQD EARNRFLHS MDAYTGLTEY PAPMLQLDG FSEVRSSGLQ
351 MTRSPGALLV YLGSVLLVLG TVLMFYVREK RAWVLFSDGK IRFAMSSARS
401 ERDLQKEFPK HVESLQRLGK DLNHD*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 504 shows 96.7% identity over a 425 aa overlap with a predicted ORF (ORF 504.ng) from *N. gonorrhoeae*:

m504/g504

m504.pep	10	20	30	40	50	60
	ILVQDLPEFEVKLKKFHIDFYNTGMPRDFASDIEVTDKATGEKLETRIRVNHPLTLHGITI					
g504	10	20	30	40	50	60
	MLVQDLPEFEVKLKKFHIDFYNTGMPRDFASDIEVTDKATGEKLETRIRVNHPLTLHGITI					
m504.pep	70	80	90	100	110	120
	YQASFADGGSDLTFKAWNLDASREPVVLKATSIHQFPLEIGKHKYRLEFDQFTSMNVED					
g504	70	80	90	100	110	120
	YQASFADGGSDLTFKAWNLRDASREPVVLKATSIHQFPLEIGKHKYRLEFDQFTSMNVED					
m504.pep	130	140	150	160	170	180
	MSEGAREKSLKSTLXDVRAVTQEGKKYTNIGPSIVYRIRDAAGQAVEYKNYMLPVLQEQ					
g504	130	140	150	160	170	180
	MSEGAREKSLKSTLNDVRAVTQEGKKYTNIGPSIVYRIRDAAGQAVEYKNYMLPILQDK					
m504.pep	190	200	210	220	230	240
	DYFWITGTRSGLQQQYRWLRIPLDKQLKADTFMALREFLKDGEGRKRLVADATKGAPAEI					
g504	190	200	210	220	230	240
	DYFWLTGTRSGLQQQYRWLRIPLDKQLKADTFMALREFLKDGEGRKRLVADATKDAPAEI					
m504.pep	250	260	270	280	290	300
	REQFMLAAENTLNIFAQKGYLGLDEFITSNIPKEQDDKMQGYFYEMLYGVMNAALDETIR					
g504	250	260	270	280	290	300
	REQFMLAAENTLNIFAQKGYLGLDEFITSNIPKEQDDKMQGYFYEMLYGVMNAALDETIR					
m504.pep	310	320	330	340	350	360
	RYGLPEWQQDEARNRFLHSMDAYTGLTEYPAPMLQLDGFSEVRSSGLQMTRSPGALLV					
g504	310	320	330	340	350	360
	RYGLPEWQQDEARNRFLHSMDAYTGLTEYPAPMLQLDGFSEVRSSGLQMTRSPGALLV					
m504.pep	370	380	390	400	410	420
	YLGSVLLVLGTVMFYVREKRAWVLFSDGKIRFAMSSARSDRLQKEFPKHVESLQRLGK					
	: : : :					

743

g504 YLGSVLLVLGTVFMFYVPKKRAWVLSN-KIRFAMSSARSERDLQKEFPKHVESLQRLGK
 370 380 390 400 410

m504.pep DLNHD
 |||||
 g504 DLNHD
 420

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1365>:

a504.seq
 1 ATATTGGTTC AGGACTTGCC TTTTGAAGTC AAAGTAAAA AATTCCATAT
 51 CGATTTTAC AATACGGGTA TGCCGCGCGA TTTTGCCAGT GATATTGAAG
 101 TAACGGATAA GCAACCGGT GAGAACTCG AGCGCACCAT CCGCGTGAAC
 151 CATCCTTTGA CCTTGCACGG CATCACGATT TATCAGGCGA GTTTTGCCGA
 201 CGCGGTTTCG GATTTGACAT TCAAGGCGTG GAATTTGGGT GATGCTTCGC
 251 GCGAGCCTGT CGTGTGAAG GCAACATCCA TACACCAGTT TCCGTTGGAA
 301 ATTGGCAAAC ACAATATCG TCTTGAGTTC GATCAGTTTA CTTCTATGAA
 351 TGTGGAGGAC ATGAGCGAGG GCGCGGAACG GGAAAAAGC CTGAAATCCA
 401 CGCTGAACGA TGTCGCGGCC GTTACTCAGG AAGGTAAAA ATACACCAAT
 451 ATCGGCCCTT CCATTGTTTA CCGTATCCGT GATGCGGCAG GGCAGGCGGT
 501 CGAATATAAA AACTATATGC TGCCGGTTT GCAGGAACAG GATTATTTTT
 551 GGATTACCGG CACGCGCAGC GGCTTGCAAG AGCAATACCG CTGGCTGCGT
 601 ATCCCTTGG ACAAGCAGTT GAAAGCGGAC ACCTTTATGG CATTGCTGTA
 651 GTTTTGAAG GATGGGGAAG GCGCGAAACG TCTGGTTGCC GACGCAACCA
 701 AAGGCGCACC TGCCGAAATC CGCGAACAAT TCATGCTGGC TCGGGAAC
 751 ACGCTGAACA TCTTGCACA AAAAGGCTAT TTGGGATTGG ACGAATTTAT
 801 TACGTCCAAT ATCCCGAAG AGCAGCAGGA TAAGATGCAG GGCTATTCT
 851 ACGAATGCT TTACGGCGTG ATGAACGCTG CTTTGGATGA AACCATACGC
 901 CGGTACGCT TGCCGAAATG GCAGCAGGAT GAAGCGCGGA ATCGTTTCT
 951 GCTGCACAGT ATGGATGCGT ACACGGGTTT GACCGAATAT CCGCGCCTA
 1001 TGCTGCTGCA ACTTGATGGG TTTTCCGAGG TCGCTTCGTC GGCTTTGCAG
 1051 ATGACCCGTT CCGCGGTCG GCTTTTGGTC TATCTCGGCT CGGTGCTGTT
 1101 GGTATTGGGT ACGGTATTGA TGTTTTATGT GCGCGAAAA CCGGCGTGGG
 1151 TATTGTTTTC AGACGGCAAA ATCCGTTTTC CCATGCTTTC GGCCCGCAGC
 1201 GAACGGGATT TGCAGAAGGA ATTTCCAAAA CACGTCGAGA GTCTGCAACG
 1251 GCTCGGCAAG GACTTGAATC ATGACTGA

This corresponds to the amino acid sequence <SEQ ID 1366; ORF 504.a>:

a504.pep
 1 ILVQDLPEFV KLKKFHIDFY NTGMPRDFAS DIEVTDKATG EKLERTIRVN
 51 HPLTLHGITI YQASFADGGS DLTFAWNLG DASREPVVLK ATSIHQFPLE
 101 IGKHKYRLEF DQFTSMNVED MSEGAREKS LKSTLNDVRA VTQEGKKYTN
 151 IGPSIVYRIR DAAGQAVEYK NYMLPVLQEQ DYFWITGTRS GLQQYRWLR
 201 IPLDKQLKAD TFMALREFLK DGEGRKRLVA DATKGAPAEI REQFMALAAEN
 251 TLNIFAQKGY LGLDEFITSN IPKEQQDKMQ GYFYEMLYGV MNAALDETIR
 301 RYGLPEWQDQ EARNRFLHLS MDAYTGLTEY PAPMLQLDG FSEVRSSGLQ
 351 MTRSPGALLV YLGSVLLVLG TVLMFYVREK RAWVLFSDGK IRFAMSSARS
 401 ERDLQKEFPK HVESLQRLGK DLNHD*

m504/a504 99.8% identity in 425 aa overlap

	10	20	30	40	50	60
m504.pep	ILVQDLPEFVKLKKFHIDFYNTGMPRDFASDIEVTDKATGEKLE	IRVNHPLTLHGITI				
a504	ILVQDLPEFVKLKKFHIDFYNTGMPRDFASDIEVTDKATGEKLE	IRVNHPLTLHGITI				
	70	80	90	100	110	120
m504.pep	YQASFADGGSDLTFAWNLGDASREPVVLKATSIHQFPLEIGKHKYRLEFDQFTSMNVED					
a504	YQASFADGGSDLTFAWNLGDASREPVVLKATSIHQFPLEIGKHKYRLEFDQFTSMNVED					
	130	140	150	160	170	180
m504.pep	MSEGAREKSLKSTLXDVRVAVTQEGKKYTNIGPSIVYRIRDAAGQAVEYKNYMLPVLQEQ					

744

```

|||||
a504 MSEGAEEREKSLKSTLNDVRAVTQEGKKYTNIGPSIVYRIRDAAAGQAVEYKNYMLPVLQEQ
      130      140      150      160      170      180

      190      200      210      220      230      240
m504.ppep DYFWITGTRSGLQQQYRWLRIPLDKQLKADTFMALREFLKDGEGRKRLVADATKGAPAEI
|||||
a504 DYFWITGTRSGLQQQYRWLRIPLDKQLKADTFMALREFLKDGEGRKRLVADATKGAPAEI
      190      200      210      220      230      240

      250      260      270      280      290      300
m504.ppep REQFMLAENTLNIFAQKGYLGLDEFITSNIPKEQQDKMQGYFYEMLYGMNAALDETER
|||||
a504 REQFMLAENTLNIFAQKGYLGLDEFITSNIPKEQQDKMQGYFYEMLYGMNAALDETER
      250      260      270      280      290      300

      310      320      330      340      350      360
m504.ppep RYGLPEWQQDEARNRFLHSMDAYTGLTEYPAPMLLQLDGFSEVRSSGLQMTSPGALLV
|||||
a504 RYGLPEWQQDEARNRFLHSMDAYTGLTEYPAPMLLQLDGFSEVRSSGLQMTSPGALLV
      310      320      330      340      350      360

      370      380      390      400      410      420
m504.ppep YLGSVLLVLGTVLMFYVREKRAWVLFSDGKIRFAMSSARSERDLQKEFPKHVESLQRLGK
|||||
a504 YLGSVLLVLGTVLMFYVREKRAWVLFSDGKIRFAMSSARSERDLQKEFPKHVESLQRLGK
      370      380      390      400      410      420

m504.ppep DLNHDX
|||||
a504 DLNHDX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1367>:

```

g505.seq
1  atgtttcgtt tacaattcag gctgtttccc cctttgcgaa ccgccatgca
51  catcctgttg accgcccctgc tcaaatgcct ctcctctgtg tcgctttcct
101 gtctgcacac gctgggaaac cggctcggac atctggcgtt ttacctttta
151 aaggaagacc gcgcgcgcac cgtcgccaat atgcggcagg cgggtttgaa
201 ccccgacacg cagacggtca aagccgtttt tgcggaaacg gcaaaatgcg
251 gtttggaact tgccccgcg tttttcaaaa aaccggaaga catcgaaaca
301 atgttcaaag cggtagacag ctgggaacac gtgcagcagg ctttggaaca
351 gggcgaaggg ctgctgttca tcacgccgca catcggcagc tacgatttgg
401 gcggacgcta catcagccag cagcttcctg tccacctgac cgccatgtac
451 aagccgccga aaatcaaagc gatagacaaa atcatgcagg cgggcagggt
501 gcgcggcaaa ggcaaaaccg cgccaccgga catacaaggg gtcaaacaaa
551 tcatcaaggc cctgcgcgcg ggcgaggcaa ccatcatcct gcccgaccac
601 gtcccttctc cgcaggaagg cggcggcgtg tggcgaggatt ttttcggcaa
651 acctgcatac accatgacac tggcggaaca attggcacac gtcaaaggcg
701 tgaaaaccct gtttttctgc tgcgaacgcc tgcggacagg acaaggcttc
751 gtgttgaca tccgccccgt ccaaggggaa ttgaacggca acaaagccca
801 cgatgccgcc gtgttcaacc gcaataccga atattggata cgcggttttc
851 cgacgcagta tctgtttatg tacaaccgct ataaaacgcc gtaa

```

This corresponds to the amino acid sequence <SEQ ID 1368; ORF 505.ng>:

```

g505.pep
1  MFRLLQRLFP PLRTAMHILL TALLKCLSL SLSCLHTLGN RLGHAFYLL
51  KEDRARIVAN MRQAGLNPD TQTKAVFAET AKCGLELAPA FFKKPEDIET
101 MFKAVHGEH VQALDKGEG LLFITPHIGS YDLGGYISQ QLPFHLTAMY
151 KPPKIKAIK IMQAGVRGK GKTAPTGIQK VKQIIKALRA GEATIILPDH
201 VPSPQEGGV WADFFGKPAY TMTLAAKLAH VKGVKTLFFC CERLPDQGF
251 VLHIRPVQGE LNGNKAHDA VFNRNTEYWI RRFTQYLFM YNRYKTP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1369>:

745

m505.seq (partial)

```

1  GGCATGTTTC GTTTACAATT CAGGCTGTTT CCCCCTTTGC GAACCGCCAT
51  GCACATCCTG TTGACCGCCC TGCTCAAATG CCTCTCCCTG CTGCCGCTTT
101 CCTGTCTGCA CACGCTGGGA AACCGGCTCG GACATCTGGC GTTTTACCTT
151 TTAAGGAAG ACCGCGCGCG CATCGTCGCC AATATGCGGC AGGCGGGTTT
201 GAACCCCGAC CCCAAAACGG TCAAAGCCGT TTTGCGGAA ACGGCAAAAG
251 GCGGTTTGGG ACTTGCCCCC GCGTTTTTCA GAAAACCGGA AGACATAGAA
301 ACAATGTTCA AAGCGGTACA CGGCTGGGAA CATGTGCAGC AGGCTTTGGA
351 CAAACACGAA GGGCTGCTAT TCATCACGCC GCACATCGGC AGTACGATT
401 TGGGCGGACG CTACATCAGC CAGCAGCTTC CGTTCCTGCT GACCGCCATG
451 TACAAACCGC CGAAAATCAA AGCGATAGAC AAAATCATGC AGGCGGGCAG
501 GGTTCGCGGC AAAGGAAAAA CCGCGCTTAC CAGCATACAA GGGGTCAAAC
551 AAATCATCAA AGCCTGCGT TCGGGCGAGC AACCATCGTC CTGCCCGACC
601 ACGTCCCCTC CCCTCAAGAA GCGGGGGAAG GCGTATGGGT GGATTTCTTC
651 GGCAAACCTG CCTATACCAT GACGCTGGCG GCAArATTGG CACACGTCAA
701 AGGCGTGAAA ACCCTGTTTT TCTGCTGCGA ACGCCTGCCT GGCGGACAA
751 GTTTCGATTG GCACATCCGC CCGTCCAAG GGAATTGAA CGGCGACAAA
801 GCCCATGATG CCGCGTGTG CAACCGCAAT GCCGAATATT GGATACGCCG
851 TTTCCGACG CATATC....

```

This corresponds to the amino acid sequence <SEQ ID 1370; ORF 505>:

m505.pep (partial)

```

1  MFRLQFRLFP PLRTAMHILL TALLKCLSLP LSLCLHTLGN RLGHlafYLL
51  KEDRARIVAN MRQAGLNPD P KTVKAVFAET AKGGLLELAPA FFRKPEDIET
101 MFKAVHGW EHVQQALDKHEG LLFITPHIGS YDLGGYISQ QLPFPLTAMY
151 KPPKIKAI DKIMQAGRV RKGKTAPT SIQGVKQIIKAL RS GEATIVLPDH
201 VPSPQEGG EG VVWVDFGK PA YMTLAAXL A HVGKVKTL FF CCERLPGGQ G
251 FDLHIRPV QG ELNGDKA HDA AVFNRNAE YW IRRFPTHI...

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 505 shows 93.7% identity over a 287 aa overlap with a predicted ORF (ORF 505.ng) from *N. gonorrhoeae*:

m505/g505

	10	20	30	40	50	60
m505.pep	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSLCLHTLGNRLGHlafYLLKEDRARIVAN					
g505	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSLCLHTLGNRLGHlafYLLKEDRARIVAN					
	10	20	30	40	50	60
m505.pep	MRQAGLNPDPKTVKAVFAETAKGGLLELAPAFRRKPEDIETMFKAVHGW EHVQQALDKHEG					
g505	MRQAGLNPDPTQTVKAVFAETAKGGLLELAPAFRRKPEDIETMFKAVHGW EHVQQALDKHEG					
	70	80	90	100	110	120
m505.pep	MRQAGLNPDPKTVKAVFAETAKGGLLELAPAFRRKPEDIETMFKAVHGW EHVQQALDKHEG					
g505	MRQAGLNPDPTQTVKAVFAETAKGGLLELAPAFRRKPEDIETMFKAVHGW EHVQQALDKHEG					
	70	80	90	100	110	120
m505.pep	LLFITPHIGSYDLGGYISQQLPFPLTAMYKPPKIKAI DKIMQAGRV RKGKTAPT SIQGVKQIIKAL RS					
g505	LLFITPHIGSYDLGGYISQQLPFPLTAMYKPPKIKAI DKIMQAGRV RKGKTAPT SIQGVKQIIKAL RS					
	130	140	150	160	170	180
m505.pep	LLFITPHIGSYDLGGYISQQLPFPLTAMYKPPKIKAI DKIMQAGRV RKGKTAPT SIQGVKQIIKAL RS					
g505	LLFITPHIGSYDLGGYISQQLPFPLTAMYKPPKIKAI DKIMQAGRV RKGKTAPT SIQGVKQIIKAL RS					
	130	140	150	160	170	180
m505.pep	VKQIIKALRSGEATIVLPDHVPSPQEGGEGVWVDFGKPAYTMTLAAXLAHVKGKVKTLFF					
g505	VKQIIKALRSGEATIVLPDHVPSPQEGGEGVWVDFGKPAYTMTLAAXLAHVKGKVKTLFF					
	190	200	210	220	230	240
m505.pep	VKQIIKALRSGEATIVLPDHVPSPQEGGEGVWVDFGKPAYTMTLAAXLAHVKGKVKTLFF					
g505	VKQIIKALRSGEATIVLPDHVPSPQEGGEGVWVDFGKPAYTMTLAAXLAHVKGKVKTLFF					
	190	200	210	220	230	240
m505.pep	CCERLPGGQGF DLHIRPVQ GELNGDKAHDA AVFNRNAE YW IRRFPTHI					
g505	CCERLPGGQGF DLHIRPVQ GELNGDKAHDA AVFNRNAE YW IRRFPTHI					
	240	250	260	270	280	290
m505.pep	CCERLPGGQGF DLHIRPVQ GELNGDKAHDA AVFNRNAE YW IRRFPTHI					
g505	CCERLPGGQGF DLHIRPVQ GELNGDKAHDA AVFNRNAE YW IRRFPTHI					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1371>:

a505.seq

```

1   ATGTTTCGTT TACAATTCAG GCTGTTTCCC CCTTTGCGAA CCGCCATGCA
51  CATCCTGTTG ACCGCCCTGC TCAAATGCCT CTCCTGCTG CCGCTTTCCT
101 GTCTGCACAC GCTGGGAAAC CGGCTCGGAC ATCTGGCGTT TTACCTTTTA
151 AAGGAAGACC GCGCGCGCAT CGTCGCCAAT ATGCGTCAGG CAGGCATGAA
201 TCCCGACCCC AAAACGGTCA AAGCCGTTT TCGGAAACG GCAAAAGCGG
251 GTTTGGAAct TGCCCCGCG TTTTTCAGAA AACCGGAAGA CATAGAAACA
301 ATGTTCAAAG CGGTACACGG CTGGGAACAT GTGCAGCAGG CTTTGGACAA
351 ACACGAAGGG CTGCTATTCA TCACGCCGCA CATCGGCAGC TACGATTGCG
401 GCGGACGCTA CATCAGCCAG CAGCTTCCGT TCCCGCTGAC CGCCATGTAC
451 AAACCGCCGA AAATCAAAGC GATAGACAAA ATCATGCAGG CGGGCAGGGT
501 TCGCGGCAAA GAAAAACCG CGCCTACCAG CATACAAGGG GTCAAACAAA
551 TCATCAAAGC CCTGCGTTCG GCGGAAGCAA CCATCGTCTC GCCCGACCAC
601 GTCCCTCCC CTCAAGAAGG CGGGGAAGGC GTATGGGTGG ATTTCTTCGG
651 CAAACCTGCC TATACCATGA CGCTGGCGGC AAAATTGGCA CACGTCAAAG
701 GCGTGAAGAC CCTGTTTTTC TGCTGCGAAC GCCTGCCTGG CGGACAAGGT
751 TTCGATTGCG ACATCCGCCC CGTCCAAGGG GAATTGAACG GCGACAAGGC
801 CCATGATGCC GCCGTGTTCA ACCGCAATGC CGAATATTGG ATACGCCGTT
851 TTCCGACGCA GTATCTGTTT ATGTACAACC GCTACAAAT GCCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1372; ORF 505.a>:

a505.pep

```

1   MFRLLQFRLFP PLRTAMHILL TALLKCLSL PLSCSLHTLGN RLGHlafYLL
51  KEDRARIVAN MRQAGMNPDP KTVKAVFAET AKGGLLELAPA FFRKPEDIET
101 MFKAVHGWEH VQALDKHEG LLFITPHIGS YDLGGYISQ QLPFPLTAMY
151 KPPKIKAIK IMQAGRVRGK GKTAPTSIQG VKQIIKALRS GEATIVLPDH
201 VPSPQEGGEG VVWDFGKPA YMTLAAKLA HVKGVKTLFF CCERLPGGQG
251 FDLHIRPVQG ELNGDKAHDA AVFNRNAEYW IRRFPTQYLF MYNRYKMP*

```

m505/a505 99.0% identity in 287 aa overlap

	10	20	30	40	50	60
m505.pep	MFRLLQFRLFP	PLRTAMHILL	TALLKCLSL	PLSCSLHTLGN	RLGHlafYLL	KEDRARIVAN
a505	MFRLLQFRLFP	PLRTAMHILL	TALLKCLSL	PLSCSLHTLGN	RLGHlafYLL	KEDRARIVAN
	10	20	30	40	50	60
m505.pep	MRQAGLNPD	PKTVKAVFAET	AKGGLLELAPA	FFRKPEDIET	MFKAVHGWEH	VQALDKHEG
a505	MRQAGMNPDP	KTVKAVFAET	AKGGLLELAPA	FFRKPEDIET	MFKAVHGWEH	VQALDKHEG
	70	80	90	100	110	120
m505.pep	LLFITPHIGS	YDLGGYISQ	QLPFPLTAMY	KPPKIKAIK	IMQAGRVRGK	GKTAPTSIQG
a505	LLFITPHIGS	YDLGGYISQ	QLPFPLTAMY	KPPKIKAIK	IMQAGRVRGK	GKTAPTSIQG
	130	140	150	160	170	180
m505.pep	VKQIIKALRS	GEATIVLPDH	VPSPQEGGEG	VVWDFGKPA	YMTLAAKLA	HVKGVKTLFF
a505	VKQIIKALRS	GEATIVLPDH	VPSPQEGGEG	VVWDFGKPA	YMTLAAKLA	HVKGVKTLFF
	190	200	210	220	230	240
m505.pep	CCERLPGGQG	FDLHIRPVQ	GELNGDKAHDA	AVFNRNAEY	WIRRFPTHI	
a505	CCERLPGGQG	FDLHIRPVQ	GELNGDKAHDA	AVFNRNAEY	WIRRFPTQYLF	MYNRYKMPX
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1373>:

747

m505-1.seq

```

1  ATGTTTCGTT TACAATTCAG GCTGTTTCCC CCTTTGCGAA CCGCCATGCA
51  CATCCTGTTG ACCGCCCTGC TCAATGCCT CTCCTGCTG CCGCTTTCCT
101 GTCTGCACAC GCTGGGAAAC CGGCTCGGAC ATCTGGCGTT TTACCTTTTA
151 AAGGAAGACC GCGCGCGCAT CGTCGCCAAT ATGCGGCAGG CGGGTTTGAA
201 CCCCGACCCC AAAACGGTCA AAGCCGTTTT TCGGAAACG GCAAAAGGCG
251 GTTTGGAAct TGCCCCGCG TTTTTCAGAA AACCGGAAGA CATAGAAACA
301 ATGTTCAAAG CGGTACACGG CTGGGAACAT GTGCAGCAGG CTTTGACAA
351 ACACGAAGGG CTGCTATTCA TCACGCCGCA CATCGGCAGC TACGATTGG
401 GCGGACGCTA CATCAGCCAG CAGCTTCCGT TCCGCTGAC CGCCATGTAC
451 AAACCGCCGA AATCAAAGC GATAGACAAA ATCATGCAGG CGGGCAGGGT
501 TCGCGGCAAA GGAACAAACG CGCCTACCAG CATACAAGGG GTCAAACAAA
551 TCATCAAAGC CCTGCGTTGG GCGGAAGCAA CCATCGTCCT GCCCGACCAC
601 GTCCCTCTCC CTCAAGAAGG CCGGGAAGGC GTATGGGTGG ATTTCTTCGG
651 CAAACCTGCC TATACCATGA CGCTGGCGGC AAAATTGGCA CACGTCAAAG
701 GCGTGAAAC CCTGTTTTTC TGCTGCGAAC GCCTGCCTGG CCGACAAGGT
751 TTCGATTGTC ACATCCGCCG CGTCCAAGGG GAATTGAACG GCGACAAGC
801 CCATGATGCC GCGGTGTTCA ACCGCAATGC CGAATATTGG ATACGCCGTT
851 TTCGACGCA GTATCTGTTT ATGTACAACC GCTACAAAAT GCGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1374; ORF 505-1>:

m505-1.pep

```

1  MFRLQFRLFP PLRTAMHILL TALLKCLSLP LSLCLHTLGN RLGHAFYLL
51  KEDRARIVAN MRQAGLNPD KTVKAVFAET AKGGLLELAPA FFRKPEDTET
101 MFKAVHGEH VQALDKHEG LLFITPHIGS YDLGGYISQ QLFFPLTAMY
151 KPPKIKAIK IMQAGRVGK GKTAPTSIQG VKQIKALRS GEATIVLPDH
201 VPSQEGGEG VWVDFGKPA YMTLAAKLA HVKGVKTLFF CCERLPGGQG
251 FDLHIRPVQG ELNGDKAHD AVFNRAEYW IRRFPTQYLF MYNRYKMP*

```

m505-1/g505 94.3% identity in 298 aa overlap

	10	20	30	40	50	60
m505-1.pep	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSLCLHTLGNRLGHAFYLLKEDRARIVAN					
g505	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSLCLHTLGNRLGHAFYLLKEDRARIVAN					
	10	20	30	40	50	60
m505-1.pep	MRQAGLNPDPTVKAVFAETAKGGLLELAPAFRRKPEDTETMPKAVHGEHVQALDKHEG					
g505	MRQAGLNPDPTVKAVFAETAKGGLLELAPAFRRKPEDTETMPKAVHGEHVQALDKHEG					
	70	80	90	100	110	120
m505-1.pep	MRQAGLNPDPTVKAVFAETAKGGLLELAPAFRRKPEDTETMPKAVHGEHVQALDKHEG					
g505	MRQAGLNPDPTVKAVFAETAKGGLLELAPAFRRKPEDTETMPKAVHGEHVQALDKHEG					
	70	80	90	100	110	120
m505-1.pep	LLFITPHIGSYDLGGYISQQLFFPLTAMYPKPKIKAIKIMQAGRVGKGKTAPTSIQG					
g505	LLFITPHIGSYDLGGYISQQLFFPLTAMYPKPKIKAIKIMQAGRVGKGKTAPTSIQG					
	130	140	150	160	170	180
m505-1.pep	LLFITPHIGSYDLGGYISQQLFFPLTAMYPKPKIKAIKIMQAGRVGKGKTAPTSIQG					
g505	LLFITPHIGSYDLGGYISQQLFFPLTAMYPKPKIKAIKIMQAGRVGKGKTAPTSIQG					
	130	140	150	160	170	180
m505-1.pep	VKQIKALRSGEATIVLPDHVPSQEGGEGVWVDFGKPAYTMTLAAKLAHVKGKTLFF					
g505	VKQIKALRSGEATIVLPDHVPSQEGGEGVWVDFGKPAYTMTLAAKLAHVKGKTLFF					
	190	200	210	220	230	240
m505-1.pep	VKQIKALRSGEATIVLPDHVPSQEGGEGVWVDFGKPAYTMTLAAKLAHVKGKTLFF					
g505	VKQIKALRSGEATIVLPDHVPSQEGGEGVWVDFGKPAYTMTLAAKLAHVKGKTLFF					
	190	200	210	220	230	240
m505-1.pep	CCERLPGGQGFVLDHIRPVQSELNGDKAHDAAVFNRAEYWIIRRFPTQYLFMYNRYKMPX					
g505	CCERLPGGQGFVLDHIRPVQSELNGDKAHDAAVFNRAEYWIIRRFPTQYLFMYNRYKMPX					
	240	250	260	270	280	290

m505-1/a505 99.7% identity in 298 aa overlap

	10	20	30	40	50	60
m505-1.pep	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSLCLHTLGNRLGHAFYLLKEDRARIVAN					
a505	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSLCLHTLGNRLGHAFYLLKEDRARIVAN					
	10	20	30	40	50	60
	70	80	90	100	110	120

748

```

m505-1.pep  MRQAGLNPDPKTVKAVFAETAKGGLELAPAFFRKPEDIMTFKAVHGWHEHVQALDKHEG
              |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a505          MRQAGMNPDPKTVKAVFAETAKGGLELAPAFFRKPEDIMTFKAVHGWHEHVQALDKHEG
              70      80      90      100     110     120

              130     140     150     160     170     180
m505-1.pep  LLFITPHIGSYDLGGRYISQQLPFPLTAMYKPPKIKAIKDIMQAGRVRGKGTAPTSTIQG
              |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a505          LLFITPHIGSYDLGGRYISQQLPFPLTAMYKPPKIKAIKDIMQAGRVRGKGTAPTSTIQG
              130     140     150     160     170     180

              190     200     210     220     230     240
m505-1.pep  VKQIIKALRSGEATIVLPDHVPSQEGGEGVWVDFFGKPAYTMTLAAKLAHVKGVKTLFF
              |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a505          VKQIIKALRSGEATIVLPDHVPSQEGGEGVWVDFFGKPAYTMTLAAKLAHVKGVKTLFF
              190     200     210     220     230     240

              250     260     270     280     290     299
m505-1.pep  CCEERLPGGQGFDLHIRPVQGELNGDKAHDAAVFNRNAEYWIRRFPTQYLFMYNRYKMPX
              |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a505          CCEERLPGGQGFDLHIRPVQGELNGDKAHDAAVFNRNAEYWIRRFPTQYLFMYNRYKMPX
              250     260     270     280     290

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1375>:

```

g506.seq
1  ATGGCGGTAT TTGATGAAGT CGGGCGCATC GCCCATGGCT GCGGCGGTGT
51  TGTCAACAA AGCCTGTTTC TGCGCGTCGT TCATCAGGTT GAACAAGGCG
101 CGCGGTTGGC TGAAGTAGTC GTCATCGTCT TGGCGGTAGT CCCAGTGTGC
151 CGCGTCGCGG TTGATTTTCA AAGGCGGTTT GCGGAAGTCG GGTGTGTGCT
201 GCCATTGGCC GAAGCTGTTG GGTTCGTAGT GCGGCAGGCT GCCGTAGTTG
251 CCGTCGCGCG GGCCTTGTCG GTCGCGCTGG TTGCTGTGAA CAGGCAACG
301 CGGACGATTG ACGGGGATTT GGCGGAAGTT CACACCCAAG CGGTAACGTT
351 GCGCGTCGCG GTAATTGAAC AAACGGGCTT GCAACATTTT ATCCGGGCTC
401 GCGCCGATAC CGGGAACGAG GTTGCTCGGT GCGAAGGCGG ATTGTTCCAC
451 ATCGGCGAAG AAGTTTTTCG GATTGCGGTT CAACTCGAAT TCGCCCACTT
501 CAATCAGCGG ATAGTCTTTT TTCGCGCAAA CTTTGGTCAA GTCAAACGGA
551 TGATAAGGCA CTTTTTCGCG ATCGGCTTCA GGCATGACTT GGATGTACAT
601 CGTCCATTTT GGGAACTCGC CGCGCTCGAT GGCTTCGTAC AGGTCCGCTC
651 GATGGCTTTT CCGGTGCTCG GCGATGATTT TTGCAGCTTC TTCGTTGGTC
701 AGGTTTTTAA TCCCTTGCTG GCTGCGGAAA TGGAATTTCA CCAAAAACG
751 TTCGCCGCTC TCGTTCCAGA AGCTGTAGGT ATGCGAACCG AAGCCGTGCA
801 TATGGCGGTA GCTGGCGGGA ATACCGCGGT CGCTCATCAC GATGTAACCT
851 TGGTGCAGGG CTTGCGGCAG CAGCGTCCAG AAGTCCCAGT TGTTTGTGGC
901 GGAACGCATA TTGGTGCGCG GATCGCGTTT GACGGCTTTG TTCAGGTCGG
951 GGAATTTGCG CGGGTCGCGC AGGAAGAACA CGGGCGTGTT GTTGCCGACC
1001 ACATCCAGT TGCCTTCTTC GGTATAGAAT TTCAACGCAA AACCGCGGAT
1051 GTCGCGTTCC GCATCGGCTG CGCCGCGCTC GCCTGCCACG GTGGTGAAAC
1101 GGGCGAACAT CTCGGTTTTT TTGCCGACTT CGCTGAAAAT TTTGGCGCGG
1151 GTGTATTGGT TGATGTCGTG TGTTACGATA AACGTACCGA ACGCGCCCGA
1201 ACCTTTGGCG TGCATACGGC GTTCGCGGAT GACTTCGCGC ACGAAGTCGG
1251 CGAGTTTTTC ATTACGCCAC AAATCTTGCG TCAGCAGGGG GCCGCGCGGG
1301 CCGGCGGTCA GGCTGTTTTG ATTGTCGGCA ACGGCGCGCG CGTTGTTTCA
1351 GGTTCAGATG GTTACGGGGC ATTTGGAGGT AGTCATCGCT CTGTTCCTT
1401 TTCTCAGGTT GGTCAAATGG GGGGCAAACG GCTTACAGTA CGATTTGGCG
1451 GAAAGCGTAT TCGTAACCGG TTTCTTGATT GTAATAAATT TCTGAATCG
1501 ACATTTTATT TTCCTTTTGC AAAAATATG GATGCGATTA TACGCCAAGA
1551 TTTTCGTAT TAA

```

This corresponds to the amino acid sequence <SEQ ID 1376; ORF 506.ng>:

```

g506.pep
1  MAVFDEVGRI AHGCGGVVKQ SLFLRVVHVQ EQGARLAEVV VIVLAVVPVC
51  RVAVDFFRRF GEVGLLLPLA EAVGFVVRQA AVVAVGAALS VALVAVNRAT
101 RTIDGDLAEV HTQAVTLRVG VIEQTGLQHF IRARADTGNE VARCEGGLFH
151 IGEEVFGIAV QLEFAHFNQR IVFFRPNFGQ VKRMIRHFFG IGPRHDLDVH

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1377>:

1	ATGGCGGTAT	TTGATGAAGT	CGGGCGCGTC	GCCCATTTGCG	GCGGCGGTGT
51	TGCCGAACAA	TGCCTGTTTC	TGCGCGTCGT	TCATCAGGTT	GAACAGGGCG
101	CGCGTTGGC	TGAAATAGTC	GTATCGTCT	TGGCGGTAGT	CCCAGTGTGC
151	CGCGTCGCCG	TTGATTTTCA	AAGGCGTTCG	GCGGAATCg	GGTTGTTGCT
201	GCCATTGGCC	GAACTGTyG	GGTTCGTAGT	GCGGCGAGCT	CcCGyAGTTG
251	CCGTGCGCGC	GGCCTTGCCC	GyGCGStgr	TtGCTGTgAA	CASGGCAACG
301	CGGACGATTG	ACGGGAATTT	GGCGGAAGTT	TACGCCCAA	CGGTAGCGTT
351	GTGCGTCGCG	GTAATTGAAC	AAACGCGCTT	GCAGCATTTT	ATCTsGGCTG
401	GCGCCGACAC	CGGGAACGAG	GTGTCTCGT	GCGAAGGCGG	ATTGTTCCAC
451	ATCGGCGAAG	AAGTTTTCGG	GATTGCGGTT	CTCAACCGGA	TGATAAGGTA
501	CTTTTTCGCG	GCTTGCTTCA	GATTCAGACTT	GGATGTACAT	GCTCCATTTC
551	GGAAACTCGC	CGCGTTCGAT	G3CTTcsTAT	AAGTCGCGCT	GATGGCTTTC
601	GCGTCTGTCG	GCGATGATTT	T3GCGGCTTC	TTCGTTGGTC	ASGTTTTTAA
651	TGCCTTGTTG	GGTGCGGAAA	TGGAATTTCA	CCCAAAAACG	CTCGCCTGCT
701	TCGTTCCAGA	AGCTGTAGTT	ATGCGAACCG	AAGCCGTGCA	TATGGCGGTA
751	GCCGCGCGGG	ATGCGCGGGT	GCCTATCAC	GATGGTAACT	TGTTGCGAGT
801	CTTCGGGCAG	CACGCTCCAG	AAGTCCCAGT	TGTTTGTGCG	AGAGCGGATA
851	TTGGTGCGCG	GGTCGCGTTT	GACGGCTTTG	TTCAGGTCGG	GGAACTTACG
901	CGGTCGCGCG	AGGAAGAAC	C6GGCGTGTT	GTTGCCGACC	ACATCCAGT
951	TGCCTTCTCT	GGTATAAAAT	TTCAAGGCCAA	AACCCGCGAT	GTCGCGTTCT
1001	GCATCGGCTG	CGCGCGCTTC	GCTCGCCACG	GTTGTGAAC	TGGCAGAACAT
1051	CTCGGTTTTT	TTCGCCGACTT	GCGTGAAGAT	TCCTTTGGCG	TGGCATACGGC
1101	GTTCCGGGGAT	GACTTCGCGC	ACGAAGTCGG	CGAGTTTTTC	AGTCATCGCT
1151	CTTGTTCTCTT	TTCTCAGGTT	GGTCAAATGG	GGGTAAACGG	CTTACAGTAC
1201	GATTTGGCGG	AAAGCGTATT	CGTAACCCGT	TTCTTGATTG	CAATAAATTT
1251	CTTGAATCGA	CATTTTATTT	CCCTTTTGTA	AAAACTATGG	ATGCGACTAT
1301	ACGCCAAGAT	TTTCGCTATT	AA		

1	MAVFDEVGRV	AHCGGGVAEQ	CLFLRVVHQV	EQGARLAEIV	VIVLAVVPVC
51	<u>RVAVDFQRRF</u>	<u>GESGLLLPLA</u>	<u>BAVGFVVRQA</u>	<u>AXVAVGAALP</u>	<u>VAXXAVNXAT</u>
101	RTIDGNLAEV	YAQTVALCVG	VIEQTRLQHF	IXAGADTGNE	VARCEGGLFH
151	IGEEVFGIAV	QLEFAHFNQF	IVFFRPNFGF	VKMIRYRFFR	VCFRHDLDVH
201	<u>RPPFKLAAFD</u>	<u>GEXFVALMAF</u>	<u>AVGDDDFGGF</u>	<u>FVGQVFNALL</u>	<u>GAEMEFHPKT</u>
251	<u>LACFVPEAVG</u>	<u>MRTXEAHVMAV</u>	<u>AGDGAAVAHH</u>	<u>DGNLVQCFCFQ</u>	<u>QREPEVPVCG</u>
301	RAHIGARVAF	DGFVQVGELT	RVAQEEHGRV	VADHIPVAFF	GIKFGKTDAD
351	VAPICIGCAAF	ACHGGETGEH	LGFPADFAED	FGAGVFGDVV	RYGKRTERAR
401	TFGVHTAFGD	DFAHEVGEFF	IQPMILRQQR	AARTGGQAVL	IVGNRRRAVH
451	QGMGYRAFGG	SHRSSEFSQV	QGMGGKRLTV	RFGGKRIRNR	FLDCNKFLES
501	TFYFFPVKTM	DATIRODFRY	*		

m506/g506

[illegible]

750

	70	80	90	100	110	120
m506.pep	GESGLLLPLAEAVGFVVRQAAXVAVGAALPVAXXAVNXATRTIDGNLAEVYAQTVALCVG					
g506	GEVGLLLPLAEAVGFVVRQAQAVVAVGAALSVALVAVNRATRTIDGDLAEVHTQAVTLRVG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m506.pep	VIEQTRLQHFIXAGADTGNEVARCEGGLFHIGEEVFGIAVQLEFAHFNQRIVFFRPNFGQ					
g506	VIEQTLQHFIRARADTGNEVARCEGGLFHIGEEVFGIAVQLEFAHFNQRIVFFRPNFGQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
m506.pep	VKRMIRYFFRVCFRHDLDVHRPFRKLAAFDGFXXVALMAFAVVGDDFGGFFVGVFNALL					
g506	VKRMIRHFFGIGFRHDLDVHRPFRKLAALDGFVQVALMAFAVVGDDFCSFFVGVFNPLL					
	190	200	210	220	230	240
	250	260	270	280	290	300
m506.pep	GAEMEFHPKTLACFVPEAVGMRTEAVHMAVAGGDAVAHHDGNLVQCFGQQRPEVPVVC					
g506	AAEMEFHPKTFARFVPEAVGMRTEAVHMAVAGGNTAVAHHDGNLVQGFQQRPEVPVVC					
	250	260	270	280	290	300
	310	320	330	340	350	360
m506.pep	RAHIGARVAFDGFVQVGEELTRVAQEEHGRVVADHIPVAFPGIKFQGTADVAFCIGCAAF					
g506	GTHIGARIAFDGFVQVGEFARVAQEEHGRVVADHIPVAFPGIEFQRTADVAFRIGCAAL					
	310	320	330	340	350	360
	370	380	390	400	410	420
m506.pep	ACHGGTGEHLGFFADFAEDFGAGVFGDVVRYGKRTERARTFGVHTAFGDDFAHEVGEFF					
g506	ACHGGTGEHLGFFADFAENFGAGVFGDVVRYGKRTERARTFGVHTAFGDDFAHEVGEFF					
	370	380	390	400	410	420
	430	440	450	460	470	480
m506.pep	IQPQILRQQAARTGGQAVLIVGNRRVAVHGMGYRAFGGSHRSCSFSQVGMGKRLTV					
g506	IQPQILRQQAARAGGQAVLIVGNRAVAVHGMGYGAFGGSHRSCSFSQVGMGKRLTV					
	430	440	450	460	470	480
	490	500	510	520		
m506.pep	RFGGKRIRNRFLDCNKFLESTFYFPFVKTMDATIRQDFRY					
g506	RFGGKRIRNRFLDCNKFLESTFYFPFAKTMDAIRQDFRY					
	490	500	510	520		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1379>:

a506.seq

```

1  ATGGCGGTAT TTGATGAAGT CCGGCGCGTC GCCCATTGCG GCGGCGGTGT
51  TGCCGAACAA TGCCTGTTTC TCGCGCTCGT TCATCAGGTT GAACAGGGCG
101 CGCGGTGGC TGAATAGTC GTCATCGTCT TGGCGGTAGT CCCAGTGCGC
151 CGCGTCGCG TTAGTTTCA AAGCGGTTTC GCGGAAGTCG GGCTGCTGCT
201 GCCATTGGCC GAAGCTGTTG GGTTCGTAGT GCGGCAGGCT GCCGTAGTTG
251 CCGTCGGCGC GTCCTGTCC GTCGCGCTGG TTGCTGTGAA CAGGGCAACG
301 CCGACGGTTG ACAGGGATTG GCGGGAAGTT CACGCCAAG CGGTAGCGTT
351 GCGCGTCGCG GTAATTGAAC AAACGCGCCT GCAACATTTT ATCTGGGCTG
401 GCGCGACAC CCGGAACGAG GTTGCTCGGT GCGAAGGCGG ATTGTTCCAC
451 ATCGCGAAG AAGTTTTCG GATTGCGGTT CAACTCGAAT TCGCCCACTT
501 CAATCAGCG ATAGTCTTTT TTCGCCCAA CTTTGGTCAA GTCAAACGGA
551 TGATACGGCA CTTTTCGCG ATCGGCTTCA GGCATGACTT GGATGTACAT
601 CGTCCATTTC GGAACTCGC .CGCGCTCGAT GGCTTCGTAC AGGTCGCGCT

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751

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651 GATGGCTTTC ACGGTCCTCG GCGATGATTT TGGCGGCTTC TTCGTTGGTC
701 AGGTTTTTAA TGCCTTCTTG GGTGCGGAAA TGGAATTTC AAAAAAACG
751 CTCGCTGCT TCGTTCAGAG AGCTGTAGGT ATGCGAACCG AAGCCGTGCA
801 TATGGCGGTA GCCGGCGGGG ATGCCGCGGT CGCTCATCAC GATGGTAACT
851 TGGTGCAGTG CTTCGGGCAG CAGCGTCCAG AAGTCCAGT TGT'TGTGGC
901 AGAGCGCATA TTGGTGCAGG GGTGCGGTTT GACGGCTTTG TTCAGGTCGG
951 GGAACCTACG CGGGTCGCGC AGGAAGAAC ACGGCGTGTT GTTGCCGACC
1001 ACATCCAGT TGCCTTCTTC GGTATAGAAC TTCAACGCAA AACCGCGGAT
1051 GTCGCGTTCT GCATCGGCTG CGCCGCGTTC GCCTGCCACG GTGGTGAAAC
1101 GGGCGAACAT CTCGGTTTTT TTGCCGACTT CGCTGAAGAT TTTGGCGCGG
1151 GTGTATTTGG TGATGTCGTG CGTTACGGTA AACGTACCGA ACGCGCCCGA
1201 ACCTTTGGCG TGCATACGGC GTTCGGGGAT GACTTCGCGC ACGAAGTCGG
1251 CGAGTTTTC ATTACGCCAC AAATCCTGCG CCAGCAGAGG GCCGCGAGGA
1301 CCGGCGGTCA GGCTGTTTTG ATTGTGCGCA ACAGGCGCGC CGTTGTTTAT
1351 GGTCAGATGG GTTACAGGGC ATTTGGAGGT ANTATCGCT CTTGTTCTCT
1401 TTCTCAGGTT GGTCAAAT.G GGGGTAAACG GCTTACAGTA CGATT'TGGCG
1451 GAAAGCGTAT TCGTAACCGG TTTCTTGATT GCAATAAAT TCTTGAATCG
1501 ACATTTTATT TCCCTTTTGT AAAAATATG GATGCGACTA TACGCCAAGA
1551 TTTTCGCTAT TAA

```

This corresponds to the amino acid sequence <SEQ ID 1380; ORF 506.a>:

```

a506.pep
1 MAVFDEVGRV AHCGGGVAEQ CLFLRVVHQV EQGARLAEIV VIVLAVVPVR
51 RVAVDFQRRF GEVGLLLPLA EAVGFVVRQA AVVAVGASLS VALVAVNRAT
101 RTVDRDLAEV HAQAVALRVG VIEQTRLQHF IWAGADTGN E VARCEGGLFH
151 IGEVFGIAV QLEFAHFNQR IVFFRPNFGQ VKRMIRHFFR IGFRLDLVH
201 RPFRLAALD GFVQVALMAF TVVGDDFGGF FVGQVFNALL GAEMEFHFKT
251 LACFVPEAVG MRTEAVHMAV AGGDAVAHH DGNLVQCFGQ QRPEVPVVCG
301 RAHIGARVAF DGFVQVGEIT RVAQEEHGRV VADHIPVAF GIELQRKTAD
351 VAFICGAAF ACHGGETGEH LGFFADFAED FGAGVFGDVV RYGRTERAR
401 TFGVHTAFGD DFAEVGEFF IQPQLRQQR AARTGGQAVL IVGNRRVAVH
451 GQMGYRAFGG XHRSCSFSQV GQXGKRLTV RFGGKRIRNR FLDCNKFLS
501 TFFFPFKTM DATIRQDFRY *

```

m506/a506 94.8% identity in 520 aa overlap

	10	20	30	40	50	60
m506.pep	MAVFDEVGRVAHCGGGVAEQCLFLRVVHQVEQGARLAEIVVIVLAVVPVCRVAVDFQRRF					
a506	MAVFDEVGRVAHCGGGVAEQCLFLRVVHQVEQGARLAEIVVIVLAVVPVRRVAVDFQRRF					
	10	20	30	40	50	60
m506.pep	GESGLLLPLAEAVGFVVRQAAXVAVGAALPVAXXAVNXATRTIDGNLAEVYAQTVALCVG					
a506	GEVGLLLPLAEAVGFVVRQAAXVAVGASLSVALVAVNRATRTVDRDLAEVHAQAVLRVG					
	70	80	90	100	110	120
m506.pep	VIEQTRLQHFIXAGADTGN E VARCEGGLFHIGEEVFGIAVQLEFAHFNQRIVFFRPNFGQ					
a506	VIEQTRLQHFIWAGADTGN E VARCEGGLFHIGEEVFGIAVQLEFAHFNQRIVFFRPNFGQ					
	130	140	150	160	170	180
m506.pep	VKRMIRYFFRVCFRHLVDVHRPFRKLAAFDGFXVALMAFAVVGDGFGGFVVGQVFNALL					
a506	VKRMIRHFRIGFRHLVDVHRPFRKLALDGFVQVALMAFTVVGDDGFGGFVVGQVFNALL					
	190	200	210	220	230	240
m506.pep	GAEMEFHFKTLACFVPEAVGMRTAVHMAVAGGDAVAHH DGNLVQCFGQQRPEVPVVCG					
a506	GAEMEFHFKTLACFVPEAVGMRTAVHMAVAGGDAVAHH DGNLVQCFGQQRPEVPVVCG					
	250	260	270	280	290	300

752

	310	320	330	340	350	360
m506.pep	RAHIGARVAFDGFVQVQV	ELTRVAQEEHGRV	VADHIPVAFFG	IKFQGKTADVA	FCIGCAAF	
a506	RAHIGARVAFDGFVQVQV	ELTRVAQEEHGRV	VADHIPVAFFG	IELQRTADVA	FCIGCAAF	
	310	320	330	340	350	360
	370	380	390	400	410	420
m506.pep	ACHGGETGEHLGFFADFA	EDFGAGVFGDV	VRYGKRT	ARTFGVHTA	FGDDFAHEV	GEFF
a506	ACHGGETGEHLGFFADFA	EDFGAGVFGDV	VRYGKRT	ARTFGVHTA	FGDDFAHEV	GEFF
	370	380	390	400	410	420
	430	440	450	460	470	480
m506.pep	IQPQILRQQR	AARTGGQAVL	LIVGNRR	AVVHGQMG	YRAFGGSHR	SCSFSQVQMG
a506	IQPQILRQQR	AARTGGQAVL	LIVGNRR	AVVHGQMG	YRAFGGXHR	SCSFSQVQXG
	430	440	450	460	470	480
	490	500	510	520		
m506.pep	RFGGKRIRNR	FLDCNKFLE	STFYFPFV	KTM	DATIRQDFRYX	
a506	RFGGKRIRNR	FLDCNKFLE	STFYFPFV	KTM	DATIRQDFRYX	
	490	500	510	520		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1381>:

g507.seq

```

1  ATGCTCTTGC CGGCTTTGCA ACAAGGCGGC GGCTTCCTGA GCGGCGGCGG
51  TTTCGGCCTC GTCGGGCAGG TTCAGGGCTT GGTTTTCTTG CTTCAGACGG
101 CCTTTGCGCT CTTCTGTGCTT GGCAACGGTT TGTTCCGGCAT GGGCAAGCTG
151 CTGCTGCTTC AACGCCAGTT CGCGGCGGAT GCGGTTTGCC TCGTCCTGCT
201 GGGTTTGGAA GGCAGCGTTG AGCGTGGCTT GGACTTCTTC CAATTGCGGC
251 AGACGCTCTT CGTGTTCGGC AACCTGCATC GCCCATTCGG CCAATTCGGT
301 TTGCTTTTCT TCGACCTGCA ACTCGTTTTC CTCAAGCTGC ACGCGGATTT
351 GCTGCTGCTC CTGCCGGATG CGTTGCAACT GCGCCTGCGC TGCCTGCTTG
401 TCGCGTTTCA TCGCTTGGTG CAGGTTTTCG CCGTGGCGGA TTTGTTCTTC
451 CAAACGGGCA ATCTGCTCGC GCAACACGCC GCGTTTGTTC CTCAATTCGT
501 GTACTGCCTG CTGCTGCGAC TGTTCGGCAG TCTGCAAGGC GTGTACTTCG
551 TTATTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1382; ORF 507.ng>:

g507.pep

```

1  MLLPALQQGG GFLSGGGFGL VGQVQGLVFL LQTAFALFVL GNLFMGMKL
51  LLLQRQFAAD AVCLVLLGLE GSVERGLDFF QFGOTLFFVG NLHRPFROFG
101 LLFFDLQLVF LKLHADLLL LPDALQLRLR CLLVAFDALV QVLPVADLFF
151 QTGNLLAQHA AFVAQFVYCL LLRLFGSLQG VYFVI*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1383>:

m507.seq

```

1  ATGCTCTTGC TGACTTTGCA ACAAGGCGGC TGCTTCCTGC GCGGCGGCGG
51  TTTCGGCTTC GTCGGGCAGG TTAAAGGCTT GGTTTTCTTG TTTAGACGA
101 CCTTTGCGCT CTTCTGTGCTT GGCAATCGTT TGTTCCGGCAT GGGCAAGCTG
151 CTGCTGCTTC AACGCCAGTT CGCGGCGGAT GCGGTTTGCC TCGTCCTGCT
201 GGGTTTGGAA GGCAGCGTTG AGCGTGGCTT GGGCTTCTTC CAATTGCGGC
251 AGACGCTCCT CGTGTTCGGC AACCTGCATC GCCCATTCGG CCAGCTCGGT
301 TTGTTTTTCT TCGACCTGCA ACTCGTTTTC TTCAAGCTGC ACGCGGATTT
351 GCTGCTGCTC TTGATGAATG CGTTGTAAC TCGCCTGCGC TGCCTGCTTG
401 TCGCGTTTCA TCGCTTGGTG CAGGTTTTCG TGATGGCGGA TTTGTTCTTC
451 CAAACGGGCA ATCTGCTCGC GCAACACGCC GCGCTTGTTC CTCAATTCAT
501 GCACTGCCTG CTGCTGCGAC TGTTCGGCAG TCTGCAAGGC GTGTACTTCG
551 TCCTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1384; ORF 507>:

m507.pep

```

1  MLLLTLLQGG CFLRGGGFGF VGQVXGLVFL FQTTAFALFVL GNRLFMMGKL

```

753

51 LLLQRQFAAD AVCLVLLGLE GGVERGLGFF QFGQTLLVFG NLHRPFRQLG
101 LFFFDLQLVF FKLHADLLLL LMNALXLRRL CLLVAFDALV QVLLMADLFF
151 QTGNLLAQHA ALVAQFMHCL LLRLFGSLQG VYFVV*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 507 shows 87.0% identity over a 185 aa overlap with a predicted ORF (ORF 507.ng) from *N. gonorrhoeae*:

m507/g507

		10	20	30	40	50	60
m507.pep		MLLLTLQGGCFLRGGGFGFVGQVXGLVFLFQTTFALFVLGNRLF	GMGKLLLLLQ	RQFAAD			
		: : :					
g507		MLLPALQGGGFLSGGGFLVGQVCGLVFLQTAFALFVLGNLFGMGK	LLLLLQ	RQFAAD			
		10	20	30	40	50	60
		70	80	90	100	110	120
m507.pep		AVCLVLLGLEGGVERGLGFFQFGQTLLVFGNLHRPFRQLGLFFFDL	QLVFFK	LHADLLLL			
		: : : :					
g507		AVCLVLLGLEGSVERGLDFFQFGQTLFVFGNLHRPFRQFGLLFFDL	QLVFLKL	HADLLLL			
		70	80	90	100	110	120
		130	140	150	160	170	180
m507.pep		LMNALXLRRLCLLVAFDALVQVLLMADLFFQTGNLLAQHAALVAQFM	HC	LLRL	FGSLQG		
		: : : :					
g507		LPDALQLRLCLLVAFDALVQVLPVADLFFQTGNLLAQHAAFVAQFVY	C	LLRL	FGSLQG		
		130	140	150	160	170	180
m507.pep		VYFVV					
		:					
g507		VYFVI					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1385>:

```
a507.seq
  1  ATGCTCTTGC  TGGCTTTGCA  ACAAGGCGGC  AGCTTCCTGC  GCGGCGGCGG
51  TTTCCGGCTTC  GTCAGGCAGA  TTCAGGGCTT  GGTTTTCCTG  TTTCAGACGA
101 CTTTTCGGCT  CTTCTGCTT  GGCACCGGTT  TGTTCCGGAT  GGCACAGCTG
151 CTGCTGCTTC  AACGCCAGTT  CGCGGCGGAT  GCGGTTTGCC  TCGTCTGTCT
201 GGGTTTGGAA  GGCGGCATTG  AGTGTGGCTT  GGTTTCTTC  CAATTCGGGC
251 AGACGCTCTT  CGTGTTCCGC  AACTGCATC  GCCCATCCG  CCAATTCGGT
301 TTGCTTTTCT  TCCGCCTGCA  ACTCGTTTTC  TTCAAGCTGC  ACGCGGATTT
351 GCTGCTGCTC  CTGATGGATG  CGCTGEATCT  GCGCCTCGGC  CGCCTGCTTG
401 TCGCGTTCGA  TGCGTTGGTG  CAGSTTTTGC  TGATGGCGGA  TTTGTTCTTC
451 CAAACGGGCA  ATCTGTTCCG  GCAACACGCC  GCSTTTGTTG  CCCAATTCGT
501 GCACCGCCTG  CTGCTGCGAC  TGTTCGGCAG  TCTGCAAGGC  GTGTACTTCG
551 TCGTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1386; ORF 507.a>:

a507.pep

1	MLLLALQGGG	SFLRGGGFGF	VRQIQGLVFL	<u>FQTTFALFVL</u>	GNGLFGMGKL
51	LLLRQRFAD	AVCLVLLGLE	GGIECGLGFF	QFGQTLFVFG	NLHRPFRQFG
101	LLFRLLQLVF	FKLHADLLLL	LMDALHLRLR	RLLVAFDALV	<u>QVLLMADLFF</u>
151	OTGNLFAOHA	AFVAQFVHRL	LLRLFGSLOG	VYFVV*	

m507/a507 89.7% identity in 185 aa overlap

	10	20	30	40	50	60
m507.pap	MLLLTLQGGGCFLRGGGFGFVGQVXGLVFLFQTTTFFALFVLGNRLF	GMGKLLLLLQRFQFAAD				
	:		:			
a507	MLLLALQGGGFLRGGGFGFVRQIQGLVFLFQTTTFFALFVLGNLFG	MGKLLLLLQRFQFAAD				
	10	20	30	40	50	60
	70	80	90	100	110	120

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```

m507.pep    AVCLVLLGLEGGVERGLGFFQFGQTLVFGNLRPFRQGLGFFDLQLVFFKLHADLLLL
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a507        AVCLVLLGLEGGIECLGFFQFGQTLFVFGNLRPFRQFGLLFFRLQLVFFKLHADLLLL
              70      80      90      100     110     120

              130     140     150     160     170     180
m507.pep    LMNALXLRRLRCLLVAFDALVQVLLMADLFFQTGNLLAQHAALVAQFMHCLLLRFLGSLQG
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a507        LMDALHLRLRLRLVAFDALVQVLLMADLFFQTGNLFAQHAAFAQFVHRLLRLFLGSLQG
              130     140     150     160     170     180

m507.pep    VYFVVX
|||||
a507        VYFVVX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1387>:

```

g508.seq
1  ATGGTAGCGT TTGGCGTTGA TCAGGGCTTC CTGCTGCTGC AACAGGGCGG
51  TTTGGGTGGC GGCCTGAAGC TCGGCAGCT TGGTTGCAG GGTTCGTACC
101 CGGGCGTATT GCTCCCTGCC CTGTTCTGA ATCTGCGCGA GTTTTCCTG
151 CACGGCGATG TATTCTTCGT CCAGCGTGTG TACGGTTTCG GTCAACTCGT
201 CGAGCTTGAT GTGCTGCTCG TCGTTTGA ACTCGGTTT ATAGGCGAGG
251 GCAAGCTCTT GCCGGCGTTC CTGCCAGTCC AGGGTTGCT GTTCGAGCCG
301 GGCGATTGTC TGCCGGTAGT TTTGTTTTTG CGGGTTGAGT TTGTGGACGG
351 CGACTTCGGC AAGCCGTAT TGGCGGTTGG CTTCCAACAG GGCAAGCTGC
401 GCCTGTTTCA GACGGCCTTG CTGCTCTTGG CGGCTGTGCG CGGTGGTTTG
451 CTGCTGGTGT TCGAGTTCGG CGGCGGCTTC CTGCAAAGTA GCGATGTCGT
501 CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1388; ORF 508.ng>:

```

g508.pep
1  MVAFGVDQGL LLLQQGGLGG GLKLRQLGLQ GLYAGVLLPA LFLNLRFFLL
51  HGDVFFVQRV YGFGQLVELD VLLVLELGF IGEKLLPAF LPVQGLLFEP
101 GDLLPVVFL RVEFVDGDFG KPVLA VGFOQ GKLRLFOTAL LLLAAVRGGL
151 LLVFEFGGGF LQSSDVV

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1389>:

```

m508.seq
1  ATGGTAGCGT TTGGCGTTGA TCAGGGCTTC CTGCTGCTGC AACAGGGCGG
51  TTTGGGTGGC GGCCTGAAGC TCGGCAGCT TGGTTGCAG GGTTCGTACT
101 TTAGCGTATT GCTCCCTGCC CTGTTCTGA ATCTGCGCGA GTTTCCTTG
151 CACAACAATA TATTCTTCGT CCAAGGTCTG TACGGCTTCG CTAATTCTT
201 CAAGCTTGAT GTGCTGCTCG TCGTTTGA ACTCGGTTT ATAGGCGAGG
251 GCAAGCTCTT GCTGGCGTTC CTGCCAGTCG AGGGTTGCT GTTCAAGCTG
301 GGCGATTGTC TGCCGGTAGT TTTGTTTTTG CTGGTTGAGT TTGTGGACGG
351 CGACTTCGGC AAGCCGTAT TGGCGGTTGG CTTCCAACAG GGCAAGCTGC
401 GCCTGTTTCA GACGGCCTTG CTGCTCTTGG CGGCTGTGCG CGGTGGTTTG
451 CTGCTGGTGT TCGAGTTCGG CGGCGGCTTC CTGCAAAGTA ACGATGTCGT
501 CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1390; ORF 508.ng>:

```

m508.pep
1  MVAFGVDQGF LLLQQGGLGG GLKLRQLGLQ GLHFSVLLPA LFLNLRFFLL
51  HNNIFFVQGL YGFAEFKLD VLLVLELGF IGEKLLAF LPVEGLLFKL
101 GDLLPVVFL LVEFVDGDFG KPVLA VGFOQ GKLRLFOTAL LLLAAVRGGL
151 LLVFEFGGGF LQGNDDV*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 508 shows 86.8% identity over a 167 aa overlap with a predicted ORF (ORF 508.ng) from *N. gonorrhoeae*:

m508/g508

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	10	20	30	40	50	60
m508 . pep	MVAFGVDQGFLLLLQQGGGLGGLKLRQLGLQGLHFSVLLPALFLNLRFLHNNIFFVQGL					
g508	MVAFGVDQGLLLLLQQGGGLGGLKLRQLGLQGLYAGVLLPALFLNLRFFLHGDVFFVQRV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m508 . pep	YGFAXFFKLDVLLVVLELGFIGEGKLLLAFLPVEGLLFLKGLDLPVVLFLLVFVDGDFG					
g508	YGFQQLVELDVLLVVLELGFIGEGKLLPAFLPVQGLLFPDGLLPVVLFLRVEFVDGDFG					
	70	80	90	100	110	120
	130	140	150	160		
m508 . pep	KPVLA VG FQQGKLR L FQTALLLLAAVRGGLLVFEFGGGLQGNDDV					
g508	KPVLA VG FQQGKLR L FQTALLLLAAVRGGLLVFEFGGGLQSSDVV					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1391>:

```

a508 . seq
1  ATGGTAGCGT TTGGCGITGA TCAGGGCTTC CTGCTGCTGC AACAGGGCGG
51  TTTGGGTGGC GGCCTGAAGC TCGGCAGCT TGGTTGCAG GGTTCGTACG
101 CGGGCGTATT GTTCCCTACC CTGCTCCTGA ATCTGCGCGA GTTTCCTCTG
151 TACGACAATA TATTCTCGT CCAAACTCTG TACGGCTTCG CTCAACTCTT
201 CGAGCTTGAT GTGCTGCTCG TCGTTTGGGA ACTCGGTTTC ATAGGCGAGG
251 GCAAGCTCTT GCTGGCGTTC CTGCCAATCG AAGGTTTGTG GTTCAAGCTG
301 GGCAATTTGC TGTGTGCTAGT TTTGTTTTTG CTGGTTGAGC TTGTGGACGG
351 CGACTTCGGC AAGCCCGTAT TGGCGGTTGG CTTCCAACAG GGCAAGCTGC
401 GCCTGTTTCA GACGACCTTG CTGCTCTTGG CGGCTGTGCG CGGCGGTTTG
451 CTGCTGCTGT TCGAGTTCGG CGGCGGCTTC CTGCAAAATG GCGATGTCGT
501 CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1392; ORF 508.a>:

```

a508 . pep
1  MVAFGVDQGF LLLQQGGLGG GLKLRQLGLQ GLYAGVLFPT LLLNLRFL
51  YDNIFVQTL YGFAQLFELD VLLVVLELGF IGEGKLLAF LPIEGLLFLK
101 GNLLLVVFL LVELVDGDFG KPVLA VG FQQ GKLR L FQT LL LLA VRGGL
151 LLVFEFGGF LQNGDVV*

```

m508/a508 88.6% identity in 167 aa overlap

	10	20	30	40	50	60
m508 . pep	MVAFGVDQGFLLLLQQGGGLGGLKLRQLGLQGLHFSVLLPALFLNLRFLHNNIFFVQGL					
a508	MVAFGVDQGFLLLLQQGGGLGGLKLRQLGLQGLYAGVLFPTLLNLRFLLYDNIFVQTL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m508 . pep	YGFAXFFKLDVLLVVLELGFIGEGKLLLAFLPVEGLLFLKGLDLPVVLFLLVFVDGDFG					
a508	YGFAQLFELDVLVVLELGFIGEGKLLLAFLPIEGLLFLKGNLLVVFLLVVELVDGDFG					
	70	80	90	100	110	120
	130	140	150	160		
m508 . pep	KPVLA VG FQQGKLR L FQTALLLLAAVRGGLLVFEFGGGLQGNDDVX					
a508	KPVLA VG FQQGKLR L FQTLLLLAAVRGGLLVFEFGGGLQNGDVVX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1393>:

g509 . seq

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```

1  atgggtcgctg tatgtgatga acgggctgta cagcggacgt tgggtggccca
51  attcgcgcaa caaggcggct tgtttttgct cttcgttcag gctgtttag
101 tcttccaagc ctgctgtgtg gaaaagctcg gcaaccacat cggcgtgttt
151 gcctgcgtgt tggcgaggt cgagcggcat catgtggaag ccgaacacgg
201 acacggaacg gatgaggtct gccaaacggc cttcggcaag caggcggctg
251 ccgttgtcga taagggaacg ttgcaatttt ttcaaatcat cgagaaattt
301 ttgggcccga gcataacgct cgagaaagcc gaatttgcag cccatgccc
351 aaccgagcga gcgcgctttg cccatagcgc gcgccataat gtaggcaatg
401 gcgcggcggt aagggttctt ggtgcggcg atttcttcgt caggcgagag
451 cgctgccagt gccattacgt cgtcgttgac ttgacgcgg cggtatggaa
501 gcggcagttc gcggtaaagt ttgtcgagtt cgctgcggt aaaaacggaac
551 acggcatcgg cgtggcggcg gaaggcaaag cgcagggttt cgccagaaac
601 aaacggaatt cgctcgcggt cgccgccgat ccagccgccc attttaagga
651 tatteggaac gcggacatcg ggataggccg tctgaaagtc gtgttccatc
701 ttgcggtaga gtttgggcag ggcttcaaaa aagctcatcg gyaagatgga
751 cagccggtt ttgatttcgt cgttgacgct gagtttggg cggcgcttt
801 cgctggtctg ccacaagccc agaagcacgg tgcgatttc gcggcgagc
851 cgtgccagcg cgtcggtatt ggtgcagcgt tcgcgttgcg gcagcagcgc
901 gcggatgcgg cggttgaaat tcaaaacggc ttggcggttc acttcggctc
951 ggtgcgcggc caaaacggcg gtaacggacg tattgtccaa ctgccgctgc
1001 accgatttgc cgtcggtttt ccccgctttg agcctgcgga cgggttccgc
1051 caggctgcct tctgctgcgt tgtggcggcg atcttcgtgg atttgcgggc
1101 ggcgttcgtg gtgcacgtct tcggcgatat tcagaatctg ggcgaaacagc
1151 ccgcaggcaa gcgtcagatc gtaggtctgc cgttcgtcca attgcggcaa
1201 tactttttca atcaatgccg cgctgtcgtc ggaagtggac aagagtttga
1251 ccgtttcgac aaccaacggc gaggcttctt cgtgcaggag gttgaacagg
1301 gactgtttca aaaattccgc gtccgcgcgc aaagccgcgt ccttcggatt
1351 gttcaggata tgcagtgcga tgattttcct ctcatgtccg taaatactgt
1401 aaatgtacct caaatgccgc atccgtgcc aaccgttcac actttaacca
1451 ctcatgtccc gaaatgccgt ctgaagtga acgccgccg acggcggcgt
1501 tacaatcgcc cgcaactggt tttttccgaa catcatcatg accgcgaccg
1551 aacacgacaa cgacgacgca ctctgctgc ggtacagccg ccacatcctc
1601 ttggacgaaa tcggcatcga agggcagcag aagctttccg ccgcgcatat
1651 tttggtcgtc ggctgcggcg gattgggcgc cgccgccctt gccctatctc
1701 gccgcctcgg gggtcggcac gctga

```

This corresponds to the amino acid sequence <SEQ ID 1394; ORF 509.ng>:

g509.pep

```

1  MVAVCDERAV ORTLVAQFAQ OGGFLFLFVQ AVVVFQACVL BKLGNHIGVF
51  ACVLAQVERH HVEAEHGHGT DEVCQTAFGK QAAAVVDKGT LQFFQIIEKF
101 LGRSIRLEKA EFAAHAQTER ARFAHSARHN VGNGAAVRFF GAGDFFVRRE
151 GCQCHYVVVD FDAADGKRQF AVKFVEFAAV KTEHGIGVAA BGKAQGFAFN
201 KRIAVAVAAD PAADFKDIRN ADIGIGRLKV VFHLAVEFGQ GFKKAHREDG
251 HAVVDFVVD AEFVAARFAGL PQAQKHGVDF AAQPCQRVGI GAAAFALRQR
301 ADAAVEIQNG LALHFGRVRG QNGGNRIVQ LPLHRFAVGF PRFEPADGFR
351 QAAFCCVVAG IFVDLAAAFV VHVFGDIQNL GEQPAQKROI VGLPFVQLRQ
401 YFFNQCRVV GSGQEFDRFD NRRGFFVQE VEQGLFQKFR VRRQSRVLR
451 VQDMQLHDFP LIAVNTVNP QMPHPCQTVH TLTHVPKCR LKLNAARRRR
501 YNRPQLFFSE HHDRDRTRQ RRRTPAAVQP PHPLGRNRHR RAAEAFRRAY
551 FGRRLRRIGR RRPCISPFR GSAR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1395>:

m509.seq

```

1  ATGGTCGCTG TATGTGATAA ACGGGCTGTA CAGAGGACGT TGATGGCTCA
51  ATTCGCGCAA CAGGGCGGTT TGTTTTGTCT CTTGCTTCAG GCGGTGTAG
101 TCTTCCAAGC CTGCGTGTGG GAAAAGCTCG GCAACCACAT CGGCGTGT
151 GCCTGCGTGT TGGCGCAAGT CGAGCGGCAT CATGTGAAAG CCGAACACGG
201 ATACGGAACG GATGAGGTCT GCCAAACGGC CTTGCGCAAG CAGACGGCTG
251 CCGTTGTCTG TAAGGGAACG TTGCAATTTT TTCAAATCAT CCAGAACTC
301 TTGTGCCGAA GCATAAGSCT CGAGAAAGCC GAATTTGCAG CCCATACCCA
351 AACCAGACGC GCGCGCTTTG CCCATAGCGC GCGCCATAAT GTAGGCGATG
401 GCGCGGCGGT AGGGTTCTTC GCGCGGGCGC ATTTCTTCGT CGGGCGATTT
451 GTCGGACAAC GCCGTACAT CGCGTTGAC TTTGACGCGG CGGATGGAGA
501 GCGGCAGTTC GCGGTAGAGT TTGTCGAGTT CGCCGCGATA GAACGGGAAC

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551 ACGGCATCGG CGTGGCGGCG GAAGGCAAAG CGCAGGGTTT CGGCAGAAAC
601 AAACGGATTG CCGTCGCGGT CGCCGCCGAT CCAGCCGCCG ATTTTGAGGA
651 TGTCCGGAAC GCGGACGCCG GGATAGGCCG TCTGAAAGTC GTGTTCATC
701 TTGCGGTAGA GCTTGGGCAG GGCTTCGAAA AAGCTCATCG GGAAGATGGA
751 CACGCCGTTG TTGATTTCGT CGTTGACGCT GAGTTTGTGG CGGCGCGTTT
801 CGCTGGTCTG CCACAAGCCC AGCAGGATAG TGTGATTtC GCgGCGCAGC
851 CGTGCCAGCG CGTCGCGATT GGTGACGCGT TCgCGTTGCG GCAACAGTGC
901 GCGGATGCGG CGGTTGAAGC TTAAGACGGT TTGGCGTTGC ACTTCGGTCG
951 GGTGCGCGGT CAAAACG3CG GTAACGGACG TATTGTCCAA CTGCCGCTGC
1001 ACCGATTTCG CGTCGCGCTTT CCCCCTTTG AGCCTGCGGA CGGTTCCGT
1051 CAGGCTGCCT TCCGCGCCGC CGCGTCCGGC TTCTTCGTGG ATTTGGCGGC
1101 GGCCTTCGTG GTGCACGTCT TCGGCGATGT TCAAATCTG GGCGAACAGG
1151 CCGCAGGCCA AGGTTAAATC GTGGGTTTGT TGTTCGTCCA ATTGCGGCCA
1201 TACTTTTTCA ATCAATGCCG CGCTGTCGTC GGAAGTGGAC AAGAGTTTGA
1251 CTGTTTCGAC AACCAACGGC GAGGCTTCTT CGTGCAAGAG GTTGAACAGG
1301 GATTGTTTCA GAAATTCCGC GTCCGCCGCC AAAGCCCGCT CTTTGGATT
1351 GTTCAGAATA TGCAGTTGCA TGATTTTCT CTCTCGTCTG CCGTAAATAT
1401 TGTAATATGTA CCCCATAATG CGCATCCGTG CCAAACCGTT CACACTTTAA
1451 CCGCCCGTGT CCCGAAATGC CGTCTGAAGT TGAACGCCGC CCGACGGCAG
1501 CGTTACAATC GCCCGCAACT GTTTTtTTCC GAACATCATC ATGACCACGA
1551 CCGAACACGA CAACGACGAT GCATTCTTGC TGCGGTACAG CCGCCACATC
1601 CTCTTGACG AAATCGGCAT CGAAGGGCAG CAGAACTTT CCGCCGCGCA
1651 TATTTTGGTC GTCGCTGCG GCGGTTGGG TGCCGCCGCA CT.GCCCTAC
1701 CTTGCCGCTT CGGGTGTCCG CACGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1396; ORF 509>:

m509.pep

```

1  MVAVCDKRAV QRTLMAQFAQ QGGLFLLFVQ AVVVFQACVL EKLGNHIGVF
51  ACVLAQVERH HVKAEHGYGT DEVCQTAFGK QTAAVVDKGT LQFFQIIQKL
101 LCRSIRLEKA EFAAHTQTER ARFAHSARHN VGDGAAGVFF GAGDFFVGRF
151 VGQRRYIAVD FDAADGERQF AVEFVEFAAI EAEHGIGVAA EGKAQGFGRN
201 KRIAVAVAAD PAADFEDVRN ADAGIGRLKV VFHLAVELGQ GFKAHREDG
251 HAVVDFVUDA EFVAARFAGL PQAQDSDVDF AAQPCQRVGI GAAAFALRQC
301 ADAAVEAXDG LALHFGRVRG QNGGNRIVQ LPLHRFAVGF PRFEPADGFR
351 QAAFRAAASG FFVDLAAAFV VHVFGDVQNL GEQAAGQGXI VGLLFVQLRQ
401 YFFNQCRVV GSGQEFDCFD NQRRGFFVQE VEQGLFQKFR VRRQSRVLWI
451 VQNMQLHDFS LSSAVNIVNV PQMPHPCQTV HTLTARVPKC RLKLNARRQ
501 RYNRPQLFFS EHHHDHRT RRCIPAAVQ PPHPLGRNRH RRAAETFRRA
551 YFGRRLRRFG CRRTXPTLPL RVSAR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 509 shows 87.8% identity over a 575 aa overlap with a predicted ORF (ORF 509.ng) from *N. gonorrhoeae*:

m509/g509

	10	20	30	40	50	60
m509.pep	MVAVCDKRAVQRTLMAQFAQQGGLFLLFVQAVVVFQACVLEKLGNHIGVFACVLAQVERH					
g509	MVAVCDERAVQRTLVQAQFQQGGLFLLFVQAVVVFQACVLEKLGNHIGVFACVLAQVERH					
	10	20	30	40	50	60
	70	80	90	100	110	120
m509.pep	HVKAHGYGTDEVCQTAFGKQTAAVVDKGTLQFFQIIQKL LCRSIRLEKA EFAAHTQTER					
g509	HVEAHHGHTDEVCQTAFGKQAAAVVDKGT LQFFQII EKFLGRSIRLEKA EFAAHTQTER					
	70	80	90	100	110	120
	130	140	150	160	170	180
m509.pep	ARFAHSARHNVDGAAGVFFGAGDFFVGRFVGQRRYIAVD FDAADGERQFAVEFVEFAAI					
g509	ARFAHSARHNVDGAAVRFFGAGDFFVRREGQCHYVVD FDAADGKRQFAVKFEFAAV					
	130	140	150	160	170	180

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	190	200	210	220	230	240
m509.pep	EAEHGIGVAAEGKAQGFGRNKR	IAVAVAADPAADFEDVRNADAG	IGRLKVVFHLAVELGQ			
	:::					
g509	KTEHGIGVAAEGKAQGFARNKRI	AVAVAADPAADFEDIRNADIG	IGRLKVVFHLAVEFCQ			
	190	200	210	220	230	240
	250	260	270	280	290	300
m509.pep	GFEKAHREDGHAVVDFVVD	AEFVAARFAGLPQAQ	QDSVDFAAQPCQ	RVGIGAAAFALRQ	QC	
g509	GFKKAHREDGHAVVDFVVD	AEFVAARFAGLPQAQ	KHGVDFAAQPCQ	RVGIGAAAFALRQ	QR	
	250	260	270	280	290	300
	310	320	330	340	350	360
m509.pep	ADAAVEAXDGLALHFG	RVRGQNGGNGRIVQL	PLHRFAVGFP	RFEPADGFRQA	AFRAAASG	
g509	ADAAVEIQNGLALHFG	RVRGQNGGNGRIVQL	PLHRFAVGFP	RFEPADGFRQA	AFCCVVAG	
	310	320	330	340	350	360
	370	380	390	400	410	420
m509.pep	FFVDLAAAFVHVFGD	VQNLGEQAAGQXIV	GLLFVQLRQYFF	NQCRAVVGSGQ	EFDCFD	
g509	IFVDLAAAFVHVFGD	IQNLGEQPAQKQIV	GLFFVQLRQYFF	NQCRAVVGSGQ	EFDRFD	
	370	380	390	400	410	420
	430	440	450	460	470	480
m509.pep	NQRRGFFVQVEVEQGL	FQKFRVRRQSRVL	WIVQNMQLHDFS	LSSAVNIVNVP	QMPHPCQTV	
g509	NQRRGFFVQVEVEQGL	FQKFRVRRQSRVL	RIVQDMQLHDFLI	-AVNTVNVP	QMPHPCQTV	
	430	440	450	460	470	
	490	500	510	520	530	540
m509.pep	HTLTARVPKCRLKLN	AARRQRYNRPQLFF	SEHHHDHRT	RQRRCPAAVQPP	PHPLGRNRH	
g509	HTLTTHVPKCRLKLN	AARRRRYNRPQLFF	SEHHHDHRT	RQRRRTPAVQPP	PHPLGRNRH	
	480	490	500	510	520	530
	550	560	570			
m509.pep	RRAAETFRRAYFG	RRLRRFGCRR	TCPTLPLRVSAR			
g509	RRAAEAFRRAYFG	RRLRRIGRR	PCPISPGRSAR			
	540	550	560	570		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1397>:

```

a509.seq
1  ATGGTCGCTG TATGTGATGA ACGGACTGTA CAGTGGACGT TGATGGCTCA
51  ATTCGCGCAA CAGGGCGGCT TGTTTTGTCT CTTCGTTGAG GCTCTTGTAG
101 TCTTCCAAGC CTGCGTGTTG GAAAAGCTCG GCAACCACAT CGGCGTGTTC
151 GCCTGCGTGT TGGCGCAGGT CGAGCGGCAT CATGTGGAAG CCGAACACGG
201 ATACGGAACG GATGAGGTCT GCCAAACGGC CTTCGGCAAG CAGGCGGCTG
251 CCGTTGTCGA TAAGGGAATG TTGCAATTTT TTCAAATCAT CGAGAAATTC
301 TTGTGCCGAA GCATAAGGCT CGAGAAAGCC GAATTTGCAG CCCATACCCA
351 AACCGAGCGC GCGCGCTTTG CCCATAGCGC GCGCCATAAT GTAGGCAATG
401 GCGCGACGGT AGGTTTCTTC GCGCGGGGCG GTTCTTCGCT CGGGCGATTT
451 GTCGGACAAC GCCATCACAT CGCCGTTGAC TTTGACGCGG CGGATGGAGA
501 GCGGCAGTTC GCGGTAGAGT TTGTGAGATT CGCCACGGTA AAAACGGAAC
551 ACGGCATCGG CGTGGCGGCG GAAGGCAAAA CGCAAGGTTT CGGCAGAAAC
601 GAACGGATTG CCGTCGCGGT CGCCGCCGAT CCAGCCGCCG ATTTTGAGGA
651 TGTCCGGAAC GCGGACATCG GGATAGGCCG TCTGAAAGTC GTGTTCCATC
701 TTGCGGTAGA GCTTGGGCAG GGCTTCAAAA AAGCTCATCG GAAAGATGGA
751 CACGCCGTTG TTGATTTGCT CGTTGACGCT GAGTTTGIGG CGGCGCGTTT
801 CGCTGGTCTG CCACAAGCCC AGCAGGATAG TGTCGATTTC GCGGCGCAGC
851 CGTGCCAGCG CGTCGGCATT GGTACAGCGT TCGCGTTGCG GCAGCAGCGC

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901 GCGGATGCGG CGGTTGAAAT TCAAGACGGT CTGGCGTTGC ACTTCGGTCG
951 GGTGCGCGGT CAAAACGGCG GTAACGGACG TATTGTCCAA CTGCCGCTGC
1001 ACCGATTTGC CGTCCGCTTT CCCCGCTTTG AGCCTGCGGA CGGTTTCCGT
1051 CAGGCTGCCT TCCGCGCCGC CGCGTCCGGC TTCTTCGTGG ATTTGGCGGC
1101 GCGGTTTCGT GTGCACGTCT TCGGCGATGT TCAAAATCTG GCGGAACAGG
1151 CCGCAGGCCA AGGTTAAATC GTGGGTTTGT TGTTCGTCCA ATTGCGGCAG
1201 TACTTTTTC AATCAATGCCG CGCTGTCTGC GGAAGTGGAC AAGAGTTTGA
1251 CCGTTTCGAC AACCAACGGC GAGGCTTCTT CGTGCAGGAG GTTGAACAGG
1301 GATTGTTTCA GAAATTCGCG GTCCGCGCCG AAAGCCGCGT CCTTTGGATT
1351 GTTCAGAATA TGCAGTTGCA TGATTTTCTT CTCATTGCCG TAAATACTGT
1401 AAATGTACCT CAAATGCCGC ATCCGTGCCA AACCGTTCAC ACTTTAACCG
1451 CCCGTGTCCC GAAATGCCGT CTGAAGTTGA ACGCCGCCCG ACGGCAGCGT
1501 TACAATCGCC CACAACGTGT TTT.TCCGAA CATCATCATG ACCACGACCG
1551 AACACGACAA CGACGATGCA TTCCTGCTGC GGTACAGCCG CCACATCCTC
1601 TTGGACGAAA TTGGCATCGA AGGCAGCAG AACTTTCCG CCGCGCATAT
1651 TTTGGTCGTC GGCTGCGCGC GTTTGGGTGC CGCCG.CCCT GGCCTATCTC
1701 GCCGTTCCG GCATCGGCAC GCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1398; ORF 509.a>:

```

a509.pep
1  MVAVCDERTV QWTILMAQFAQ QGGLFLLFVE AVVVFOACVL EKLGNHIGVF
51  ACVLAQVERH HVEAEHGYGT DEVCQTAFGK QAAAVVDKGM LQFFQIIEKF
101 LCRSIRLEKA EFAAHTQTER ARFAHSARHN VNGATVGGF GAGGFFVGRF
151 VGQRHHIAVD FDAADGERQF AVEFVEFATV KTEHGIGVAA EGKTQGFGRN
201 ERIAVAVAAD PAADFEDVRN ADIGIGRLKV VFHLAVELGQ GFKKAHRKDG
251 HAVVDFVDA EFVAARFAGL PQAQDSDVF AAQPCQRVGI GTAFALRQQR
301 ADAAVEIQDG LALHFGRVRG QNGNGRIVQ LPLHFAVGF PRFEPADGFR
351 QAAFRAAASG FFDLAAAFV VHVFGDVQNL GEQAAGQG*I VGLLFVQLRQ
401 YFFNQCRVV GSGQEFDRFD NQRRGFFVQE VEQGLFQKFR VRRQSRVLWI
451 VQNMQLHDFS LIAVNTVNVP QMPHPCQTVH TLTARVPKCR LKLNAARRQR
501 YNRQQLFXSE HHHHDHRTRO RRCIPAAVQP PHELGRNWHR RAAETFRRAY
551 FGRRLLRRFGC RXPCPISPLP ASAR*

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m509/a509 93.0% identity in 575 aa overlap

m509.pep	10	20	30	40	50	60
	MVAVCDKRAVQRTILMAQFAQQGGLFLLFVQAVVVFOACVLEKLGHNHIGVFACVLAQVERH					
a509	MVAVCDERTVQWTILMAQFAQQGGLFLLFVEAVVVFOACVLEKLGHNHIGVFACVLAQVERH					
m509.pep	70	80	90	100	110	120
	HVKAHEHGYGTDEVCQTAFGKQTAAVVDKGTLLQFFQIIQKLLCRSIRLEKAEFAAHTQTER					
a509	HVEAEHGYGTDEVCQTAFGKQAAAVVDKGM LQFFQIIEKFLCRSIRLEKAEFAAHTQTER					
m509.pep	130	140	150	160	170	180
	ARFAHSARHNVDGAAVGGFFGAGDFFVGRFVGRQRRYIAVDFDAADGERQFAVEFVEFAAI					
a509	ARFAHSARHNVNGATVGGFFGAGGFFVGRFVGRQRRHIAVDFDAADGERQFAVEFVEFATV					
m509.pep	190	200	210	220	230	240
	EAEHGIGVAAEGKAQGFGRNKRIVAVVAADPAADFEDVRNADAGIGRLKVVFHLAVELGQ					
a509	KTEHGIGVAAEGKTQGFGRNERIAVAVVAADPAADFEDVRNADAGIGRLKVVFHLAVELGQ					
m509.pep	250	260	270	280	290	300
	GFKAHREDGHAVVDFVDAEFVAARFAGLPQAQDSDVFAAQPCQRVGIGAFALRQQR					
a509	GFKKAHRKDGHAVVDFVDAEFVAARFAGLPQAQDSDVFAAQPCQRVGIGTAFALRQQR					
	310	320	330	340	350	360

m509.pep	ADA AVEAXDGLALHFGSRVRGQNGGNRIVQLPLHRFAVGFPFRFEPADGFRQA AFR AASG					
a509	ADA AVEIQDGLALHFGSRVRGQNGGNRIVQLPLHRFAVGFPFRFEPADGFRQA AFR AASG	310	320	330	340	350 360
m509.pep	FFVDLAAA FVVHVFGDVQNLGEQAAGQGXI VGLLFVQLRQYFFNQCRAVVGS GQEFDCFD	370	380	390	400	410 420
a509	FFVDLAAA FVVHVFGDVQNLGEQAAGQGXI VGLLFVQLRQYFFNQCRAVVGS GQEFDRFD	370	380	390	400	410 420
m509.pep	NQRRGFFVQEVEQGLFQKFRVRRQSRVLWIVQNMQLHDFS LSSAVNIVNVPQMPHP CQTV	430	440	450	460	470 480
a509	NQRRGFFVQEVEQGLFQKFRVRRQSRVLWIVQNMQLHDFS LI-AVNTVNVPQMPHP CQTV	430	440	450	460	470
m509.pep	HTLTARVPKCR LKLNAARRQRYNRPQLFFSEHHHDH DTRQRR CIPAAVQPPHPLGRNRH	490	500	510	520	530 540
a509	HTLTARVPKCR LKLNAARRQRYNRPQLFXSEHHHDH DTRQRR CIPAAVQPPHPLGRNWH	480	490	500	510	520 530
m509.pep	RRAAETFRRAYFGRRLRRFGCRRTXPTLP LRV SARX	550	560	570		
a509	RRAAETFRRAYFGRRLRRFGCRXPCFIPSP LFA SARX	540	550	560	570	

```
g510.seq
1  atgccttcgc ggacaccgca gggaaaaagg ggttattcct gccccaagcg
51  ggatagtgcc ttttggcagg cgttggtcca atcgggttatt tacgcgcgcaa
101 aatcgccyatt tgccaaatcg gcgcggttca gggagggtttt caataggtcg
151 tggacgacgt tgcgcgcggc cataatgacg attttttcgc tgcgcgcgac
201 gcggccgect tcgcggatgg cttcggtttt gccgttgagc attccgactg
251 cctgcaacag tgtgtctttt tctctcgccg gcgtgttgac agtcagccgg
301 ggcgtgcatg acttcgatgt agacttgttc gatgttcate ctttaatect
351 tattactacg tttctctacc ttggggagag cgcactgaca atgcgctga
```

g510.pep
1 MPSRTPOGKR GYSCPKRDSA FWQALSISVI LRAKSPIAKS PPFREVFNRS
51 WTTLSAAIMT IFSLSATRPP SRMASALPLS IPTACNSVSF SSAGVLTCSR
101 GVHDFDVDLF DVHPLILIAA FPAVGGGALP VR*

```
m510.seq
1  ATGCCTTCGC GGACACCGCA GGGnAAAAGG GGTATTCTCT GCGCCAAGCG
51  GGATAGTGGT TTTTGGCAGG CCGTGTCCAT ATCGGCTATT TTACGCGCAA
101 AATCGCCGAT TGCCAAATCG CGGTGGCTTA CGAGAGCTTT CAACAGGTGC
151 TGGACGACGT TGAGCGCGGC CATAATGACG ATTTTTTCGC TGTCCGCGAC
201 GCGTCGCGCT TCGCGGATGG CTTGCGCTTT GCCGTTGAGC ATTCGGACTG
251 CCTGCAACAG TGTGTCTTTT TCTTCTGCCG GCGTGTTCAC GGTGACGCGG
301 GGCCTGCaWg ACTTcSaTgT GGACTTGTTC GATGTTGCAT CTTTAACTCG
351 TATTGCTGCG TTTCTTGCCA TTGGGGGAGG CGCGCTGCCA GTGCGCTGTA
```

m510.pep

1	MPSRTPQGKR	GYSCAKRDSA	FWQALSISAI	LRAKSPIAKS	PPFREVENRS
51	WTTLSAAIMT	IFSLSATRPP	SRMASALPLS	IPTACNSVSF	SSAGVLTCSR
101	GVXDFXVDLF	DVHPLILIAA	FPAIGGGALP	VR*	

Computer analysis of this amino acid sequence gave the following results:

761

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 510 shows 96.2% identity over a 132 aa overlap with a predicted ORF (ORF 510.ng) from *N. gonorrhoeae*:

m510/g510

	10	20	30	40	50	60
m510.pep	MPSRTPQGKRGYSCAKRDSA FWQALSISAILRAKSPIAKSPPFREVFNRSWTTLSAAIMT					
g510	MPSRTPQGKRGYSCPKRDSA FWQALSISVILRAKSPIAKSPPFREVFNRSWTTLSAAIMT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m510.pep	IFSLSATRPPSRMASALPLSIPTACNSVSFSSAGVLT VSRGVXDFXVDLFDVHPLILIAA					
g510	IFSLSATRPPSRMASALPLSIPTACNSVSFSSAGVLT VSRGVHDFDVLFDVHPLILIAA					
	70	80	90	100	110	120
	130					
m510.pep	FPAIGGGALPVRX					
g510	FPAVGGGALPVRX					
	130					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1403>:

a510.seq

```

1  ATGCCTTCGC GGACACCGCA GGGAAAAAGG GGTATTTCCT GCGCCAAGCG
51 GGATAGTGCT TTTTGGCAGG CGTTGTCCAT ATCGGCTATT TTACGCGCAA
101 AATGCGCGAT TGCCAAATCG CCGCCGTTCA GGGAGGTTT CAACAGGTCTG
151 TGGACGACGT TGAGCGCGGC CATAATGACG ATTTTTTCGC TGTCGCGCAG
201 GCGTCCGCCT TCGCGGATGG CTTGGCTTT GCCGTGAGC ATTCGACTG
251 CCTGCAACAG TGTGTCTTT TCTTCTGCG GCGTGTGAC GGTGAGCCGG
301 G.CGTGCATG ACTTCGATGT GGA CTGTGTTGATGTTTC GATGTTTCATC CTTAATCTCT
351 TATTGCTGCG TTTCTGCGG TTGGGGGAGG CCGCTGCCA GTGCGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1404; ORF 510.a>:

a510.pep

```

1  MPSRTPQGKR GYSCAKRDSA FWQALSISAI LRAKSPIAKS PPFREVFNR
51 WTTLSAAIMT IFSLSATRPP SRMASALPLS IPTACNSVSF SSAGVLT VSR
101 XVHDFDVLDF DVHPLILIAA FPAVGGGALP VR*

```

m510/a510 97.0% identity in 132 aa overlap

	10	20	30	40	50	60
m510.pep	MPSRTPQGKRGYSCAKRDSA FWQALSISAILRAKSPIAKSPPFREVFNRSWTTLSAAIMT					
a510	MPSRTPQGKRGYSCAKRDSA FWQALSISAILRAKSPIAKSPPFREVFNRSWTTLSAAIMT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m510.pep	IFSLSATRPPSRMASALPLSIPTACNSVSFSSAGVLT VSRGVXDFXVDLFDVHPLILIAA					
a510	IFSLSATRPPSRMASALPLSIPTACNSVSFSSAGVLT VSRXVHDFDVLFDVHPLILIAA					
	70	80	90	100	110	120
	130					
m510.pep	FPAIGGGALPVRX					
a510	FPAVGGGALPVRX					
	130					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1405>:

g512.seq

```

1  atgaaagtgc ttgttttagg tgcgggtgtt gccggcgat cctccgtgtg

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762

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51  gtatctggca gaggccggac atgaagtaac ggtcatcgac cgcaccgagg
101 gtgtggcgat ggaaaccagt tttgccaatg caggccagct ttcttacggc
151 tataccacgc cttgggcgc acccggtatt ccgaccaaag cactgaaacg
201 gctgtttaa agccatccgc ctttactgtt ccgccctgac ggcggcctgt
251 atcaaatcga atggtctgtg cggaatgctc aaaactgcac ggcaacgcgc
301 tatcaaatca ataaagagcg catggtcagg atttccgaat acagccgtga
351 aatgttccgc cgttttgaag cgcaaaccga catgaatttt gagggacgca
401 aaaaaggac gttgcagatt ttccgccaaa ccgaagaagt cgaagcggca
451 aaacaagaca ttgccgtttt ggaacgctac ggcgtgccgt accgccgtct
501 gaagcccgaa gaatgcgcag aattcgagcc tgcgtggca cgcgttaccg
551 ccaaaattgt cggcggctcg cacctgcctg cggatgcgac cggcgactgc
601 cgcctcttca ccgaaaacct gtacaaattg tgtcaagaga agggggtacg
651 gttctacttc aaccaaacca tcagccgcat cgaccacaac gggctgcgca
701 tcaaagccgt tgaacgaaa cagggcggtt tgaacagat gccgttgtct
751 gcgcgctcgg ctgcttcagc aggactgtgt tggcgcagtt ggatctcaat
801 ctgcccattt atcccgtaa aggtatttcc ttga

```

This corresponds to the amino acid sequence <SEQ ID 1406; ORF 512.ng>:

g512.pep

```

1  MKVLVLGAGV AGVSSVWYLA EAGHEVTVID RTEGVAMETS FANAGQLSYG
51  YTPWAAPGI PTKALKRLFK SHPPLLFRPD GGLYQIEWLW RMLQNCTATR
101 YQINKERMVR ISEYSREMFR RFEAQDTMNF EGRKKGTLQI FRQTEEEVAA
151 KQDIAVLERY GVPYRRLKPE ECAEFEPALA RVTAKIVGGL HLPADATGDC
201 RLFTENLYKL CQEKGVRFYF NQTISRIDHN GLRIKAVETK QGGLKQMPLS
251 ARSAASAGLC WRSWISICPF IPSKAIP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1407>:

m512.seq (partial)

```

1  ..GTTTGGAAAC GCTACGGCGT GCCGTACCGC CGTCTGAAAC CCGAAGAATG
51  TGCAGAAATT GAGCCTGCGC TGGCACGCGT TACCGCCAAA ATTGCCGGCG
101 GCCTGCACCT GCCTGCAGAT GCGACCGCG ACTggCGCCT CTTCACTGAA
151 AACCTATACA AATTGTGTCA GGAAAAGGGC GTACGGTTTC ATTTCAACCA
201 AAACATCAGC CGCATCGACC ACAACGGGCT GCGCATCAAA ACCGTTGAAA
251 CCAAACAGGG CGGTTTGAAG CAGATGCCGT TGTCTGCGCG CTCGGTTGCT
301 TCAGCAGGAC GGTTTTGGCG CAGTTGGATC TCAATCTGCC CATTATCCC
351 GTCAAAGGCT ATTCCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1408; ORF 512>:

m512.pep (partial)

```

1  ..VLERYGVPYR RLKPEECAEF EPALARVTAK IAGGLHLPAD ATGDWRLFTE
51  NLYKLCQKEG VRFHFNONIS RIDHNLRIK TVETKQGLK QMPLSARVA
101 SAGRFWRWI SICPFIPSKA IP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 512 shows 93.4% identity over a 122 aa overlap with a predicted ORF (ORF 512.ng) from *N. gonorrhoeae*:

m512/g512

m512.pep				10	20	30
				VLERYGVPYRRLKPEECAEFEPALARVTAK		
g512						
	130	140	150	160	170	180
m512.pep	40	50	60	70	80	90
	IAGGLHLPADATGDWRLFENLYKLCQKEKGVRFHFNONISRIDHNLRIKTVETKQGLK					
g512	: : : : : :					
	190	200	210	220	230	240
m512.pep	100	110	120			
	QMPLSARSVASAGRFWRWISICPFIPSKAIP					
g512	:					
	QMPLSARSAASAGLCWRSWISICPFIPSKAIP					

```
a512.seq
1  ATGAAAGTGC TTGTTTTAGG TGCTGGTGTT GCCGGCGTAT CTTCCGCGTG
51  GTATCTGGCA GAGGCAGGAC ATGAAGTAAC GGTATCTGAC CGCGCCGAGG
101 GCGTGGCGAT GGAACCAGAT TTTGCCAACG CAGGCCAGCT TTCTTACGGC
151 TATACACAGC CTTGGGCTGC ACCCGGTATT CCGACCAAAG CACTGAAATG
201 GCTGTTTAAA AGCCATCCGC CTTTGCTGTT TCGCCCCGAC GGCAGCCTGT
251 ATCAAATCGA ATGGCTGTGG CAGATGCTGC AACACTGCAC GGCAGCGCGC
301 TATCAATATCA ATAAGAGCGC CATGGTCAAG ATGTCCGAAT ACAGCCGTGA
351 AATGTTCCCG CGTTTGAAG CGCAAAACGG CATGAATTTT GAGGGACGCA
401 AAAAAGGGAC GTTGCAGATT TTCCGCCAAA CCAAAGAAGT C3AAGCGCCA
451 AAACAAGACA TTCCCGTTTT GGAACGCTAC GCGGTGCCGT ACCGCCGTCT
501 GAAGCCCGCA GAATGCGCAG AATTCTGAGCC TCGCTTGSCA CGCGTTACTG
551 CCAAATATGC CGCGGCGCTG CACCTGCGCG CAGCAGCGAC CGGCGATTGC
601 CGCCTCTTCA CTGAAAACCT GTACAAATTG TGTACAGAAA AGGGCGTACG
651 GTTTCATTTT AACCAAACCA TCAGCCGCAT CGACCACAAC GGGCTGCGCA
701 TCAAACCGT TGAACAGCAA CAGGGCGGTT TGAAGCAGAT GCCGTTGTCT
751 GCGCGCTCGG CTGCTTCAGC AGGACGGTTT TGCGCAAGT GGATCTCAAT
801 CTGCCGATT ATCCCGTCAA AGGCTATTCC TTGA
```

a512.pep

1	MKVLVLGAGV	AGVSSAWYLA	EAGHEVTVID	RAEGVAMETS	FANAGQLSYG
51	YTPPWAAPI	PTKALKWLFL	SHPLLFRPD	GSLYQIEWLW	QMLQHCCTAAR
101	YQINKRMVR	MSEYSREMR	RFEAQTGMNF	EGRKKGTLOI	FRQKVEEAA
151	KQDIAVLRY	GVFPYRLKPE	ECAEFEPALA	RVTAKIAGGL	HLPADATGDC
201	LRFTENLYKL	CQEKGVRFHF	NQTSRIDHN	GLRIKTVETK	QGGLKQMPLS
251	ARSAASAGRF	WRKWISICRF	IPSKAIP*		

```

m512.pep                                10      20      30
                                         VLERYGVPYRLRKPEECAEFEPALARVTAK
                                         |||||
a512      TGMNFEGRKKGTLQIFRQTKVEAAKQDIAVLERYGVPYRLRKPEECAEFEPALARVTAK
           130      140      150      160      170      180

           40      50      60      70      80      90
m512.pep      IAGGLHLPADATGDWRLFTENLYKLCQEKGVRFHFNQNISRIDHNGLRIKTVETKQGGGLK
           |||||
a512      IAGGLHLPADATGDCRLFTENLYKLCQEKGVRFHFNQTIISRIDHNGLRIKTVETKQGGGLK
           190      200      210      220      230      240

           100      110      120
m512.pep      QMPLSARSVASAGRFWRSWISICPFIPSKAIPX
           |||||:|||||:|||||
a512      QMPLSARSAASAGRFWRKWISICRFIPSKAIPX
           250      260      270

```

```

g513.seq
1  ATGGGTTCCG  CGCCGAACGC  CGCCGCGGCC  GCCGAAGTGA  AACACCCTGT
51  TTCGCAAGGT  ATGATTCAA  TGCTGGGCGT  GTTGTGCGAT  ACCATCATCG
101  TTGTTCTTG  CACCGCCTTC  ATCATCTTGA  TTTACCAACA  GCCTTATGGC
151  GATTTGACG  GTGCGGCGCT  GAcgcAGGCG  GCGATTGTCA  GCCAAGTGGG
201  GCAATGGGGC  GCGGGTTTCC  TCGCGCTCAT  CCTGTTTATG  TTTGCCPTTT
251  CCACCGTTAT  CGGCAACTAT  GCCTATGCCG  AGTCCAACGT  CCAATTTCATC
301  AAAAGCCATT  GGCTGATTAC  CGCCGTTTTC  CGTATGCTGG  TTTTGGCGTG
351  GGCTCTATT  GCGCGGGTTG  CCAATGTGCC  TTTGGTCTGG  GATATGGCGG
401  ATATGGCGAT  GGGCATCATG  CGGTGGATCA  ACCTCGTCGC  CATCCTGCTG
451  CTCTCGCCat  TGGCGTTTAT  GCTGCTGCGC  GATTACACCG  CCAAGCTGAA

```

764

501 AATGGGCAAA GACCCCGAGT TCAAACCTTc cgAACATCCG GGCCTGAAAC
 551 GCCGCATCAA ATCCGATGTT TGGTAA

This corresponds to the amino acid sequence <SEQ ID 1412; ORF 513.ng>:

g513.pep

1 MGSAPNAAAA AEVKHPVSQG MIQMLGVFVD TIIVCSCTAF IILIYQQPYG
 51 DLSGAALTQA AIVSQVGQWG AGFLAVILEM FAFSTVIGNY AYAESNVQFI
 101 KSHWLITAVF RMLVLAWVYF GAVANVPLVW DMADMAMGIM AWINLVAILL
 151 LSPLAFMLLR DYTAKLKMKG DPEFKLSEHP GLKRRIKSDV W*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1413>:

m513.seq

1 ATGGGTTCCG CGCCGAACGC CGCCGCCGCC GCCGAAGTGA AACACCCTGT
 51 TTCGAAGGT ATGATTCAAA TGCTGGGCGT GTTTGTCGAT ACCATCATCG
 101 TTTGTTCTTG CACCGCCTTC ATCATCTTGA TTTACCAACA GCCTTATGGC
 151 GATTTGAGCG GTGCGGCGCT GAcgcAGGCG GCGATTGTCA GCCAAGTGGG
 201 GCAATGGGGC GCGGCTTTC TCGCCGTCAT CCTGTTTATG TTTGCCTTTT
 251 CCACCGTTAT CGGCAACTAT GCCTATGCCG AGTCCAACGT CCAATTCATC
 301 AAAAGCCATT GGCTGATTAC CGCCGTTTTC CGTATGCTGG TTTTGGCGTG
 351 GGTCTATTTT GCGCGGTTG CCAATGTGCC TTTGGTCTGG GATATGGCGG
 401 ATATGGCGAT GGGCATCATG GCGTGGATCA ACCTCGTCGC CATCCTGCTG
 451 CTCTCGCCat TGGCGTTTAT GCTGCTGCGC GATTACACCG CCAAGCTGAA
 501 AATGGGCAAA GACCCCGAGT TCAAACCTTc cgAACATCCG GGCCTGAAAC
 551 GCCGCATCAA ATCCGATGTT TGGTAA

This corresponds to the amino acid sequence <SEQ ID 1414; ORF 513>:

m513.pep

1 MGSAPNAAAA AEVKHPVSQG MIQMLGVFVD TIIVCSCTAF IILIYQQPYG
 51 DLSGAALTQA AIVSQVGQWG AGFLAVILEM FAFSTVIGNY AYAESNVQFI
 101 KSHWLITAVF RMLVLAWVYF GAVANVPLVW DMADMAMGIM AWINLVAILL
 151 LSPLAFMLLR DYTAKLKMKG DPEFKLSEHP GLKRRIKSDV W*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 513 shows 99.5% identity over a 191 aa overlap with a predicted ORF (ORF 513.ng) from *N. gonorrhoeae*:

m513/g513

	10	20	30	40	50	60
m513.pep	MGSAPNAAAAAEVKHPVSQGMQMLGVFVDTIIVCSCTAFIILIYQQPYGDLSGAALTQA					
g513	MGSAPNAAAAAEVKHPVSQGMQMLGVFVDTIIVCSCTAFIILIYQQPYGDLSGAALTQA					
	10	20	30	40	50	60
	70 80 90 100 110 120					
m513.pep	AIVSQVGQWGAGFLAVILFMFAFSTVIGNYAYAESNVQFIKSHWLITAVFRMLVLAWVYF					
g513	AIVSQVGQWGAGFLAVILFMFAFSTVIGNYAYAESNVQFIKSHWLITAVFRMLVLAWVYF					
	70	80	90	100	110	120
	130 140 150 160 170 180					
m513.pep	GAVANVPLVWDMADMAMGIMAWINLVAILLSPLAFMXLRDYTAKLKMKGKDPEFKLSEHP					
g513	GAVANVPLVWDMADMAMGIMAWINLVAILLSPLAFMLLRDYTAKLKMKGKDPEFKLSEHP					
	130	140	150	160	170	180
	190					
m513.pep	GLKRRIKSDVW					
g513	GLKRRIKSDVW					
	190					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1415>:

a513.seq

765

```
1  ATGAACGAGA  ACCTTACCGA  ATGGCTGCAC  GGCTGGGTCG  GCGCCATCAA
51  CGATCCGATG  TGGTCATACT  TGGTTTATNT  GCTTTTGGGT  ACGGGGCTTT
101 TCTTCACCGT  AACCACGGGC  TTTGTCCAAT  TCCGCCTGTT  CGGGCGCAGC
151 ATCAAAGAAA  TGCTCGGCGG  CCGCAAACAG  GGGGACGACC  CTCACGGCAT
201 CACGCCGTTT  CAGGCATTTG  TAACCGGCCT  TGCCAGCCGC  ETGGGCGTGG
251 GCAATATCGC  GGGCGTGGCC  ATCGCCATCA  AAGTCGGCGG  ACCGGGCGCG
301 GTGTTTGGGA  TGTGGGTAAC  CGCCTTAATC  GGTATGAGTT  CGGCGTTTGT
351 CGAATCTTCG  CTGGCGCAGC  TCTTTAAAGT  CCGCGACTAC  GACAACCACC
401 ATTTCCGGGG  CGGCCCTGCC  TACTACATCA  CTCAAGGCGT  GGGCAGAAAA
451 TGGCTGGGCG  TGTGTTCGCG  CCTGAGCCTG  ATTTTCTGTT  TCGGCTTTGT
501 GTTTGAAGCG  GTTCAGACCA  ATACCATTGC  CGATACCGTC  AAAGCGGCGT
551 GGGGTGTTGG  GCCTCATTAT  GTCGGCGTCG  CCCTGGTGAT  TTTAACC CGG
601 CGGATATATC  TCGGCGGCAT  CAGGCGCATA  TCTAAAGCGG  CGGAAATCGT
651 CGTCCCCCTG  ATGGCGGTTT  TGTACCTCTT  TATCGCGGCT  TTCATCATTT
701 TGACCAATAT  TCCGATGATT  CCGGACGTGT  TCGGTCAGAT  TTTTTCGGGC
751 GCGTTCAAAT  TCGACGCGGC  AGCAGGCGGC  TTA CTGCGG  GTCTGATTTC
801 GCAAACGATG  ATGATGGGCA  TCAAACGCGG  CCTGTATTCC  AACGAGGCGG
851 GTATGGGTTT  CGCGCCGAAC  GCCGCCGCCG  CCGCCGAAGT  GAAACACCCT
901 GTTTCCCAAG  GTATGATTCA  AATGCTGGGC  GTGTTTGTCT  ATACCATCAT
951 CGTTTGTCTT  TGCACCGCCT  TCATCATCTT  GATTTACCAA  CAGCCTTACG
1001 GCGATTTGAG  CGGTGCGGCG  CTGACGCAGG  CGGCGATTGT  CAGCCAAGTG
1051 GGGCAATGGG  GCGCGGGCTT  CCTCGCGCTC  ATCCTGTTTA  TGTTCGCCTT
1101 TTCCACCGTT  ATCGGCAACT  ATGCCTATGC  CGAGTCCAAC  GTCCAATTCA
1151 TCAAAGCCA  TTGGCTGATT  ACCGCCGTTT  TCCGTATGCT  GGTTTGGCG
1201 TGGGTCTATT  TCGGCGCGGT  TGCCAATGTG  CCTTTGGTCT  GGGATATGGC
1251 GGATATGGCG  ATGGGCATTA  TGGCGTGGAT  CAACCTTGTC  GCCATCTGCG
1301 TGCTCTCGCC  CTTGGCGTTT  AIGCTGCTGC  GCGATTACAC  CGCCAAGCTG
1351 AAAATGGGCA  AAGACCCCGA  GTTCAAACCT  TCCGAACATC  CGGGCCTGAA
1401 ACGCGGTATC  AAATCCGACG  TTTGGTAA
```

This corresponds to the amino acid sequence <SEQ ID 1416; ORF 513.a>:

```
a513.pep
1  MNENFTEWLH  GWVGAINDPM  WSYLVYXLLG  TGLEFTVTTG  FVQFRLFGRS
51  IKEMLGGRKQ  GDDPHGITPF  QAFVTGLASR  VGVGNIAGVA  IAIKVGGPGA
101 VFWMWVTALI  GMSSAFVESS  LAQLFKVRDY  DNHHFRGGPA  YYITQGLGQK
151 WLGVLFALSL  IFCFGVFEEA  VQNTIADTV  KAAWGWEPHY  VGVALVILTA
201 PIIFGGIRRI  SKAAEIVVPL  MAVLYLFIAL  FIILTNI PMI  PDVFGQIFSG
251 AFKFDAAAGG  LLGLISQTM  MMGIKRLYS  NEAGMGSAPN  AAAAAEVKHP
301 VSQGMQMLG  VFVDTIIVCS  CTAFIILIYQ  OPYGDLSGAA  LTQAAIVSQV
351 GQWGAGFLAV  ILFMFAFSTV  IGNYAYAESN  VQFIKSHWLI  TAVFRMLVLA
401 WVYFGAVANV  PLVWDMADMA  MGIMAWINLV  AILLLSPLAF  MLLRDYTAKL
451 KMGKDPEFKL  SEHPGLKRRI  KSDVW*
```

m513/a513 100.0% identity in 191 aa overlap

```

                                     10      20      30
m513.pep                               MGSAPNAAAAAEVKHPVSQGMQMLGVFVD
                                     |||
a513      DAAAGLLGLISQTM MMGIKRLYSNEAGMGSAPNAAAAAEVKHPVSQGMQMLGVFVD
               260      270      280      290      300      310

               40      50      60      70      80      90
m513.pep      TIIVCSCTAFIILIYQQPYGDLSGAALTQAAIVSQVGWAGFLAVILFMFAFSTVIGNY
               |||
a513      TIIVCSCTAFIILIYQQPYGDLSGAALTQAAIVSQVGWAGFLAVILFMFAFSTVIGNY
               320      330      340      350      360      370

               100      110      120      130      140      150
m513.pep      AYAESNVQFIKSHWLITAVFRMLVLAVVYFGAVANVPLVWDMADMAMGIMAWINLVAILL
               |||
a513      AYAESNVQFIKSHWLITAVFRMLVLAVVYFGAVANVPLVWDMADMAMGIMAWINLVAILL
               380      390      400      410      420      430

               160      170      180      190
m513.pep      LSPLAFMLLRDYTAKLMGKDPEFKLSEHPGLKRRIKSDVWX
               |||
```

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a513 LSPLAFMLLRDYTAKLMGKDPEFKLSEHPGLKRRIKSDVWX
440 450 460 470

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1417>:

g515.seq
1 atggttcaaa tacaggttgt gcgcgcgcgc gccgttgccc gtggtctgca
51 ttccgagttt gcgcgcgcgc taactgccga ggaaatagcc ttcgacaatg
101 ccgttttgaa tcacgaagcg cggcgcggtg gcaacacctt ccgcatcaaa
151 atagctgctg cggaagagcg ggggatgtg cggttcttcg cgcaggttga
201 ggaaatcggg caggactttt ttgccgatgc tgcgatcag gaaactgctt
251 tggcggtaga gcgcgcgcgc ggagagtgtg ccgacgaggt gtccgatcag
301 cccgcccgaa acggtggtat cgaagaggac ggggtagctg cctgtcggga
351 tgctgcggct gccgagtcgg cgcaaagtgc ggcggcgccg cgtttgaccg
401 atggtttcgg gctgtccat atccgatgg cggcaggcgg aatcgtacca
451 gtagtcgcgc tgcattccgt ttctgtcggc ggcgacgacg ctgcaggaaa
501 tgctgtggtg cgtgctttgc cgggtgtcgg caaaaccgtg ggtgttgccg
551 taaacgtatt ggtactgtcc ggtttgcacc gccgcgcctt cggagttttc
601 gatgcggctg tccgtgtcca acgctgcctg ttccgattgt tttgccaaagc
651 cgacggcggc ttccgtatcc aaatccatt cgtggttaaag gtcggggctg
701 ccgatgtgtt gcgccatcaa ctcggggtcg gcaagtcggc cgcaaccgtc
751 ttcggcggtg tggcgggcga tgcggcggc ggcgcggacg gtgtcgcgca
801 gggcttgctt ggagaagcg gcggtgccgg cgcgcgcctt gcgtttgccg
851 acgtaaacgg taatgtccag cgatttgtcc tgcgtggaact cgatttgttc
901 gatttcgccc aagcgacgc tgacgctttg tccgagcgat tcgctgaagt
951 cggcttcggc ggcggtcgcg cccgctgctt ttgccaagtc gagcgtgcgg
1001 cggcagaggt cgaggagttc ggaagcgggt tgggtgaaca gcataacaat
1051 ctttcttggt ggagcgttgt ggcattttta

This corresponds to the amino acid sequence <SEQ ID 1418; ORF 515.ng>:

g515.pep
1 MVQIQVVRAA GVARGLHSEF ARAVTAEIEA FDNVLNHEA RRGNTFRIK
51 IAAERAGDV RFFAQVEEIG QDFFADAVDQ ETALAVERAA GECADDEVSDQ
101 PARNGGIEED GVAACRDAAG AESAQSAAGG GLTDGFGAVH IRMAAGGIVP
151 VVALHSVFVG GDDAAGNAV V RALPVCCKTV GVAVNVLVLS GLHRRAFGVF
201 DAAVRVQRCL FALFCQADGG FRIQIPFVVK VGVADVLRHQ LGVKSGATV
251 FGGVAGDVGG GADGVAQGLF GEVGGAGAAF AFADVNGNVQ RFVLELDLF
301 DFAQAHADAL SERFAEVGFG GGRARCFCQV ERAABVEEF GSGVVEQHNN
351 LSWSVVAF*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1419>:

m515.seq (partial)
1 ..GGAAAGAGCG GGGGATGTGC GTTCTTCGCG CAGGTTGAGG AAATCGGGCA
51 GGACTTTTCT GCCGATGCTG TCGATCAGGA AACTGCTTTG GCGGTAGAGC
101 GCGCCGCCCG AGAGTGCGCC GACGAGGTGT CCGATAAGAC CGCCCGAAAC
151 GGTGGTATCG AAGAGGACCG GGTAGCTGCC TGTCCGGATG CTGCGGCTGC
201 CGAGTCGGCG CAAAGTGCGG CCGGCGGCGG TTTGACCGAT GGTTCGGGG
251 CTGTCCATAT CCGGATGGCG GCAGGCGGAA TCGTACCAGT AGTCGCGCTG
301 CATGCCGTTT TCGTCGGCGG CAACGACGCT GCAGGAAATG CTGTGGTGCG
351 TGCCTTGCCG GTGTGCGGCA AAACCGTGGG TGTGCCGTA AACGTATTGG
401 TAATGGCCCG TTGACCCGCG CGCGCCTTCG GAGTTTTCGA TCGCTCATC
451 CTCGTTTCAAG GCGGCTTGTT CGCATTGTTT TGCCAAGCCG ACGGCGGCTK
501 CCGTATCCAA ATCCCATTCG TGGTAAAGGT CCGGGTCGCC GATGTGTTTT
551 GCCATCAGAC AGGCATCGGC AAGTCCGGCG CAACCGTCTT CCGCGGTGTG
601 CCGGCGGATG TCGATGGCGG CTTGACGGT GTCTTGCAAG GCTTTTTCGG
651 AGAAGTCGGC AGTACTGGCG CGGCCTTTCG GTTTGCCGAC GTAAACGGTA
701 ATGTCCAGCG ACTTGTCTTG CTGGAACGCG ATTTGTTsGA TTTsGCCAG
751 CCGCACGCTG ACGCTTTGTC CCAATGATTC GCTGAAATCG GCTTCGGCGG
801 CGGTTGCGCC CGTCGCTTTT GCCAAGTCGA GCGTGGCGCG GCAGAGGTG
851 AGGAGTTCGG AAGCGGTGTG GTTgAACAGC ATAGAAATCT TTCTTGATGA
901 TGCTTTGCGG CATTTTAA

This corresponds to the amino acid sequence <SEQ ID 1420; ORF 515>:

m515.pep (partial)

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```

1  ..GKSGGCAFFA QVEEIGQDFS ADAVDQETAL AVERAAGECA DEVSDKTARN
51  GGIEEDGVAA CRDAAAESA QSAAGGLTD GFGAVHIRMA AGGIVPVVAL
101 HAVFVGGNDA AGNAVVRALP VCGKTVGVAV NVLVMAGLHR RAFGVFDALI
151 LVQGGFLFALF CQADGGXRIQ IPFVVKVGVA DVFCHQTGIG KSGATVFGGV
201 AGDVGDFG VLQFFGEVG STGAFAFAD VNGNVQRLVL LELDLXDXAQ
251 PHADALSQXF AEIGFGGCA RRFCQVERAA AEVEEFGSGV VEQHRNLSXX
301 CFAAF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 515 shows 85.9% identity over a 304 aa overlap with a predicted ORF (ORF 515.ng) from *N. gonorrhoeae*:

m515/g515

```

                                10      20      30
m515.pep                      GKSGGCAFFAQVEEIGQDFSADAVDQETALA
                                ::|  |||||  |||||  |||||  |||||  |||||
g515      AEEIAFDNAVLNHEARRGGNTFRIKIAAAERAGDVRFFAQVEEIGQDFFADAVDQETALA
                                30      40      50      60      70      80

                                40      50      60      70      80      90
m515.pep      VERAAGECADEVSDKTARNGGIEEDGVAAACRDAAAESAQSAAGGLTDGFGAVHIRMAA
|||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
g515      VERAAGECADEVSDOPARNGGIEEDGVAAACRDAAAESAQSAAGGLTDGFGAVHIRMAA
                                90      100     110     120     130     140

                                100     110     120     130     140     150
m515.pep      GGIVPVVALHAVFVGGNDAAGNAVVRALPVCCKTVGVAVNVLMAGLHRRRAFGVFDALIL
|||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
g515      GGIVPVVALHSVFVGGDDAAGNAVVRALPVCCKTVGVAVNVLVLSGLHRRRAFGVFDAAVR
                                150     160     170     180     190     200

                                160     170     180     190     200     210
m515.pep      VOGGLFALFCQADGGXRIQIPFVVKVGADVDFCHQTGIGKSGATVFGGVAGDVGDFG
||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
g515      VQRCFLFALFCQADGGFRIQIPFVVKVGADVLRHLQGVGKSGATVFGGVAGDVGGGADGV
                                210     220     230     240     250     260

                                220     230     240     250     260     270
m515.pep      LQGFGEVGVSTGAFAFADVNGNVQRLVLELDLXDXAQPHADALSQXFAEIGFGGGCAR
||:  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
g515      AQGLFGEVGGAGAAFAFADVNGNVQRFVLELDLDFDAQAHADALSERFAEVFGGGRAR
                                270     280     290     300     310     320

                                280     290     300
m515.pep      RFCQVERAAAEVEEFGSGVVEQHRNLSXXCFAAF
|||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
g515      CFCQVERAAAEVEEFGSGVVEQHNNLSWWSVVAF
                                330     340     350

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1421>:

a515.seq

```

1  ATGGTTCAAA TAAAGGTGTT GCGCGCCGCC GCGTTGCCCC GTGGTCTGCA
51  TTCCGAGTTT GCGCGCGCTG TAACTGCTGA GGAATAGCC TTCGACAATG
101 CCGTTTGTAA TCACGAAGCG CGGTGCGGTG GCAACGCTT CCGCATCAAA
151 ATAGCTGCTG CGGAAAGAGC GGGGGATGTG CGGTTCTTCG CGCAGGTGA
201 GGAATCGGG CAGGACTTTT TTGCCGATGC TGTCGATCAG GAACTGCTT
251 TGGCGGTAGA GCGCTCCGCC GGAGAGTGCG CCGACGAGGT GTCCGATAAG
301 ACCGCCCCGA ACGGTGGTAT CGAAGAGGAC GGGGTAGTTG CCTGTCCGGA
351 TGCTGCGGCT GCCGAGTCGG CGCAAAGTGC GCGGGCGGCG GGTTCGACCG
401 ATGGTTTCGG GGCTGTCCAT ATCCGGATGG CGGCAGGCGG AATCGTACCA
451 GTAGTCGCGC TGCAAGCCGT TTTCGTGCGC GGCAACGACG CTCAGGAAA
501 TGCTGTGGTG CGTGCTTTGC CGGTGTGCGG CAAACCGTA GGTGTTGCCG

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551 TAAACGTATT GGTAATGGCC GGTTCGCACC GCCGCGCCTT CGGAGTTTTC
601 EATGCGCTCA TCCTCGTTCA GGGCGGCTTG TTCGCATTGT TTTGCCAAGC
651 CGACGCGGCG TTCCTGATCC AAATCCCATT CGTGGTAAAG GTCGGGGTCCG
701 CCGATGTGTT GCGCCATCAA CTCGGGGTCG GCAAGTCCGG CGCAACCGTC
751 TTCGCGCGTG TGGCGGGCGA TGTCNNNNGC GCGCGGACG GTGTCGCGCA
801 GGGCTTGTTT GGAGAAATCG GCGGTGCCGG CGCGGCCTTT GCGTTTGCCG
851 ACGTAAACGG TAATGTCCAG CGACTGTGCC TGCTGAAACT CGATTGTGTT
901 GATTTCGCCC AGCCGCACGC TGACGCTTTG TCCCAATGAT TCGCTGAAAT
951 CGGCTTCGGC GCGGTTGCG CCCGTCGCTT TTGCCAAGTC GAGCGTGCGG
1001 CGGCAGAGGT CGAGGAGTTC GGAAGCGGTG TGGTTGAACA GCATAGAAAT
1051 CTTTCTTGAT GATGCTTTGC GGCATTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1422; ORF 515.a>:

```

a515.pep
1  MVQIKVVRAA  GVARGLHSEF  ARAVTAEEIA  FDNAVLNHEA  RCGNAPRIK
51  IAAAERAGDV  RFFAQVEEIG  QDFFADAVDQ  ETALAVERSA  GECADSVSDK
101  TARNGGIEED  GVVACRDAAA  AESAQSAAGG  GLTDGFGAVH  IRMAAGGIVP
151  VVALHAVFVG  GNDAAAGNAV  RALPVCCKTV  GVAVNVLMVA  GLHRRAFGVF
201  DALILVQGG  FALFCQADGG  FRIQIPFVVK  VGVADVLRHQ  LGVGKSGATV
251  FGGVAGDVXX  GADGVAQGLF  GEIGGAGAAF  AFADVNGNVQ  RLVLKLDLF
301  DFAQPHADAL  SQ*FAEIGFG  GGCARRFCQV  ERAAAEVEEF  GSGVVEQHRN
351  LS**CFAAF*

```

m515/a515 92.1% identity in 304 aa overlap

```

m515.pep                                10      20      30
                                GKSGGCAFFAQVEEIGQDFSADAVDQETALA
                                ::|  |||||  |||||  |||||  |||||
a515      AEEIAFDNAVLNHEARCGGNAFRIKIAAAERAGDVRFFAQVEEIGQDFFADAVDQETALA
           30      40      50      60      70      80

m515.pep           40      50      60      70      80      90
VERAAGECADEVSDKTARNGGIEEDGVAAACRDAAAESAQSAAGGGLTDGFGAVHIRMMA
||:|||||  |||||  |||||  |||||  |||||  |||||
a515      VERSAGECADEVSDKTARNGGIEEDGVVACRDAAAESAQSAAGGGLTDGFGAVHIRMMA
           90      100     110     120     130     140

m515.pep           100     110     120     130     140     150
GGIVPVVALHAVFVGNDAAAGNAVVRALPVCCKTVGVAVNVLMAGLHRRAFGVFDALIL
|||||  |||||  |||||  |||||  |||||  |||||
a515      GGIVPVVALHAVFVGNDAAAGNAVVRALPVCCKTVGVAVNVLMAGLHRRAFGVFDALIL
           150     160     170     180     190     200

m515.pep           160     170     180     190     200     210
VQGGFLFALFCQADGGXRIQIPFVVKVGADVLFCHQTGIGKSGATVFGGVAGDVGDFGV
|||||  |||||  |||||  |||||  |||||  |||||
a515      VQGGFLFALFCQADGGFRIQIPFVVKVGADVLRHQLGVGKSGATVFGGVAGDVXXGADGV
           210     220     230     240     250     260

m515.pep           220     230     240     250     260     270
LQGGFFGEVSGTGAAFAFADVNGNVQRLVLELDLXDQAQPHADALSQXFAEIGFGGGCAR
||:||||  ||:||||  |||||  |||||  |||||  |||||
a515      AQGLFGEIGGAGAAFAFADVNGNVQRLVLLKLDLFDFAQPHADALSQXFAEIGFGGGCAR
           270     280     290     300     310     320

m515.pep           280     290     300
RFCQVERAAAEVEEFGSGVVEQHRNLSXXCFAAFX
|||||  |||||  |||||  |||||  |||||
a515      RFCQVERAAAEVEEFGSGVVEQHRNLSXXCFAAFX
           330     340     350     360

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1423>:

```

g515-1.seq
1  ATGTTTCAAA  TACAGTTGT  GCGCGCCGCC  GCGGTGCCC  GTGGTCTGCA

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51  TTCCGAGTTT GCGCGCGCTG TAACTGCCGA GGAATAGCC TTCGACAATG
101 CCGTTTTGAA TCACGAAGCG CGCGCCGCTG GCAACACCTT CCGCATCAAA
151 ATAGCTGCTG CCGAAAGAGC GGGGGATGTG CGGTTCTTCG CGCAGGTTGA
201 GGAATACGGG CAGGACTTTT TTGCCGATGC TGTCGATCAG GAAACTGCTT
251 TGGCGGTAGA GCGCGCCGCC GGAGAGTGTG CCGACGAGGT GTCCGATCAG
301 CCCGCCCGAA ACGGTGGTAT CGAAGAGGAC GGGGTAGCTG CCTGTCCGGA
351 TGCTGCGGCT GCCGAGTCGG CGCAAAGTGC GCGGGCGCGG GGTTCGACCG
401 ATGTTTTCGG GGCTGTCCAT ATCCGATGCG CCGCAGGCGG AATCGTACCA
451 GTAGTCGCGC TGCATTCCGT TTTCGTGCGC GGCACGACG CTGCAGGAAA
501 TGCTGTGGTG CGTGCTTTGC CGGTGTGCGG CAAAACCGTG GGTGTGCGG
551 TAAACGTATT GGTAGTGTCC GGTTCGACC GCCGCGCCTT CGGAGTTTTC
601 GATGCGGCTG TCCGTGTCCA ACGCTGCCTG TTCGATTGT TTTGCCAAGC
651 CGACGGCGCG TTCCGTATCC AAATCCCAT CTGGTAAAG GTCGGGGTCG
701 CCGATGTGTT GCGCCATCAA CTCGGGGTCG GCAAGTCCGG CGCAACCGTC
751 TTCCGGCGTG TGGCGGGCGA TGTCGGCGGC GCGCGGACG GTGTCGCGCA
801 GGGCTTTGTT GGAGAAGTCG GCGGTGCGCG CGCGGCCTTT CGGTTTGCGG
851 ACGTAAACGG TAATGTCCAG CGATTGTGCC TGCTGGAAC CGATTGTGTT
901 GATTTCCGCC AAGCGCACGC TGACGCTTTC TCCGAGCGAT TCCTGAAAT
951 CGGCTTCGGC GCGGGTCGCG CCCGCTGCTT TTGCCAAGTC GAGCGTGCAG
1001 CCGCAGAGGT CGAGGAGTTC GGAAGCGGTG TGGTTGAACA GCATAACAAT
1051 CTTCTTGGT GGAGCGTGT GGCATTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1424; ORF 515-1.ng>:

g515-1.pep

```

1  MVQIQVVRAA GVARGLHSEF ARAVTAEEIA FDNVLNHEA RRGNTFRK
51  IAAERAGDV RFFAQVEEIG QDFFAVDQ ETALAVERAA GECADSVSDQ
101 PARNGGIEED GVAACRDAAA AESAQSAAGG GLTDGFGAVH IRMAAGGIYP
151 VVALHSEFVG GNDAAAGNAV RALPVCCKTV GVAENVLVVS GLHRRAFGVF
201 DAAVRVORCL FALFCQADGG FRIQIPFVVK VGVADVLRHQ LGVKGSGATV
251 FGGVAGDVGG GADGVAQGLF GEVGGAGAA AFADVNGNVQ RVLLELDLF
301 DFAQAHADAL SERFAEVGFG GGRARCFQCV ERAAEVEEF GSGVVEQHNN
351 LSWNSVVF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1425>:

m515-1.seq

```

1  ATGGTTCAAA TACAGGTTGT GCGCGCCGCC GCGGTTGCCC GTGGTCTGCA
51  TACCGAGTTT GCGCGCGCTG TAACTGCTGA GGAATAGCC TTCGACAATG
101 CCGTTTTGAA TCACGAAGCG CGGTGCGGTG GCAACGCTT CCGCATCAAA
151 ATAGCTGCTG CCGAAAGAGC GGGGGATGTG CGGTTCTTCG CGCAGGTTGA
201 GGAATACGGG CAGGACTTTT TTGCCGATGC TGTCGATCAG GAAACTGCTT
251 TGGCGGTAGA GCGCGCCGCC GGAGAGTGTG CCGACGAGGT GTCCGATAAG
301 ACCGCCCGAA ACGGTGGTAT CGAAGAGGAC GGGGTAGCTG CCTGTCCGGA
351 TGCTGCGGCT GCCGAGTCGG CGCAAAGTGC GCGGGCGCGG GGTTCGACCG
401 ATGTTTTCGG GGCTGTCCAT ATCCGATGCG CCGCAGGCGG AATCGTACCA
451 GTAGTCGCGC TGCATGCCGT TTTCGTGCGC GGCACGACG CTGCAGGAAA
501 TGCTGTGGTG CGTGCTTTGC CGGTGTGCGG CAAAACCGTG GGTGTGCGG
551 TAAACGTATT GGTAAATGGC GGTTCGACC GCCGCGCCTT CGGAGTTTTC
601 GATGCGCTCA TCCTCGTTCA GGGCGGCTTG TTCGATTGT TTTGCCAAGC
651 CGACGGCGCG TTCCGTATCC AAATCCCAT CTGGTAAAG GTCGGGGTCG
701 CCGATGTGTT TTGCCATCAG ACAGGCATCG GCAAGTCCGG CGCAACCGTC
751 TTCCGGCGTG TGGCGGGCGA TGTCGATGGC GGCTTTGACG GTGCTTGCA
801 GCGCTTTTTC GGAGAAGTCG CCACTACTGG CGCGGCCTTT CGGTTTGCGG
851 ACGTAAACGG TAATGTCCAG CGACTGTGCC TGCTGGAAC CGATTGTGTT
901 GATTTCCGCC AGCCGCACGC TGACGCTTTC TCCCAATGA

```

This corresponds to the amino acid sequence <SEQ ID 1426; ORF 515-1>:

m515-1.pep

```

1  MVQIQVVRAA GVARGLHTEF ARAVTAEEIA FDNVLNHEA RCGGNAFRK
51  IAAERAGDV RFFAQVEEIG QDFFAVDQ ETALAVERAA GECADSVSDK
101 TARNGGIEED GVAACRDAAA AESAQSAAGG GLTDGFGAVH IRMAAGGIYP
151 VVALHSEFVG GNDAAAGNAV RALPVCCKTV GVAENVLVMA GLHRRAFGVF
201 DALILVQGLL FALFCQADGG FRIQIPFVVK VGVADVFCQG TGIGKSGATV
251 FGGVAGDVGG GFDGVLQGF GEVGTGAAG AFADVNGNVQ RVLLELDLF
301 DFAQPHADAL SQ*

```

m515-1/g515-1 91.7% identity in 312 aa overlap

	10	20	30	40	50	60
g515-1.pep	MVQIQVVRAAGVARGLHSEFARAVTAEEIAFDNVLNHEARRGGNTFRKIAAAERAGDV					
m515-1	MVQIQVVRAAGVARGLHTEFARAVTAEEIAFDNVLNHEARCGGNAFRKIAAAERAGDV					
	10	20	30	40	50	60

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	70	80	90	100	110	120
g515-1.pep	RFFAQVEEIGQDFFADAVDQETALAVERAAGECADEVSDQPARNGGIEEDGVAACRDAAA					
m515-1	RFFAQVEEIGQDFFADAVDQETALAVERAAGECADEVSDKTARNGGIEEDGVAACRDAAA					
	70	80	90	100	110	120
g515-1.pep	AESAQSAAGGGLTDGFGAVHIRMAAGGIVPVVALHSVFVGGNDAAGNAVVRALPVCCKTV					
m515-1	AESAQSAAGGGLTDGFGAVHIRMAAGGIVPVVALHAFVVGNDAGNAVVRALPVCCKTV					
	130	140	150	160	170	180
g515-1.pep	GVAVNVLVVSGLHRRAFGVFDAAVRVQRCLFALFCQADGGFRIQIPFVVKVGVDVLRHQ					
m515-1	GVAVNVLVNAGLHRRAFGVFDALILVQGGFLALFCQADGGFRIQIPFVVKVGVDVFCCHQ					
	190	200	210	220	230	240
g515-1.pep	LGVGKSGATVFGGVAGDVGGGADGVAQGLFGEVGGAGAAFAFADVNGNVORFVLELDLF					
m515-1	TGIKSGATVFGGVAGDVGGGADGVLQGFGEVGGAGAAFAFADVNGNVORFVLELDLF					
	250	260	270	280	290	300
g515-1.pep	DFAQAHADALSERFAEVGFGGRARCFCQVERAAAEVEEFGSGVVEQHNNLSWWSVVAFX					
m515-1	DFAQPHADALSQX					
	310	320	330	340	350	360

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1427>:

a515-1.seq

```

1  ATGGTTCAAA TAAAGGTTGT GCGCGCCGCC GCGCTTGCCC GTGGTCTGCA
51  TTCCGAGTTT GCGCGCGCTG TAACTGCTGA GGAAATAGCC TTCGACAATG
101 CCGTTTGTAA TCACGAAGCG CGGTGCGGTG GCAACGCCCT CCGCATCAAA
151 ATAGCTGCTG CGGAAAGAGC GGGGGATGTG CCGTCTTTCG CGCAGGTTGA
201 GGAAATCGGG CAGGACTTTT TTGCCGATGC TGTCGATCAG GAAACTGCTT
251 TGGCGGTAGA GCGCTCCGCC GGAGAGTCCG CCGACGAGGT GTCCGATAAG
301 ACCGCCCGAA ACGGTGGTAT CGAAGAGGAC GGGGTAGTTG CCTGTCGGGA
351 TGCTGCGGCT GCCGAGTCCG CGCAAAGTGC GCGCGGCGCG GGTTTGACCG
401 ATGGTTTCGG GGCTGTCCAT ATCCGGATGG CCGCAGGCGG AATCGTACCA
451 GTAGTCGCGC TGCATGCCGT TTTCGTCCGC GCGAACGACG CTGCAGGAAA
501 TGCTGTGGTG CGTGCTTTGC CCGTGTGCGG CAAACCCGTA GGTGTGCGCG
551 TAAACGTATT GGTAAATGCC GGTTCGACC GCCGCGCCTT CGGAGTTTTC
601 GATGCGCTCA TCCTCGTTCA GGGCGGCTTG TTCGCATTGT TTTGCCAAGC
651 CGACGGCGGC TTCCGTATCC AAATCCCATC CGTGATAAG GTCCGGGTGC
701 CCGATGTGTT GCGCCATCAA CTCGGGGTGC GCAAGTCCGG CGCAACCGTC
751 TTCCGGCGGT TGCGGGGCGA TGTCCGCGGC GCGCGGACG GTGTGCGCGA
801 GGGCTTGTTT GGAGAAATCG CCGGTGCCCG CCGCGCCTTT GCGTTTGCCG
851 ACGTAAACGG TAATGTCCAG CGACTTGTC TGCTGAAACT CGATTGTGTC
901 GATTTGCCCC AGCCGCACGC TGACGCTTTC TCCCAATGA

```

This corresponds to the amino acid sequence <SEQ ID 1428; ORF 515-1.a>:

a515-1.pep

```

1  MVQIKVVRAA GVARGLHSEF ARAVTAEIEA FDNVNLNHEA RCGGNAFRIK
51  IAAAERAGDV RFFAQVEEIG QDFFADAVDQ ETALAVERSA GECADDEVSDK
101 TARNGGIEED GVVACRDAAA AESAQSAAGG GLTDGFGAVH IRMAAGGIVP
151 VVALHAFVFG GNDAAAGNAV RALPVCCKTV GVAVNVLVMA GLHRRAFGVF
201 DALILVQGGF FALFCQADGG FRIQIPFVKV VGVADVLRHQ LGVGKSGATV
251 FGGVAGDVGG GADGVAQGLF GEIGGAGAAF AFADVNGNVQ RLVLKLDLF
301 DFAQPHADAL SQ*

```

m515-1/a515-1 94.9% identity in 312 aa overlap

	10	20	30	40	50	60
a515-1.pep	MVQIKVVRAAGVARGLHSEFARAVTAEIEAFDNVNLNHEARCGGNAFRIKIAAAERAGDV					
m515-1	MVQIQVVRAAGVARGLHTEFARAVTAEIEAFDNVNLNHEARCGGNAFRIKIAAAERAGDV					
	10	20	30	40	50	60
a515-1.pep	RFFAQVEEIGQDFFADAVDQETALAVERSAGECADEVSDKTARNGGIEEDGVVACRDAAA					
	70	80	90	100	110	120

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m515-1      RFFAQVEEIGQDFFADAVDQETALAVERAAGECADEVSDKTARNGGIEEDGVAACRDAAA
              70          80          90          100          110          120

              130          140          150          160          170          180
a515-1.pep  AESAQSAAGGGLTDGFGAVHIRMAAGGIVPVVALHAVFVGGNDAAGNAVVRALPVCCKTV
              |||
m515-1      AESAQSAAGGGLTDGFGAVHIRMAAGGIVPVVALHAVFVGGNDAAGNAVVRALPVCCKTV
              130          140          150          160          170          180

              190          200          210          220          230          240
a515-1.pep  GVAVNVLMAGLHRRAFGVFDALILVQGGFALFCQADGGFRIQIPFVVKVGVDVLRHQ
              |||
m515-1      GVAVNVLMAGLHRRAFGVFDALILVQGGFALFCQADGGFRIQIPFVVKVGVDVLRHQ
              190          200          210          220          230          240

              250          260          270          280          290          300
a515-1.pep  LGVGKSGATVFGGVAGDVGGADGVAQGLFGEIGGAGAAFAFADVNGNVQRLVLLKDLF
              |||
m515-1      TGIGKSGATVFGGVAGDVGGADGVAQGLFGEIGGAGAAFAFADVNGNVQRLVLLKDLF
              250          260          270          280          290          300

              310
a515-1.pep  DFAQPHADALSQX
              |||
m515-1      DFAQPHADALSQX
              310

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1429>:

```

g516.seq
1   atgttggttcc gtaaaacgac cgccgccggtt ttggcggcaa ccttgatact
51  gaacggctgtg acgatgatgt tgcgggggat gaacaacccg gtcagccaaa
101 caatcacccg caaacacggt gacaaagacc aaatccgcgc cttcgggtgtg
151 gttgccgaag acaatgccca attggaaaag ggcagcctgg tgatgatggg
201 cgggaaatac tggttcgccg tcaatcccg aagctgacgg
251 gccttttgaa ggcggggttg gacaagccct tccaaatagt tgaggatacc
301 ccgagctatg cccgccacca agccctgccg gtcaaattcg aagcgcccg
351 cagccagaat ttcagtaccg gaggtctttg cctgcgctat gataccggca
401 gacctgacga catcgccaag ctgaaacagc ttgagtttaa agcggcctaaa
451 ctcgacaatc ggaccattta cagcgctgct gtatccgcc aaggcaataa
501 ctacgccacg ccgcaaaaac tgaacgccga ttatcatttt gagcaaatgt
551 tgcccgccga tatttattat acggttactg aaaaacatac cgacaaatcc
601 aagctgtttg gaaatatctt atatacgccc cccttggtga tattggatgc
651 ggcggccgcg gtgctggtct tgcctatggc tctgattgca gccgcgaatt
701 cctcagacaa atga

```

This corresponds to the amino acid sequence <SEQ ID 1430; ORF 516.ng>:

```

g516.pep
1   MLFRKTTAAV LAATLILNGC TMMLRGMNPN VSQTITRKHV DKDQIRAFGV
51  VAEDNAQLEK GSLVMMGGKY WFAVNPEDSA KLTGLLKAGL DKPFQIVEDT
101 PSYARHQALP VKFEAPGSQN FSTGGLCLRY DTGRPDIAK LKQLEFKAVK
151 LDNRTIYTRC VSAKGYYAT PQLNADYHF EQSVPADIYY TVTEKHTDKS
201 KLFGNILYTP PLLILDAAA VLVLPALIA AANSSDK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1431>:

```

m516.seq
1   ATGTTGTTCC GTAAACGAC CGCCGCCGTT TTGGCGGCAA CCTTGATGCT
51  GAACGGCTGT ACGTTGATGT TGTGGGAAT GAACAACCCG GTCAGCGAAA
101 CAATCACCCG CAAACACGTT GACAAAGACC AAATCCGC GCCTTCGGTGTG
151 GTTGCCGAAG ACAATGCCCA ATTGAAAAG GGCAGCCTGG TGATGATGGC
201 CGGAAAATAC TGGTTCGTCG TCAATCCCGA AGATTCGCGC AAGCTGACGG
251 GCATTTTGAA GGCAGGGCTG GACAAACCCT TCCAAATAGT TGAGGATACC
301 CCGAGCTATG CTCGCCACCA AGCCCTGCCG GTCAAACCTG AATCGCCTGG
351 CAGCCAGAAT TTCAGTACCG AAGGCCTTTG CCTGCGCTAC GATACCGACA
401 AGCCTGCCGA CATCGCCAAG CTGAAACAGC TCGGTTTGA AGCGGTCAAA
451 CTCGACAATC GGACCATTTA CACGCGCTGC GTATCCGCCA AAGGCAAATA

```

501 CTACGCCACA CCGCAAAAC TGAACGCCGA TTACCATTTT GAGCAAAGTG
551 TGCCTGCCGA TATTTATTAC ACGGTACTAG AAGAACATAC CGACAAATCC
601 AAGCTGTTTG CAAATATCTT ATATACGCCC CCCTTTTGA TACTGGATGC
651 GCGGGGCGCG GTACTGGCCT TGCTTGCGGC GGCTCTGGGT GCGGTCGTGG
701 ATGCCGCCCG CAAATGA

```
m516.ppep
1      MLFRKTTAAV  LAATLMLNGC  TLMWGMNPN  VSETITRKHV  DKDQIRAFGV
51     VAEDNAQLEK  GSLVMGGGKY  WFVNPEDSA  KLTGILKAGL  DKFPQIVEDT
101    PSYARHQALP  VKLESPGSQN  FSTEGLCLRY  DTDKPADIAK  LKQLGFQAVK
151    LDNRITYTRC  VSAKGKYYAT  PQKNLADYHF  EQSPVADIYY  TVTTEHTDKS
201    KLFANILYTR  PFLILDAAGA  VLALPAAALG  AVVDAARK*
```

ORF 516 shows 90.0% identity over a 231 aa overlap with a predicted ORF (ORF 516.ng) from *N. gonorrhoeae*:

```
a516.seq
1  ATGTTGTTCC GTAAACGAC CGCCGCCGTT TTGGCGGCAA CSTTGATGTT
51  GAACGGCTGT ACGGTAAATGA TGTGGGGTAT GAACAGCCCGC TTCAGCGAAA
101 CGACCGCGTC CAAACACGTT GACAGGACC AAATCCGCGC CTCGGTGTG
151 GTTGCCGAAG ACAATGCCCA ATTGGAAGA GGCAGCCTGG TGATGATGGG
201 CGGGAATATC TGGTTCGTCG TCAATCCTGA AGATTCGGCG AAGCTGACGG
251 GCATTTTGAA GCGCGGGTTG GACAAGCAGT TTCAAATGGT TGAAGCCCAAC
301 CGCGCCTTTG CCTACCAAGC CCTGCGGTG AAATCGAAT CGCCGCGCAG
351 CCAGAATTTT AGTACCGAAG GCCTTTGCCT GCGCTACGAT ACCGACAGAC
401 CTGCGGACAT CGCCAAGCTG AAACGCTTTG AGTTTGAAG GGTCTGAATC
451 GACAATCGGA CCATTTACAC GCGCTGCGTC TCCGCCAAAG GCAAATACTA
501 CGCCACACCG CAAAACATGA ACGCGGATTA TCATTTTGAG CAAAGTGTGC
551 CTGCCGATAT TTATTACACG GTTACGAAA AACATACCGA CAAATCCAAG
601 TTGTTTGAAT ATATTGCATA TACGCCCACC ACGTTGATAC TGGATGCGGT
651 GGGCGCGGTC CTGGCCTTGC CTGTGCGGGC GTTGATTGCA GCCACGAATT
701 CCTCAGACAA ATGA
```

a516.pep

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```

1  MLFRKTTAAV LAATLMLNGC TVMMWGMNSP FSETTARKHV DKDQIRAFGV
51  VAEDNAQLEK GSVLMMGGKY WVVNPEDSA KLTGILKAGL DKQFQMVPEPN
101 FRFAYQALPV KLESPASQNF STEGLCLRYD TDRPADIAKL KQLEFEAVEL
151 DNRTIYTRCV SAKGKYATP QKLNADYHFE QSVPADIIYYT VTKKHTDKSK
201 LFENIAYTPT TLILDAVGAV LALPVAALIA ATNSSDK*

```

m516/a516 86.1% identity in 238 aa overlap

	10	20	30	40	50	60
m516.pep	MLFRKTTAAVLAATLMLNGCTLMLWGMNPNVSETITRKHV	DKDQIRAFGVVAEDNAQLEK				
a516	MLFRKTTAAVLAATLMLNGCTVMMWGMNSPFSETTARKHV	DKDQIRAFGVVAEDNAQLEK				
	10	20	30	40	50	60
m516.pep	GSVLMGGKYWVVNPEDSAKLTGILKAGLDKPFQIVEDTPSYARHQA	LPVKLESPGSQN				
a516	GSVLMGGKYWVVNPEDSAKLTGILKAGLDKQFQMVPEPNRFA-YQALP	VKLESPASQN				
	70	80	90	100	110	120
m516.pep	GSVLMGGKYWVVNPEDSAKLTGILKAGLDKPFQIVEDTPSYARHQA	LPVKLESPGSQN				
a516	GSVLMGGKYWVVNPEDSAKLTGILKAGLDKQFQMVPEPNRFA-YQALP	VKLESPASQN				
	70	80	90	100	110	
m516.pep	FSTEGCLCLRYDTPKPADIAKLKQLGFQAVKLDNRTIYTRCVSAKGKYATP	QKLNADYHFE				
a516	FSTEGCLCLRYDTPKPADIAKLKQLEFEAVELDNRTIYTRCVSAKGKYATP	QKLNADYHFE				
	120	130	140	150	160	170
m516.pep	EQSVPADIIYYTVTEEHTDKSKLFANILYTPPFLILDAAGAVLALPAAALGAV	VDAARKX				
a516	EQSVPADIIYYTVTKKHTDKSKLFENIAYTPTTLILDAVGAVLALPVAALIAATNSSDKX					
	180	190	200	210	220	230

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1435>:

g517.seq

```

1  atgcatcggg tttcagacgg cattggagtg tcagtcgtgt tctgccgatt
51  cgtaggcttc gacgattttt tgcaccagag gatgccggac aacgtcttcg
101 ccggtgaagg tatggaaata cagtcctgcc acgccgtgca gtttctcagc
151 tgcgtctttc aatcccgaatt tgatgttttt gggcaggctg atttggtctg
201 tgcgcgggt aatgacggct ttcgcgccga agccgatgag ggtcaggaac
251 attttcattt gttcgggctt ggtgttttgc gcttcgtcga ggatgatgta
301 tgcgcgggtt agcgtcttgc cgcgcataata ggcgagcggg gcgatttcaa
351 tcaggccttt ttcaatcagc ttggttacac ggtcaaagcc catcagggtca
401 tagagggcat cataaagcgg acggaggtag gggtcgactt tttgggtcag
451 gtctccgggc aggaagccca gtttctcacc ggcttcgacg gcaggccgaa
501 ctaa

```

This corresponds to the amino acid sequence <SEQ ID 1436; ORF 517.ng>:

g517.pep

```

1  MHRVSDGIGV SVVFCRFVGF DDFLHQMPD NVFAGEGMEI QSCHAVQFLT
51  CVFQSRFDVF GQVDLAGVAG NDGFRAEADA GQEHFHLFGR GVLRFVEDDV
101 CAVERPAAHI GERGFNQAF FNQLGYTVKA HQVIEGIIKR TEVGVDLFGQ
151 VSGQEAQFLT GFDGRPN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1437>:

m517.seq

```

1  ATGCATCGGG TTTCAGACGG CATTGGAATG TCAGTCGTGT TCTGCCGATT
51  CGTAGGCTTC GACGATTTTT TGCACCAAAG GATGCCGGAC AACGTCTTCG
101 CCGGTAAAGG TGTGAAATA CAGCCCTTCC ACGTTGTGCA GTTCTCACG
151 CGCATCTTTT AATCCCGATT TGATGTTTTT GGGCAGGTCG ATTTGGCTGG
201 TTTCGCCGGT AATGACGGCT TTCGCGCCGA AGCCGATGCG GGTCAGGAAC
251 ATTTTCATTT GTTCGGGCGT GGTGTTTTGC GCTTCGTGCA GGATGATGTA
301 TGCGCGGTTG AGCGTCCTGC CGCGCATATA GGCAGCGGG GCgatttcaa
351 TCAGGCCTTT TTCAATCAGC TTGTTACAC GGTCAAAGCC CATCAGGTCA
401 TAGAGGGCAT CATAAAGCGG ACGAAGGTAG GGATCGACTT TCTGGGTCAG

```

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451 GTCTCCGGGC AGGAAGCCCA GTTCTCGCC GGCTTCGACG GCTGgGCGCA
501 CTAA

This corresponds to the amino acid sequence <SEQ ID 1438; ORF 517>:

m517.pep
1 MHRVSDGIGM SVVFCRFVGF DDFLHQMPD NVFAGKGVEI QPFHVQFLT
51 RIFXSRFDVF QQVLAGVAG NDGFRAEADA QGEHFHFGF GVLRFVEDDV
101 CAVERPAAHI GERGDFNQAF FNQLGYTVKA HQVIEGIIKR TKVGIDFLGQ
151 VSGQEAQFLA GFDGWAH*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 517 shows 92.7% identity over a 164 aa overlap with a predicted ORF (ORF 517.ng) from *N. gonorrhoeae*:

m517/g517

	10	20	30	40	50	60
m517.pep	MHRVSDGIGMSVVFCRFVGFDDFLHQMPD NVFAGKGVEIQPFHVQFLTRIFXSRFDVF					
g517	MHRVSDGIGMSVVFCRFVGFDDFLHQMPD NVFAGKGVEIQSCHAVQFLTCVFQSRFDVF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m517.pep	QQVLAGVAGNDGFRAEADAGQEHFHLFGFGRVLRFEEDDVCAVERPAAHIGERGDFNQAF					
g517	QQVLAGVAGNDGFRAEADAGQEHFHLFGFGRVLRFEEDDVCAVERPAAHIGERGDFNQAF					
	70	80	90	100	110	120
	130	140	150	160		
m517.pep	FNQLGYTVKAHQVIEGIIKR TKVGIDFLGQVSGQEAQFLAGFDGWAH					
g517	FNQLGYTVKAHQVIEGIIKRTEVGVDLFGQVSGQEAQFLTGFDGRPN					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1439>:

a517.seq
1 ATGCATCGGG TTTCAGACGG CATTGGAATG TCAGTCGTGT TCTGCCGATT
51 CGTAGGCTTC GACGATTTT TGCACCAAAG GATGCCGGAC AACGTCTTCG
101 CCGGTAAAGS TGTGGAATA CAGCCCTTCC ACGCCGTGCA GTTCTCAGC
151 CGCATCTTTT AATCCCGATT TGATGTTTTT GGGCAGGTCC ATTTGGCTGG
201 TGTCGCCCGT AATGACGGCT TTCGCGCCGA AGCCGATGCG GCTCAGGAAC
251 ATTTTCATT GTTCGGCGGT GSTGTTTTGC GCTTCGTGCA GGATGATGTA
301 TGCGCCGTTG AGCGTCCTGC CGCGCATATA GCGGAGCGGG GCAATCTCAA
351 TCAGACCTTT TTCAATCAGC TTGGTGACAC GGTGGAAGCC CATCAGGTCA
401 TAGAGGGCAT CATAAAGCGG ACGAAGGTAG GGATCGACTT TCTGGGTCAG
451 GTCACCGGGC AGAAAACCCA GTTCTCGCC GGCTTCGACG GCAGGCCGCA
501 CTAA

This corresponds to the amino acid sequence <SEQ ID 1440; ORF 517.a>:

a517.pep
1 MHRVSDGIGM SVVFCRFVGF DDFLHQMPD NVFAGKGVEI QPFHAVQFLT
51 RIF*SRFDVF QQVLAGVAG NDGFRAEADA QGEHFHFGF GVLRFVEDDV
101 CAVERPAAHI GERGNLNOTF FNQLGDTVEA HQVIEGIIKR TKVGIDFLGQ
151 VTGQKTQFLA GFDGRPH*

m517/a517 93.4% identity in 167 aa overlap

	10	20	30	40	50	60
m517.pep	MHRVSDGIGMSVVFCRFVGFDDFLHQMPD NVFAGKGVEIQPFHVQFLTRIFXSRFDVF					
a517	MHRVSDGIGMSVVFCRFVGFDDFLHQMPD NVFAGKGVEIQPFHAVQFLTRIFXSRFDVF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m517.pep	QQVLAGVAGNDGFRAEADAGQEHFHLFGFGRVLRFEEDDVCAVERPAAHIGERGDFNQAF					
a517	QQVLAGVAGNDGFRAEADAGQEHFHLFGFGRVLRFEEDDVCAVERPAAHIGERGNLNOTF					

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	70	80	90	100	110	120
	130	140	150	160		
m517.pep	FNQLGYTVKAHQVIEGIIKRTKVGIDFLGQVSGQEAQFLAGFDGWAHX					
a517	FNQLGDTVEAHQVIEGIIKRTKVGIDFLGQVTGQKQFLAGFDGRPHX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1441>:

```

g518.seq
1  atgacgtttt  cggcggcaaa  gctcaacatt  tccgcactga  tgttgtgtct
51  ttccggcagga  atgaccgttt  tactttccgc  ttttttactg  ctccgaccgg
101 aaggcagcat  cttattcaac  cattttttca  gcataaatat  tctgacccca
151 agagcggcat  ctccacgggc  aaccgtgttc  agactgcata  aggcggtagc
201 attccacaag  atgccgaaaa  ccataagcaa  aatgcgtaga  aactacgccg
251 tccgaatcac  gccgcctcct  cgggcggcaa  cgcttcatta  taacagattg
301 ccccttaaaa  aatcagaccc  tgcttttgtg  gcggagtctg  aaatttga

```

This corresponds to the amino acid sequence <SEQ ID 1442; ORF 518.ng>:

```

g518.pep
1  MTFSAAKLNI  SALMLCLSAG  MTVLLSAFLL  LRPEGSILFN  HFFSINILTR
51  RAASPRATVF  RLHQAVRFHK  MKPTISKMR  NYAVRITPPP  RAATLHYNRI
101 PLKKSDFAFV  AESEI*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1443>:

```

m518.seq
1  ATGACGTTTT  CGGCGGCAAA  GCTCAACATT  TCGGCACGGA  TGTGTGTCT
51  TTCGGCAGGA  ATGACCGTTT  TACTTTCCGC  TTTTACTG  CTCCGACCGG
101 AAGGCAGCAT  CTTATTCAAC  CATTTTTCA  GCATAAATAT  TCTGACCCGA
151 AGAGCGGCAT  CTCCACAGGC  AACCCTGTT  AGACGGCATC  AGGCGCGGTT
201 TGCAAGATGC  CGTACCATAA  ACAAAGGCG  TAGAACTAC  GCCGTCCGAA
251 TCACGCGGCC  CTCGCG.GCG  GCAACGCGTC  ATTATAACAG  ATTGCCCTCC
301 GCGGCAGGCT  TAGTGCGGCG  GGAGCGCCGC  CGTTGCGCAG  TAATATTGTC
351 TAACGGGAGG  AAAAAATCAG  ACCCTGCTT  TGTGGCAGAG  TCTGAAATT
401 GA

```

This corresponds to the amino acid sequence <SEQ ID 1444; ORF 518>:

```

m518.pep
1  MTFSAAKLNI  SARMLCLSAG  MTVLLSAFLL  LRPEGSILFN  HFFSINILTR
51  RAASPRATVF  RRHQARFARC  RTINKRRRNY  AVRITPPSXA  ATRHYNRLPS
101 AAGLVRERR  RCAVILSNGR  KKSDFAFVAE  SEI*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 518 shows 74.1% identity over a 135 aa overlap with a predicted ORF (ORF 518.ng) from *N. gonorrhoeae*:

```

m518/g518

m518.pep  MTFSAAKLNISARMLCLSAGMTVLLSAFLLLRPEGSILFNHFFSINILTRRAASPRATVF
          |||||
g518      MTFSAAKLNISALMLCLSAGMTVLLSAFLLLRPEGSILFNHFFSINILTRRAASPRATVF
          |||||
          10      20      30      40      50      60

          70      80      90      100     110
m518.pep  RRHQA-RFARC-RTINKRRRNYAVRITPPSXAATRHYNRLPSAAGLVRERRRCAVILSN
          | ||| | : : ||: | ||||| ||| |||||
g518      RLHQAVRFHKMPKTISKMRNYAVRITPPRAATLHYNRLPL-----
          70      80      90      100

m518.pep  120      130
          GRKKSDFAFVAESEI
          |||||
g518      --KKSDFAFVAESEI
          110

```


The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1445>:

```
a518.seq
1  ATGACGTTTT CGGCGGCAAA GCTCAACATT TCGGCACGGA TGTGTGTCT
51  TTCGCGAGGA ATGACCGTTT TACTTTCCGC TTTTCTACTG CTCCGACCGG
101 AAGGCAGCAT CTTATTCAAC CATTTTTCAT GCATAAATAT TCTAACCCGA
151 AGA3CGGCAT CTCCACGGGC AACCCTGTTT AGACGGCATC AGGCGGTACG
201 ATTCCGCAAG ATGCCGACCA TAAACAAAAG GCGTAGAAAC TACGCCGTCC
251 GAATCAGGCC GTCCTCG.CG GCGGCAACGC GTCATTATAA CAGATTGCCC
301 TCC.....
351 .....
401 TTTGA
```

This corresponds to the amino acid sequence <SEQ ID 1446; ORF 518.a>:

```
a518.pep
1  MTFSAAKLNI SARMLCLSAG MTVLLSAFLL LRPEGSILFN HFFSINILTR
51  RAASPRATVF RRHQAVRFRK MPTINKRRRN YAVRITPSSX AATRHYNRLP
101 S..... .KKSDPAFVA ESEI*

m518/a518 79.9% identity in 134 aa overlap

          10      20      30      40      50      60
m518.pep  MTFSAAKLNISARMLCLSAGMTVLLSAFLLLRPEGSILFNHFFSINILTRRAASPOATVF
a518       MTFSAAKLNISARMLCLSAGMTVLLSAFLLLRPEGSILFNHFFSINILTRRAASPRATVF
          10      20      30      40      50      60

          70      80      90      100     110     119
m518.pep  RRHQA-RFARCTINKRRRNYAVRITPPSXAATRHYNRLPSAAGLVRERRRRCVILSNG
a518       RRHQAVRFRKMPTINKRRRNYAVRITPPSXAATRHYNRLPS-----
          70      80      90      100

m518.pep  120      130
          RKKSDPAFVAESEIX
a518       -KKSDPAFVAESEIX
          110
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1447>:

```
g519.seq
1  atggaatttt tcattatctt gttggcagcc gtcgccgttt tcggcttcaa
51  atcctttgtc gtcattcccc agcaggaagt ccacgttgtc gaaaggctcg
101 ggcgtttcca tcgcgccctg acggccggtt tgaatatttt gattcccttt
151 atcgaccgcg tcgcctaccg ccattcgctg aaagaaatcc ctttagacgt
201 acccagccag gtctgcatca cgcgcgataa tacgcaattg actgttgacg
251 gcatcatcta tttccaagta accgatccca aactcgcttc atacggttcg
301 agcaactaca ttatggcaat taccagctt gcccaaacga cgctgcgttc
351 cgttatcggy cgtatggagt tggacaaaac gtttgaagaa cgcgacgaaa
401 tcaacagtac cgtcgtctcc gccctcgatg aagccgcggy ggcttggggt
451 gtgaaagtcc tccgttacga aatcaaggat ttggttcgcy cgcaagaaat
501 ccttcgcgca atgcaggcac aaattaccgc cgaacgcgaa aaacgcgccc
551 gtattgcgga atccgaaggc cgtaaaatcg aacaaatcaa ctttgccagt
601 ggtcagcgty aagccgaaat ccaacaatcc gaaggcgagg ctgaggtgcy
651 ggtcaatgcy tccaatgccg agaaaatcgc ccgcatcaac cgcgcgcaag
701 gcgaagcgga atccctgcgc cttgttgccg aagccaatgc cgaagccaac
751 cgtcaaattg ccgcccgcct tcaaaccгаа agcggggcgg atgcggtcaa
801 tctgaagatt gcgggacaat acgttaccgc gttcaaaaat cttgccaag
851 aagacaatac gcgattaag cccgccaagg ttgccgaaat cgggaaacct
901 aattttcggc ggcatgaaaa attttcgcca gaagcaaaaa cggccaata
951 a
```

This corresponds to the amino acid sequence <SEQ ID 1448; ORF 519.ng>:

```
g519.pep
1  MEFFIILLAA VAVFGFKSFV VIPQQEVHV ERLGRFHRAL TAGLNILIPF
51  IDRVAYRHSI KEIPLDVPSQ VCITRDNTQL TVDGIYFQV TDPKLASYGS
```

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```

101 SNYIMAITQL AQTLRSVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG
151 VKVLRYEIKD LVPPQEILRA MQAQITAERE KRARIAESEG RKIEQINLAS
201 GQREAEIQQS EGEEAQAANA SNAEKIARIN RAKGEAESLR LVAEANAEN
251 RQIAAALQTO SGADAVNLKI AGQYVTAFKN LAKEDNTRIK PAKVAEIGNP
301 NFRRHEKFSP EAKTAK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1449>:

```

m519.seq (partial)
1  ..TCCGTTATCG GCGTATGGA GTTGGACAAA ACGTTTGAAG AACGCGACGA
51  AATCAACAGT ACTGTTGTTG CCGCTTTGGA CGAGGCGGCC GGGgCTTgGG
101 GTGTGAAGGT TTTGCGTTAT GAGATTAAAG ACTTGGTTCC GCCGCAAGAA
151 ATCCTTCGCT CAATCGAGGC GCAAATTACT GCCGAACGCG AAAAACGCGC
201 CCGTATCGCC GAATCCGAAG GTCGTAAAT CGAACAAATC AACCTTGCCA
251 GTGGTCAGCG CGAAGCCGAA ATCCAACAAT CCGAAGGCGA GGCTCAGGCT
301 GCGGTCAATG CGTCAAATGC CGAGAAAATC GCCCGCATCA ACCGCGCCAA
351 AGGTGAAGCG GAATCCTTGC GCCTTGTTGC CGAAGCCAAT GCCGAAGCCA
401 TCCGTCAAAT TGCCGCCGCC CTTCAAACCC AAGGCGGTGC GGATGCGGTC
451 AATCTGAAGA TTGCGGAACA ATACGTCGCT GCGTTCAACA ATCTTGCCAA
501 AGAAAGCAAT ACGCTGATTA TGCCCGCCAA TGTGCGGAC ATCGGCAGCC
551 TGATTCTGTC CGGTATGAAA ATTATCGACA GCAGCAAAAC CGCCAAaTAA

```

This corresponds to the amino acid sequence <SEQ ID 1450; ORF 519>:

```

m519.pep (partial)
1  ..SVIGRMELDK TFEERDEINS TVVAALDEAA GAWGVKVLRY EIKDLVPPQE
51  ILRSMQAQIT AEREKRARIA ESEGRKIEQI NLAGQREAE IQQSEGEAQA
101 AVNASNAEKI ARINRAKGEA ESLRLVAEAN AEAIRQIAAA LQTQGGADAV
151 NLKIAEQYVA AFNNLAKESN TLIMPANVAD IGSLISAGMK IIDSSKTAK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 519 shows 87.5% identity over a 200 aa overlap with a predicted ORF (ORF 519.ng) from *N. gonorrhoeae*:

m519/g519

m519.pep				10	20	30
				SVIGRMELDKTFEERDEINSTVVAALDEAA		
g519	YFQVTDPKLASYGSSNYIMAITQLAQTTLSVIGRMELDKTFEERDEINSTVVSALDEAA					
	90	100	110	120	130	140
m519.pep		40	50	60	70	80
		GAWGVKVLRYEIKDLVPPQEILRSMQAQITAEREKRARIAESEGRKIEQINLAGQREAE				
g519		GAWGVKVLRYEIKDLVPPQEILRAMQAQITAEREKRARIAESEGRKIEQINLAGQREAE				
		150	160	170	180	190
m519.pep		100	110	120	130	140
		IQQSEGEAQA AVNASNAEKIARINRAKGEAESLRLVAEANAENRQIAAALQTQGGADAV				
g519		IQQSEGEAQA AVNASNAEKIARINRAKGEAESLRLVAEANAENRQIAAALQTQSGADAV				
		210	220	230	240	250
m519.pep		160	170	180	190	200
		NLKIAEQYVA AFNNLAKESNTLIMPANVADIGSL-ISAGMKIIDSSKTAK				
g519		NLKIAGQYVTAFKNLAKEDNTRIKPAKVAEIGNPNFRRHEKFSP EAKTAK				
		270	280	290	300	310

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1451>:

```

a519.seq
1  ATGGAATTTT TCATTATCTT GCTGGCAGCC GTCGTTGTTT TCGGCTTCAA
51  ATCCTTTGTT GTCATCCAC AGCAGGAAGT CCACGTTGTC GAAAGGCTCG
101 GCGGTTTCCA TCGCGCCCTG ACGGCCGTT TGAATATTTT GATTCCCTTT
151 ATCGACCGCG TCGCTACCG CCATTGCTG AAAGAAATCC CTTAGACGT

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201 ACCCAGCCAG GTCTGCATCA CGCGCGACAA TACGCAGCTG ACTGTTGACG
251 GTATCATCTA TTTCCAAGTA ACCGACCCCA AACTCGCCTC ATACGGTTCG
301 AGCAACTACA TTATGGCGAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC
351 CGTTATCGGG CGTATGGAAT TGGACAAAAC GTTTGAAGAA CGCGACGAAA
401 TCAACAGCAC CGTCGTCTCC GCCCTCGATG AAGCCGCCGG AGCTTGGGGT
451 GTGAAGGTTT TGCATTATGA GATTAAAGAC TTGGTTCCGC CGCAAGAAAT
501 CCTTCGCTCA ATGCAGGCGC AAATTACTGC TGAACGCGAA AAACGCGCCC
551 GTATCGCCGA ATCCGAAGGT CGTAAATCG AACAAATCAA CCTTGCCAGT
601 GGTTCAGCGC AAGCCGAAAT CCAACAATCC GAAGGCGAGG CTCAGGCTGC
651 GGTCAATGCG TCAATGCGC AGAAAATCGC CCGCATCAAC CGCGCAAAG
701 GTGAAGCGGA ATCCTTGCGC CTTGTTGCCG AAGCCAATGC CGAAGCCATC
751 CGTCAAAATG CCGCCGCCCT TCAAACCCAA GCGGTTGCGG ATGCGGTCAA
801 TCTGAAGATT GCGGAACAAT ACGTCGCCGC GTTCAACAAT CTTGCCAAAG
851 AAAGCAATAC GCTGATTATG CCCGCCAATG TTGCCGACAT CGGCAGCCTG
901 ATTCTGCGC GTATGAAAAT TATCGACAGC AGCAAACCG CCAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1452; ORF 519.a>:

```

a519.pep
1  MEFFIILLAA VVVFGEKSEV VIPQOEHVHV ERLGRFHRAL TAGLNILIPF
51  IDRVAIRHSL KEIPLDVPSQ VCITRDNTQL TVDGIYFQV TDPKLASYGS
101 SNYIMAITQL AQTTLRSVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG
151 VKVLRVEIKD LVPPQEILRS MQAQITAERE KRARIAESG RKTEQINLAS
201 GQREAEIQQS EGEAQAAVNA SNAEKIARIN RAKGEAESLR LVAEANAELAI
251 RQIAAALQTO GGADAVNLKI AEQYVAAFNN LAKESNTLIM PANVADIGSL
301 ISAGMKIIDS SKTAK*

m519/a519 99.5% identity in 199 aa overlap

m519.pep
10 20 30
SVIGRMELDKTFEERDEINSTVVAALDEAA
|||||
a519 YFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIGRMELDKTFEERDEINSTVVSALDEAA
90 100 110 120 130 140

m519.pep
40 50 60 70 80 90
GAWGVKVLRYEIKDLVPPQEILRSMAQITAEREKRARIAESEGRKIEQINLASGQREAE
|||||
a519 GAWGVKVLRYEIKDLVPPQEILRSMAQITAEREKRARIAESEGRKIEQINLASGQREAE
150 160 170 180 190 200

m519.pep
100 110 120 130 140 150
IQQSEGEAQAAVNASNAEKIARINRAKGEAESLRLVAEANAELRQIAAALQTGGADAV
|||||
a519 IQQSEGEAQAAVNASNAEKIARINRAKGEAESLRLVAEANAELRQIAAALQTGGADAV
210 220 230 240 250 260

m519.pep
160 170 180 190 200
NLKIAEQYVAAFNNLAKESNTLIMPANVADIGSLISAGMKIIDSSKTAKX
|||||
a519 NLKIAEQYVAAFNNLAKESNTLIMPANVADIGSLISAGMKIIDSSKTAKX
270 280 290 300 310

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1453>:

```

g519-1.seq
1  ATGGAATTTT TCATTATCTT GTTGGCAGCC GTCGCCGTTT TCGGCTTCAA
51  ATCCTTTGTC GTCATCCCCC AGCAGGAAGT CCACGTTGTC GAAAGGCTCG
101 GCGGTTTCCA TCGCGCCCTG ACGGCCGGTT TGAATATTTT GATTCCTTTT
151 ATCGACCGCG TCGCCTACCG CCATTCGCTG AAAGAAATCC CTTTAGACGT
201 ACCCAGCCAG GTCTGCATCA CGCGCGATAA TACGCAATTG ACTGTTGACG
251 GCATCATCTA TTTCCAAGTA ACCGATCCCA AACTCGCCTC ATACGGTTCG
301 AGCAACTACA TTATGGCAAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC
351 CGTTATCGGG CGTATGGAAT TGGACAAAAC GTTTGAAGAA CGCGACGAAA
401 TCAACAGTAC CGTCGTCTCC GCCCTCGATG AAGCCGCCGG GGCCTGGGGT
451 GTGAAAGTCC TCCGTTACGA AATCAAGGAT TTGGTTCCGC CGCAAGAAAT
501 CCTTCGCGCA ATGCAGGCAC AAATTACCGC CGAACGCGAA AAACGCGCCC
551 GTATTGCCGA ATCCGAAGGC CGTAAATCG AACAAATCAA CCTTGCCAGT
601 GGTTCAGGTG AAGCCGAAAT CCAACAATCC GAAGGCGAGG CTCAGGCTGC
651 GGTCAATGCG TCAATGCGC AGAAAATCGC CCGCATCAAC CGCGCAAAG
701 CGAAGCGGA ATCCCTGCGC CTTGTTGCCG AAGCCAATGC CGAAGCCATC
751 CGTCAAAATG CCGCCGCCCT TCAAACCCAA GSCGGGCGG ATGCGGTCAA

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801 TCTGAAGATT GCGGAACAAT ACGTAGCCGC GTTCAACAAT CTTGCCAAAG
 851 AAAGCAATAC GCTGATTATG CCCGCCAATG TTGCGACAT CGGCAGCCTG
 901 ATTTCTGCCG GCATGAAAAT TATCGACAGC AGCAAAACCG CCAAATAA

This corresponds to the amino acid sequence <SEQ ID 1454; ORF 519-1.ng>:

g519-1.pep

1 MEFFIILLAA VAVFGPKSFV VIPQQEVHV ERLGRFHRAL TAGLNILIPF
 51 IDRVAVRHSL KEIPLDVPSQ VCITRDNTQL TVDGIIFYQV TDPKLASYGS
 101 SNYIMAITQL AQTTLRSVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG
 151 VKVLRYEIKD LVPPQEILRA MQAQITAERE KRARIAESEG RKIEQINLAS
 201 GQREAEIQQS EGEAQAANA SNAEKIARIN RAKGEAESLR LVAEANAIAI
 251 RQIAAALQTQ GGADAVNLKI AEQYVAAFNN LAKESNTLIM PANVADIGSL
 301 ISAGMKIIDS SKTAK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1455>:

m519-1.seq

1 ATGGAATTTT TCATTATCTT GTTGGTAGCC GTCGCCGTTT TCGGTTTCAA
 51 ATCCTTTGTT GTCATCCAC AACAGGAAGT CCACGTGTC GAAAGGCTGG
 101 GCGGTTTCCA TCGCGCCCTG ACGGCGGTT TGAATATTT GATTCCCTTT
 151 ATCGACCGCG TCGCCTACCG CCATTGCTG AAAGAAATCC CTTTAGACGT
 201 ACCCAGCCAG GTCTGCATCA CGCGCGACAA TACGCAGCTG ACTGTTGACG
 251 GCATCATCTA TTTCCAAGTA ACCGACCCCA AACTCGCCTC ATACGGTTCTG
 301 AGCAACTACA TTATGGCGAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC
 351 CGTTATCGGG CGTATGGAGT TGGACAAAAC GTTTGAAGAA CGCGACGAAA
 401 TCACACGTAC TGTGTGTCG GCTTTGACG AGGCGGCCGG GGCTTGGGGT
 451 GTGAAGGTTT TGCCTTATGA GATTAAAGAC TTGTTCCGC CGCAAGAAAT
 501 CCTTCGCTCA ATGCAGCGC AAATTACTGC CGAACGCGAA AACCGCGCCC
 551 GTATCGCCGA ATCCGAAGGT CGTAAATCG AACAAATCAA CCTTGCCAGT
 601 GGTACGCGCG AAGCCGAAAT CCAACAATCC GAAGGCGAGG CTCAGGCTGC
 651 GGTCAATGCG TCAATGCGG AGAAAATCGC CGCATCAAC CGCGCCAAAG
 701 GTGAAGCGGA ATCCTTGCGC CTGTTGCGG AAGCCAATGC CGAAGCCATC
 751 CGTCAAAATG CCGCGCCCT TCAAAACCAA GCGGTGCGG ATGCGGTCAA
 801 TCTGAAGATT GCGGAACAAT ACGTCGCTGC GTTCAACAAT CTTGCCAAAG
 851 AAAGCAATAC GCTGATTATG CCCGCCAATG TTGCGACAT CGGCAGCCTG
 901 ATTTCTGCCG GTATGAAAAT TATCGACAGC AGCAAAACCG CCAAATAA

This corresponds to the amino acid sequence <SEQ ID 1456; ORF 519-1>:

m519-1.

1 MEFFIILLVA VAVFGPKSFV VIPQQEVHV ERLGRFHRAL TAGLNILIPF
 51 IDRVAVRHSL KEIPLDVPSQ VCITRDNTQL TVDGIIFYQV TDPKLASYGS
 101 SNYIMAITQL AQTTLRSVIG RMELDKTFEE RDEINSTVVA ALDEAAGAWG
 151 VKVLRYEIKD LVPPQEILRS MQAQITAERE KRARIAESEG RKIEQINLAS
 201 GQREAEIQQS EGEAQAANA SNAEKIARIN RAKGEAESLR LVAEANAIAI
 251 RQIAAALQTQ GGADAVNLKI AEQYVAAFNN LAKESNTLIM PANVADIGSL
 301 ISAGMKIIDS SKTAK*

m519-1/g519-1 99.0% identity in 315 aa overlap

	10	20	30	40	50	60
g519-1.pep	MEFFIILLAAVAVFGPKSFVVIPQQEVHVVERLGRFHRALTAGLNILIPFIDRVAVRHSL					
m519-1	MEFFIILLVAVAVFGPKSFVVIPQQEVHVVERLGRFHRALTAGLNILIPFIDRVAVRHSL					
	10	20	30	40	50	60
g519-1.pep	KEIPLDVPSQVCITRDNTQLTVDGIIFYQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG					
m519-1	KEIPLDVPSQVCITRDNTQLTVDGIIFYQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG					
	70	80	90	100	110	120
g519-1.pep	RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRAMAQITAERE					
m519-1	RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMAQITAERE					
	130	140	150	160	170	180
g519-1.pep	KRARIAESEG RKIEQINLASGQREAEIQQSEGEAQAANASNAEKIARINRAKGEAESLR					
m519-1	KRARIAESEG RKIEQINLASGQREAEIQQSEGEAQAANASNAEKIARINRAKGEAESLR					
	190	200	210	220	230	240
g519-1.pep	KRARIAESEG RKIEQINLASGQREAEIQQSEGEAQAANASNAEKIARINRAKGEAESLR					
m519-1	KRARIAESEG RKIEQINLASGQREAEIQQSEGEAQAANASNAEKIARINRAKGEAESLR					

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m519-1      KRARIAESEGKIEQINLASGQREAEIQSEGEAQAAVNASNAEKIARINRAKGEAESLR
              190      200      210      220      230      240

              250      260      270      280      290      300
g519-1.pep  LVAEANAEAIRQIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLINPANVADIGSL
              |||||
m519-1      LVAEANAEAIRQIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLINPANVADIGSL
              250      260      270      280      290      300

              310
g519-1.pep  ISAGMKIIDSSKTAKX
              |||||
m519-1      ISAGMKIIDSSKTAKX
              310

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1457>:

```

a519-1.seq
1  ATGGAATTTT TCATTATCTT GCTGGCAGCC GTCGTTGTTT TCGGCTTCAA
51  ATCCTTTGTT GTCATCCAC AGCAGGAAGT CCACGTTGTC GAAAGGCTCG
101 GCGGTTTCCA TCGCGCCCTG ACGGCCGTTT TGAATATTTT GATTCCCTTT
151 ATCGACCGCG TCGCCTACCG CCATTGCTG AAAGAAATCC CTTTAGACGT
201 ACCCAGCCAG GCTGTCATCA CGCGCGACAA TACGCAGCTG ACTGTTGACG
251 GTATCATCTA TTCCAAGTA ACCGACCCCA AACTCGCCTC ATACGGTTTG
301 AGCAACTACA TTATGGCGAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC
351 CGTTATCGGG CGTATGGAAT TGGACAAAAC GTTTGAAGAA CGCGACGAAA
401 TCAACAGCAC CGTCGTCTCC GCCCTCGATG AAGCCGCGGG AGCTTGGGGT
451 GTGAAGGTTT TCGGTTATGA GATTAAAGAC TTGGTTCCGC CGCAAGAAAT
501 CCTTCGCTCA ATGCAGGCGC AAATTACTGC TGAACGCGAA AAACGCGCCC
551 GTATCGCCGA ATCCGAAGGT CGTAAATCG AACAAATCAA CCTTGCCAGT
601 GGTACGCGCG AAGCCGAAAT CCAACAATCC CAAGCGGAGG CTCAGGCTGC
651 GGTCAATGCG TCAAATCCCG AGAAAATCGC CCGCATCAAC CGCGCCAAAG
701 GTGAAGCGGA ATCCTTGCGC CTTGTTGCGG AAGCCAATGC CGAAGCCATC
751 CGTCAAAATG CCGCCGCCCT TCAAACCCAA GGCGGTGCGG ATGCGGTCAA
801 TCTGAAGATT GCGGAACAAT ACGTCGCCGC GTTCAACAAT CTTGCCAAAG
851 AAAGCAATAC GCTGATTATG CCGGCCAATG TTGCCGACAT CGGCAGCCTG
901 ATTTCTGCCG GTATGAAAAA TATCGACAGC AGCAAAACCG CCAATAAA

```

This corresponds to the amino acid sequence <SEQ ID 1458; ORF 519-1.a>:

```

a519-1.pep.
1  MEFFIILLAA VVVFGRKSFV VIPQEVHV VRLGRFHRAL TAGLNILIPF
51  IDRVA YRHS L KEIPLDVPSQ VCITRDN TQL TVDGIYFQV TDPKLASYGS
101 SNYIMAITQL AQTTLR SVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG
151 VKVLR YEIKD LVPPQEILRS MQAQITAERE KRARIAESEG RKIEQINLAS
201 QREAEIQQS EGEEAQA VNA SNAEKIARIN RAKGEAESLR LVAEANAEAI
251 RQIAAALQTQ GGADAVNLKI AEQYVAAFNN IAKESNTLIM PANVADIGSL
301 ISAGMKIIDS SKTAK*

```

m519-1/a519-1 99.0% identity in 315 aa overlap

```

              10      20      30      40      50      60
a519-1.pep  MEFFIILLAAVVVFGRKSFVVIPQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
              |||||
m519-1      MEFFIILLVAVAVFGFKSFVVIPQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
              10      20      30      40      50      60

              70      80      90      100     110     120
a519-1.pep  KEIPLDVPSQVCITRDN TQLTVDGIYFQVTDPKLASYGSSNYIMAITQLAQTTLR SVIG
              |||||
m519-1      KEIPLDVPSQVCITRDN TQLTVDGIYFQVTDPKLASYGSSNYIMAITQLAQTTLR SVIG
              70      80      90      100     110     120

              130     140     150     160     170     180
a519-1.pep  RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
              |||||
m519-1      RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
              130     140     150     160     170     180

              190     200     210     220     230     240
a519-1.pep  KRARIAESEGKIEQINLASGQREAEIQSEGEAQAAVNASNAEKIARINPAKGEAESLR
              |||||

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m519-1      KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
              190      200      210      220      230      240

              250      260      270      280      290      300
a519-1.pep  LVAEANAEAIRQIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
              |||||
m519-1      LVAEANAEAIRQIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
              250      260      270      280      290      300

              310
a519-1.pep  ISAGMKIIDSSKTAKX
              |||||
m519-1      ISAGMKIIDSSKTAKX
              310

```

Expression of ORF 519

The primer described in Table 1 for ORF 519 was used to locate and clone ORF 519. ORF 519 was cloned in pET and pGex vectors and expressed in E.coli as above described. The products of protein expression and purification were analyzed by SDS-PAGE. Figure 4A shows the results of affinity purification, and Figure 4B shows the expression in E.coli. Purified Nis-fusion protein was used to immunize mice whose sera were used for ELISA (positive result), FACS analysis (Figure 4C), western blot (Figure 1E), and a bactericidal assay (Figure 4D). These experiments confirm that 519 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipathic regions of ORF 519 are provided in Figure 8. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996; *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 519 and the amino acid sequence encoded thereby as provided herein.

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1459>:

```

g520.seq
1  atgcctgcgc ttctttcaat acgtcgggca aacgcgctgc ctttttcgcg
51  catttcggaa aggatgaagt tgctgggtgcc gttaataatg ccggcgatgg
101 atttaatcct gtttgccgcc aaaccttcgc gcacggcttt gatgattggg
151 ataccgcccg ctactgccgc ttcaaattgg acgatgacgt tttgtttttc
201 cgccagcggg aagatttcgt tgccgtattc ggcgagcagt tttttgttg
251 cggtaacgat gtgtttgccg ttttcaatgg ctttcaacac cgcttctttg
301 gcaatgcccg tgccgccgaa caattcgacc aagacatcga cgtctttacg
351 cgcgaacagt tcgaacggat cttttgacaa gggcgggcga cgggccgatt
401 ttggcgggct ttttcttcgc ttaagtcgca catggcagaa atacggattt
451 cgcgcccacg gcggcgggaa atttcctctg cgttgctccc caacacggca
501 gccgcaccgc cgccgacgct acctaagcct aaaagaccga tgtttactgg
551 cttcattgtg tctccttgta agccgactga aatgtaaata ttga

```

This corresponds to the amino acid sequence <SEQ ID 1460; ORF 520.ng>:

```

g520.pep
1  MPALLSIRRA NALPFSRISE RMKLLVPLIM PAMDILIFAA KPSRTALMIG
51  IEPATAASNW TMTFCFSASG KISLPYSASS FLLAVTMCLP FSMAFNTASL
101 AMPVPPNNST KTSTSLRANS SNGSFDKGGG RADFGGLFLR LSRTWQKYGF
151 RAPSGGKFPL RCPATRQPHR RRPYLSLKDR CLLASLCLLV SRLKCKY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1461>:

```

m520.seq
1  ATGCCTGCGC TTCTTTCAGT ACATCG.GCA AACGCGCTGC CTTTTTCGCG
51  CATTTTCGGrk AGGATGAAGT TGCTGGTGCC GTTAATAATG CCGGCGATGG
101 ATTTAATCCT GTTTGCCGCC AAACCTTCGC GCAGGGCTTT GATGATTGGG
151 ATACCGCCCG CTACTGCCGC TTCAAATTGG ACGATGACGT TTTGTTTTTC
201 CGCCAGCGGG AAGATTTCGT TGCCGTATTC GCGAGCAGT TTTTGTGTGG
251 CGGTAACGAT GTGTTTGCCG TTTTCAATGG CTTTCAACAC CGCATCTTTG

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301 GCAATGCCGG TACCGCCGaA CAATTCGACG ACGACATCGA CGTCTTCACG
351 TGCGACCACT TCGAACGGAT CTTTGACAAA GGCTGc.CGG ACGGGCAGGT
401 TTGTCGGGCT TTTTCTTCAC TCAAATCGCA CACGGCAGAA ATACGGATTT
451 CGCGCCCCAA GCGACGGGAA ATTTCTCTCG CGTTGTCCsCG CAACACGGCA
501 GCCGTACCGC CGCCGACCGT ACCCAAACCT AAAAGACCGA TGTTTACTGG
551 CTTCAATTGTG TCTCCTTGTA AGCCGACTGA AATGTAAATA TTGA

```

This corresponds to the amino acid sequence <SEQ ID 1462; ORF 520>:

```

m520.pep
  1 MPALLSVHXA NALPFSRISX RMKLLVPLIM PAMDILFAA KPSRRALMIG
 51 IPPATAASNW TMTFCFSASG KISLPYSASS FLLAVTMCLP FSMAFNTASL
101 AMPVPPNNST TTSTSSRATS SNGSLTKAXR TGRFVGLFLH SNRTROKYGF
151 RAPSDGKFPP RCXATROPYR RRPYPNLKDR CLLASLCLLV SRLKCKY*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 520 shows 87.3% identity over a 197 aa overlap with a predicted ORF (ORF 520.ng) from *N. gonorrhoeae*:

```

m520/g520
      10      20      30      40      50      60
m520.pep MPALLSVHRANALPFSRISXRMKLLVPLIMPAMDILFAAKPSRRALMIGIPPATAASNW
      |||||::||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g520      MPALLSIRANALPFSRISERMKLLVPLIMPAMDILFAAKPSRTALMIGIPPATAASNW
      10      20      30      40      50      60

      70      80      90      100     110     120
m520.pep TMTFCFSASGKISLPYSASSFLLAVTMCLPFSMAFNTASLAMPVPPNNSTTTSTSSRATS
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g520      TMTFCFSASGKISLPYSASSFLLAVTMCLPFSMAFNTASLAMPVPPNNSTKTSTSLRANS
      70      80      90      100     110     120

      130     140     150     160     170     180
m520.pep SNGSLTKAARTGRFVGLFLHSNRTROKYGFRAPSDGKFPPRCXATROPYRRRPYPNLKDR
      ||||| :||| :||| ||||| :||| ||||| ||||| ||||| ||||| :|||
g520      SNGSFDKGGRRADFGGLFLRLSRTWQKYGFRAPSGGKFPLRCPATROPYRRRPYLSLKDR
      130     140     150     160     170     180

      190
m520.pep CLLASLCLLVSRKCKY
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g520      CLLASLCLLVSRKCKY
      190

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1463>:

```

a520.seq
  1 ATGCCTGCGC TTCTTTCAGT ACATCGG.CA AACGCGCTGC CTTTTTCGCG
 51 CATTTTCGAG AGGATGAAGT TGCTGGTGCC GTTAATAATG CCGGCGATGG
101 ATTTAATCCT GTTTGCCGCC AAACCTTCGC GCAGGGCTTT GATGATTGGG
151 ATACCGCCCG CTACTGCCGC TTCAAATTGG ACGATGACGT TTTGTTTTTC
201 CGCCAGCGGG AAGATTTTCGT TGCCGTATTC GGCGAGCAGT TTTTGTGTGG
251 CGGTAACGAT GTGTTTGCCG TTTTCAATGG CTTTCAACAC CGCATCTTTG
301 GCAATGCCGG TACCGCCGAA CAATTCGACG ACGACATCGA CGTCTTCACG
351 TGCGACCACT TCGAACGGAT CTTTGACAAA GGCTG..CGG ACGGGCAGGT
401 TTGTCGGGCT TTTTCTTCAC TCAAATCGCA CACGGCAGAA ATACGGATTT
451 CGCGCCCCAA GCGACGGGAA ATTTCTCTCG CGTTGTCCCG CAACACGGCA
501 GCCGTACCGC CGCCGACCGT ACCCAAACCT AAAAGACCGA TGTTTACTGG
551 CTTCAATTGTG TCTCCTTGTA AGCCGACTGA AATGTAAATA TTGA

```

This corresponds to the amino acid sequence <SEQ ID 1464; ORF 520.a>:

```

a520.pep
  1 MPALLSVHRX NALPFSRISE RMKLLVPLIM PAMDILFAA KPSRRALMIG
 51 IPPATAASNW TMTFCFSASG KISLPYSASS FLLAVTMCLP FSMAFNTASL
101 AMPVPPNNST TTSTSSRATS SNGSLTKAXR TGRFVGLFLH SNRTROKYGF

```

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151 RAPSDGKFPP RCPATRQPYR RRPYPNLKDR CLLASLCLLV SRLKCKY*

m520/a520 98.0% identity in 197 aa overlap

	10	20	30	40	50	60
m520.pep	MPALLSVHXANALPFSRISXRMKLLVPLIMPANDLILFAAKPSRRALMIGIPPATAASNW					
a520	MPALLSVHRXNALPFSRISERMKLLVPLIMPANDLILFAAKPSRRALMIGIPPATAASNW					
	10	20	30	40	50	60
	70	80	90	100	110	120
m520.pep	TMTFCFSASGKISLPYSASSFLAVTMCLPFSMAFNNTASLAMPVPPNNSTTTSTSSRATS					
a520	TMTFCFSASGKISLPYSASSFLAVTMCLPFSMAFNNTASLAMPVPPNNSTTTSTSSRATS					
	70	80	90	100	110	120
	130	140	150	160	170	180
m520.pep	SNGSLTKAXRTGRFVGLFLHSNRTROKYGERAPSDGKFPPRCXATRQPYRRRPYNLKDR					
a520	SNGSLTKAXRTGRFVGLFLHSNRTROKYGERAPSDGKFPPRCXATRQPYRRRPYNLKDR					
	130	140	150	160	170	180
	190					
m520.pep	CLLASLCLLVSRKCKYX					
a520	CLLASLCLLVSRKCKYX					
	190					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1465>:

g520-1.seq

```

1  ATGAAGTTGC TGGTGCCGTT AATAATGCCG GCGATGGATT TAATCCTGTT
51  TGCCGCCAAA CCTTCGCGCA GGGCTTTGAT GATTGGGATA CCGCCCGCTA
101 CTGCCGCTTC AAATTGGACG ATGACGTTTT GTTTTCCGC CAGCGGGAAG
151 ATTCGTTGCG CGTATTCGGC GAGCAGTTTT TTGTTGGCGG TAACGATGTG
201 TTTGCCGTTT TCAATGGCTT TCAACACCGC TTCTTTGGCA ATGCCCGTGC
251 CGCCGAACAA TTCGACGACG ACATCGACGT CTTTACGCGC GACCAGTTCG
301 AACGGATCTT TGACAAAGGC GCGGACGGG CAGATTGGCG GGGCTTTTTC
351 TTCGCTTAAG TCGCACATGG CAGAAATACG GATTTCGCGC CCCAAGCGGC
401 GGGAAATTTT CTCTGCGTTG TCCCGCAACA CGGCAGCCGC ACCGCCGCCG
451 ACCGTACCTA AGCCTAAAG ACCGATGTTT ACTGGCTTCA TTGTGTCTCC
501 TTGTAAGCCG ACTGAAATGT AA

```

This corresponds to the amino acid sequence <SEQ ID 1466; ORF 520-1.ng>:

g520-1.pep

```

1  MKLLVPLIMP AMDLILFAAK PSRRALMIGI PPATAASNWT MTFCSASGK
51  ISLPYSASSE LLAVTMCLPF SMAFNNTASLA MPVPPNNSTT TSTSLRATSS
101 NGSLTKAADG QIWRAFSSLK SHMAEIRISR PKRREISSAL SRNTAAAPPP
151 TVPKPRPMF TGFIVSPCKP TEM*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1467>:

m520-1.seq

```

1  ATGAAGTTGC TGGTGCCGTT AATAATGCCG GCGATGGATT TAATCCTGTT
51  TGCCGCCAAA CCTTCGCGCA GGGCTTTGAT GATTGGGATA CCGCCCGCTA
101 CTGCCGCTTC AAATTGGACG ATGACGTTTT GTTTTCCGC CAGCGGGAAG
151 ATTCGTTGCG CGTATTCGGC GAGCAGTTTT TTGTTGGCGG TAACGATGTG
201 TTTGCCGTTT TCAATGGCTT TCAACACCGC ATCTTTGGCA ATGCCCGTAC
251 CGCCGAACAA TTCGACGACG ACATCGACGT CTTACAGTGC GACCAGTTCG
301 AACGGATCTT TGACAAAGGC TCGGACGGG CAGTTTGTG GGGCTTTTTC
351 TTTACTCAAA TCGCACACGG CAGAAATACG GATTTCGCGC CCCAAGCGAC
401 GGGAAATTTT CTCCGCGTTG TCCCGCAACA CGGCAGCCGT ACCGCCGCCG
451 ACCGTACCCA AACCTAAAG ACCGATGTTT ACTGGCTTCA TTGTGTCTCC
501 TTGTAAGCCG ACTGAAATGT AA

```

This corresponds to the amino acid sequence <SEQ ID 1468; ORF 520-1>:

m520-1.pep

```

1  MKLLVPLIMP AMDLILFAAK PSRRALMIGI PPATAASNWT MTFCSASGK
51  ISLPYSASSE LLAVTMCLPF SMAFNNTASLA MPVPPNNSTT TSTSSRATSS

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101 NGSLTKAADG QVCRAFSSLK SHTAEIRISR PKRREISSAL SRNTAAVPPP
151 TVPKPKRPMF TGFIVSPCKP TEM*

g520-1/m520-1 97.1% identity in 173 aa overlap

	10	20	30	40	50	60
g520-1.pep	MKLLVPLIMPAMD	LILFAAKPSRRAL	MIGIPPATAASN	WTMTFCFSASG	KISLPYSASSF	
m520-1	MKLLVPLIMPAMD	LILFAAKPSRRAL	MIGIPPATAASN	WTMTFCFSASG	KISLPYSASSF	
	10	20	30	40	50	60
	70	80	90	100	110	120
g520-1.pep	LLAVTMCLPFSMA	ENTASLAMPVPP	NNSTTTSTSLR	ATSSNGSLTKA	ADGQIWRAFSS	SLK
m520-1	LLAVTMCLPFSMA	ENTASLAMPVPP	NNSTTTSTSSR	ATSSNGSLTKA	ADGQVCRAFSS	SLK
	70	80	90	100	110	120
	130	140	150	160	170	
g520-1.pep	SHMAEIRISRPKR	REISSALSRNTAA	PPPTVPKPKRPM	FTGFIVSPCKP	TEMX	
m520-1	SHTAEIRISRPKR	REISSALSRNTAA	PPPTVPKPKRPM	FTGFIVSPCKP	TEMX	
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1469>:

a520-1.seq
1 ATGAAGTTGC TGGTGCCGTT AATAATGCCG GCGATGGATT TAATCCTGTT
51 TGCCGCCAAA CCTTCGCGCA GGGCTTTGAT GATTGGGATA CCGCCCGCTA
101 CTGCCGCTTC AAATTGGACG ATGACGTTTT GTTTTCCGCG CAGCGGGAAG
151 ATTTGCTTGC CGTATTCGGC GAGCAGTTTT TTGTTGGCGG TAACGATGTG
201 TTTGCCGTTT TCAATGGCTT TCAACACCGC ATCTTTGGCA ATGCCGGTAC
251 CGCCGAACAA TTCGACGACG ACATCGACGT CTTACGTCG GACCAGTTCG
301 AACGGATCTT TGACAAAGGC TCGGACGGG CAGGTTTGTG GGGCTTTTTC
351 TTCACTCAAA TCGCACACGG CAGAAATACG GATTTCGCGC CCCAAGCCGAC
401 GGGAAATTTT CTCCGCGTTG TCCCGCAACA CGGCAGCCGT ACCGCCGCGG
451 ACCGTACCCA AACCTAAAAG ACCGATGTTT ACTGGCTTCA TTGTGTCTCC
501 TTGTAAGCCG ACTGAAATGT AA

This corresponds to the amino acid sequence <SEQ ID 1470; ORF 520-1.a>:

a520-1.pep
1 MKLLVPLIMP AMDLILFAAK PSRRALMIGI PPATAASNWT MTFCSASGK
51 ISLPYSASSF LLAVTMCLPF SMAFNTASLA MPVPPNNSTT TSTSSRATSS
101 NGSLTKAADG QVCRAFSSLK SHTAEIRISR PKRREISSAL SRNTAAVPPP
151 TVPKPKRPMF TGFIVSPCKP TEM*

m520-1/a520-1 100.0% identity in 173 aa overlap

	10	20	30	40	50	60
a520-1.pep	MKLLVPLIMPAMD	LILFAAKPSRRAL	MIGIPPATAASN	WTMTFCFSASG	KISLPYSASSF	
m520-1	MKLLVPLIMPAMD	LILFAAKPSRRAL	MIGIPPATAASN	WTMTFCFSASG	KISLPYSASSF	
	10	20	30	40	50	60
	70	80	90	100	110	120
a520-1.pep	LLAVTMCLPFSMA	ENTASLAMPVPP	NNSTTTSTSSR	ATSSNGSLTKA	ADGQVCRAFSS	SLK
m520-1	LLAVTMCLPFSMA	ENTASLAMPVPP	NNSTTTSTSSR	ATSSNGSLTKA	ADGQVCRAFSS	SLK
	70	80	90	100	110	120
	130	140	150	160	170	
a520-1.pep	SHTAEIRISRPKR	REISSALSRNTAA	PPPTVPKPKRPM	FTGFIVSPCKP	TEMX	
m520-1	SHTAEIRISRPKR	REISSALSRNTAA	PPPTVPKPKRPM	FTGFIVSPCKP	TEMX	
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1471>:

g521.seq
1 ATGAAATCAA AACTCCCTT AATCCTAATC AACCTTTCCC TGATTTCAG
51 CCCATTGGGT GCGAATGCGG CCAAAATCTA TACCTGCACA ATCAACGGAG
101 AAACCGTTTA CACCACCAAG CCGTCTAAAA GCTGCCACTC AACCGATTG

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151 CCCCCAATCG GCAACTACAG CAGCGAACGC TATATCCTGC CCCAACTCC
201 CGAACCGGCA CCATCACCGT CAAACGGCGG ACAGGCTGTC AAATATAAAG
251 CCCCAGTCAA AACAGTATCC AAGCCGGCAA AATCCAATAC GCCGCCTCAA
301 CAAGCACCTG TAAATAACAG CAGACGCTCC ATTCTcgaag caGaattaa
351 cAatgaacgc aaagccctGa ctGaAGCCCA AAAAATGTTA TCACAagcac
401 gtCtGGCAAA AGGCGGcaAC AtcaaCCatc aaaAaatcaa cgcattgtaa
451 AGCAATGTTt tggacAGACA GCAAAATaTC Caagcactgc aaaGAgAATt
501 GGGACGTATG TAA

```

This corresponds to the amino acid sequence <SEQ ID 1472; ORF 521.ng>:

```

g521n.pep
1 MKSKLPLILI NLSLISSPLG ANAAKIYTCT INGETVYTTK PSKSCHSTD
51 PPIGNYSSER YILPQTPEPA PPSNGGQAV KYKAPVKTVS KPAKSNTTPQ
101 QAPVNNRRS ILEAELSNER KALTEAQKML SQARLAKGN INHQKINAL*
151 SNVLDROQNI QALQRELGRM *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1473>:

```

m521.seq
1 ATGAAATCAA AACTCCTCTT AATCCTAATC AACTTTTCCC TGATTTCAG
51 CCCATTGGGT GCGAATGCGG CCAAAATCTA sACCTGCACA ATCAACGGAG
101 AAACCGTTTA CACCAaCAAG CCGTCCAAAA GCTGCCACTC AACCGATTG
151 CCCCCAATCG GCAACTACAG CAGCGAACGC TATATCCCGC CCCAAACGCC
201 CGAACCGGTA TCATCACCGT CAAACGGCGG ACwGGTTGTC AAATATAAAG
251 CCCCAGTCAA AACAGTATCC AAGCCGGCAA AATCCAATAC GCCGCCTCAA
301 CAACAAGCAC CCTCAAACAA CAGCAGACGC TCCATTCTCG AAACAGAATT
351 GAGCAACGAA CGCAAAGCAT TGGTTGAAGC CCAAAAAATG TTATACAAG
401 CACGTCTGGC AAAGGGCGGC AACATCAACC ATCAAGAAAT AAATGCATTA
451 CAAAGCAATG TATTGGACAG GCAGCAAAT ATTCAAGCCC TGCAAAGGGA
501 ACTGGGGCGT ATGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1474; ORF 521>:

```

m521.pep
1 MKSKLLLLILI NLSLISSPLG ANAAKIXTCT INGETVYTXK PSKSCHSTD
51 PPIGNYSSER YIPPQTPEPV SPSNGGXVV KYKAPVKTVS KPAKSXTPPP
101 QAPSNNRRS SILETELSNE RKALVEAQKM LSQARLAKGG NINHQEINAL
151 QSNVLDROQN IQALQRELGR M*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 521 shows 90.6% identity over a 171 aa overlap with a predicted ORF (ORF 521.ng) from *N. gonorrhoeae*:

m521/g521

	10	20	30	40	50	60
m521.pep	MKSKLLLLILINFLISSPLGANAAKIXTCTINGETVYTXKPSKSCHSTDLPPIGNYSSER					
	: : : : : : : : :					
g521	MKSKLPLILINLSLISSPLGANAAKIYTCTINGETVYTTKPSKSCHSTDLPPIGNYSSER					
	10	20	30	40	50	60
	70	80	90	100	110	120
m521.pep	YIPPQTPEPVSSPSNGGXVVKYKAPVKTVSKPAKSXTPPPQAPSNNRRSILETELSNE					
	: : : : : : : :					
g521	YILPQTPEPAPSPSNGGQAVKYKAPVKTVSKPAKSNTTPP-QQAPVNNRRSILEAELSNE					
	70	80	90	100	110	
	130	140	150	160	170	
m521.pep	RKALVEAQKMLSQARLAKGGNINHQEINALQSNVLDROQNIQALQRELGRMX					
	: : : : : : : :					
g521	RKALTEAQKMLSQARLAKGGNINHQKINALXSNVLDROQNIQALQRELGRMX					
	120	130	140	150	160	170

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1475>:

```

a521.seq
1 ATGAAATCAA AACTCCCCTT AATCCTAATC AACTTTTCCC TGATTTCAG

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```

51 CCCATTGGGT GCGAATGCGG CCAAAATCTA CACCTGCACA ATCAACGGAG
101 AAACCGTTTA CACCACCAAG CCGTCCAAAA GCTGCCTCTC AACCGATTTG
151 CCCCCAATCG GCAACTACAG CAGCGAACGC TATATCCCGC CCCAACATC
201 CGAACCGACA CCATCACCGT CAAACGGCGG ACAGGCTGTC AAATATAAAG
251 CCCCGGTCAA AACAGTATCC AAGCCGGCAA AATCCAATAC GCCGCCGCCG
301 CAACAAGCAC CCTCAAACAA CAGCAGACGC TCCATTCTCG AAACAGAATT
351 GAGCAACGAA CGCAAAGCAT TGGTTGAAGC CAAAAAATG TTATCACAAG
401 CACGCTGGC AAAAGGCGGC AACATCAACC ATCAAGAAAT CAACGCATTG
451 CAAAGCAATG TATTGGACAG GCAGCAAAAT ATCCAAGCAC TGCAAAGAGA
501 ATGGGACGT ATGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1476; ORF 521.a>:

```

a521.pep
1  MKSKLPLILI NFSLISSPLG ANAAKIYTCT INGETVYTTK PSKSLSTDL
51  PPIGNYSSER YIPPQTSEPT PSPSNGGQAV KYKAPVKTVS KPAKSNTPPP
101 QQAPSNNRRR SILETELSNE RKALVEAQKM LSQARLAKGG NINHQEINAL
151 QSVLDRQON IQALQRELGR M*

```

m521/a521 94.2% identity in 171 aa overlap

	10	20	30	40	50	60
m521.pep	MKSLLLLILINFSLISSPLGANAAKIXTCTINGETVYTXKPSKXSCHSTDLPPIGNYSSER					
a521	MKSKLPLILINFSLISSPLGANAAKIYTCTINGETVYTTKPSKSLSTDLPPIGNYSSER					
	10	20	30	40	50	60
	70	80	90	100	110	120
m521.pep	YIPPQTPEPVSSPSNGGXVVVKYKAPVKTVSKPAKSXTPEPQQAPSNNRRRSILETELSNE					
a521	YIPPQTSEPTSPSNGGQAVKYKAPVKTVSKPAKSNTPEPQQAPSNNRRRSILETELSNE					
	70	80	90	100	110	120
	130	140	150	160	170	
m521.pep	RKALVEAQKMLSQARLAKGGNINHQEINALQSNVLDROQNIQALQRELGRMX					
a521	RKALVEAQKMLSQARLAKGGNINHQEINALQSNVLDROQNIQALQRELGRMX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1477>:

```

g522.seq
1  atgactgagc cgaaacacga aacgccgacg gaagagcagg ttgccgcgcg
51  caaaaaagca aaagccaaaa tccgcaccat ccgcatttgg gcgtgggtca
101 ttttgcggtt gctcgcttca accgccctgc tctcccaatg cgcgatgtcc
151 aaaccgcagg caaaacagaa aattgtcgag tcttgcataa aaaatattcc
201 gtttgctgaa aaatggcaga acgatttgaa agcgcgcggc ttggatgcgg
251 acaatacccg tctcgccgct gactactgca aatgtatgtg ggagcagcct
301 ttggacggat tgagcgagaa acagatcagc tccttcggca aactcgggtg
351 acaagaacag cttgacctgc tcggcggcgc aaacgcgttt gaaactcgag
401 acaaacaatg tgtcgcggat ttgaaagccg attga

```

This corresponds to the amino acid sequence <SEQ ID 1478; ORF 522.ng>:

```

g522.pep
1  MTEPKHETPT EEQVAARKKA KAKIRTIRIW AWVILALLAS TALLSQCAMs
51  KPQAKQKIVE SCMKNIFFAE KWQNDLKARG LDADNTRLAV DYCKCMWEQP
101 LDGLSEKQIS SFGKLGAQEQ LDLLGGANAF ETRDKQCVAD LKAD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1479>:

```

m522.seq
1  ATGACTGAGC CGAAACACGA AATGCTGACG AAAGAGCAGG TTGCCGCGCG
51  CAAAAAAGCA AAAGCCAAAA TCGCACCAT CCGCATTGCG GCGTGGGTCA
101 TTTTGGCGTT GCTCGCTTTA ACCGCCCTGC TCTCCCAATG CGCGATGTCC
151 AAACCGCAGG CAAAACAGAA AATTGTCGAG TCTTGCGTGA AGAATATTCC
201 GTTTGCCGAA AAATGGCAAA ACGATTGCGG GGCCCGCGGT TTAGATTCAA
251 ACAATACCCG CCTCGCCGTC GACTACTGCA AATGTATGTG GGAGCAGCCT

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301 TTGGACAGAT TGAGCGAGAA ACAGATTAGA TCCTTCGGCA AACTCGGCGC
 351 ACAAGAACAG CTTGACCTGC TCGGCGGCGC AAATGCCTTT GAAGCACGTG
 401 ACAAGCAGTG TGTGCGCAT TTGAAATCAG AATAA

This corresponds to the amino acid sequence <SEQ ID 1480; ORF 522>:

m522.pep

1 MTEPKHEMLT KEQVAARKKA KAKIRTIRIW AWVILALLAL TALLSQCAMS
 51 KPQAKQKIVE SCVKNIPFAE KWQNDLRARG LDSNNTRLAV DYCKCMWEQP
 101 LDRLSEKQIR SFGKLGAQEQ LDLLGGANAF EARDKQCVAD LKSE*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 522 shows 91.0% identity over a 144 aa overlap with a predicted ORF (ORF 522.ng) from *N. gonorrhoeae*:

m522/g522

	10	20	30	40	50	60
m522.pep	MTEPKHEMLTKEQVAARKKAKAKIRTIRIWAWVILALLALTALLSQCAMSKPQAKQKIVE					
	:					
g522	MTEPKHETPTEEQVAARKKAKAKIRTIRIWAWVILALLASTALLSQCAMSKPQAKQKIVE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m522.pep	SCVKNIPFAEKWQNDLRARGLDSNNTRLAVDYCKCMWEQPLDRLSEKQIRSFGLGAQEQ					
	: : :					
g522	SCMKNIPFAEKWQNDLKARGLDADNTRLAVDYCKCMWEQPLDGLSEKQISSFGLGAQEQ					
	70	80	90	100	110	120
	130	140				
m522.pep	LDLLGGANAFEARDKQCVADLKSEX					
	: : :					
g522	LDLLGGANAFETRDKQCVADLKAD					
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1481>:

a522.seq

1 ATGACTGAGC CGAAACACGA AATGCCGACG GAAGAGCAGG TTGCCGCGCG
 51 CAAAAAAGCA AAAGCCAAAA TCCGCACCAT CCGCATTGG GCATGGGTCA
 101 TTTTGGCGTT GCTCGCTTCA ACCGCCCTGC TCTCCCAATG CGCGATGTCC
 151 AAACCGCAGG CAAAACAGAA AATTGTCGAG TCTTGCGTGA AGAATATTCC
 201 GTTTGCCGAA AAATGGCAAA ACGATTGCG GGCCCGCGGT TTAGATTCAA
 251 ACAATACCG CTTACCGTC GACTACTGCA AATGTATGTG GGAGCAGCCT
 301 TTGGACAGAT TGAGCGAGAA ACAGATTAGT TCCTTCGGCA AACTCGGCGC
 351 ACAAGAACAG CTTGACCTGC TCGGCGGCGC AAATGCCTTT GAAACGCGAG
 401 ACAAGCAGTG TGTGCGCAT TTGAAATCAG AATAA

This corresponds to the amino acid sequence <SEQ ID 1482; ORF 522.a>:

a522.pep

1 MTEPKHEMPT EEQVAARKKA KAKIRTIRIW AWVILALLAS TALLSQCAMS
 51 KPQAKQKIVE SCVKNIPFAE KWQNDLRARG LDSNNTRLTV DYCKCMWEQP
 101 LDRLSEKQIS SFGKLGAQEQ LDLLGGANAF ETRDKQCVAD LKSE*

m522/a522 95.8% identity in 144 aa overlap

	10	20	30	40	50	60
m522.pep	MTEPKHEMLTKEQVAARKKAKAKIRTIRIWAWVILALLALTALLSQCAMSKPQAKQKIVE					
	:					
a522	MTEPKHEMPTTEEQVAARKKAKAKIRTIRIWAWVILALLASTALLSQCAMSKPQAKQKIVE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m522.pep	SCVKNIPFAEKWQNDLRARGLDSNNTRLAVDYCKCMWEQPLDRLSEKQIRSFGLGAQEQ					
a522	SCVKNIPFAEKWQNDLRARGLDSNNTRLTVDYCKCMWEQPLDRLSEKQISSFGLGAQEQ					
	70	80	90	100	110	120

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	130	140
m522 . pep	LDLLGGANAFEARDKQCVADLKSEX	
a522	LDLLGGANAFETRDKQCVADLKSEX	
	130	140

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1483>:

g523 . seq

```

1  atgactgtat ggtttgttgc cgctgttgcc gtcttaatca tcgaattatt
51  gacgggaacg gtttatcttt tggttgtag cgcggtttg gcgggttcgg
101 gcatctgcta cgggctgact ggcagcacgc ctgccgccgt cttgaccgcc
151 gcactgcttt ccgcgtggg catttggttc gtacatgcca aaaccgccgt
201 gggaaaagtt gaaacggatt catatcagga ttggatacc ggaaaatatg
251 ccgaaatcct ccgatacaca ggcggcaacc gttacgaagt tttttatcgc
301 ggtacgcact ggcaggcgca aaatacggg caggaagtgt ttgaaccggg
351 aacgcgcgcc ctcatcgtcc gcaaagaagg taaccttctt atcatcgcaa
401 acccttaa

```

This corresponds to the amino acid sequence <SEQ ID 1484; ORF 523.ng>:

g523 . pep

```

1  MTVWFVAAVA VLIIELLTGT VYLLVVSAA AGSGIAYGLT GSTPAAVLTA
51  ALLSALGIWF VHAKTAVGKV ETDSYQDLDT GKYAEILRYT GGNRYEVFYR
101 GTHWQAQNTG QEVFEPGTRA LIVRKEGNLL IIANP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1485>:

m523 . seq (partial)

```

1  ..GCCGTCCTAA TCATCGAATT ATTGACGGGA ACGGTTTATC TTTTGGTTGT
51  nAGCGCGGCT TTGGCGGGTT CGGGCATTGC TTACGGGCTG ACCGGCAGTA
101 CGCCTGCCGC CGTCTTGACC GnCGCTCTGC TTTCCGCGCT GGGTATTTnG
151 TTCGTACACG CCAAAACCGC CGTTAGAAAA GTTGAAACGG ATTCATATCA
201 GGATTTGGAT GCCGACAAT ATGTCGAAAT CCTCCGACAC ACAGGCGGCA
251 ACCGTTACGA AGTTTTLTAT CGCGGTACGc ACTGGCAGGC TCAAAATACG
301 GGGCAAGAAG AGCTTGAACC AGGAACCTCG GCCCTCATTG TCCGCAAGGA
351 AGGCAACCTT CTTATTATCA CACACCCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1486; ORF 523>:

m523 . pep (partial)

```

1  ..AVLIIELLTG TVYLLVVSAA LAGSGIAYGL TGSTPAAVLT XALLSALGIX
51  FVHAKTAVRK VETDSYQDLT AGQYVEILRH TGGNRYEVFY RGTWQAQNT
101 GQEELEPGTR ALIVRKEGNL LIITHP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF523 shows 91.3% identity over a 126 aa overlap with a predicted ORF (ORF 523.ng) from *N. gonorrhoeae*:

m523/g523

	10	20	30	40	50
m523 . pep	AVLIIELLTGTVYLLVVSAA LAGSGIAYGLTGSTPAAVLT XALLSALGIXF				
g523	MTVWFVAAVAVLIIELLTGTVYLLVVSAA LAGSGIAYGLTGSTPAAVLTAALLSALGIWF				
	10	20	30	40	50
	60	70	80	90	100
m523 . pep	VHAKTAVRKVETDSYQDLT AGQYVEILRH TGGNRYEVFYRGTWQAQNTGQEELEPGTRA				
g523	VHAKTAVGKVETDSYQDLT GKYAEILRYTGGNRYEVFYRGTWQAQNTGQEVFEPGTRA				
	70	80	90	100	110
	120				
m523 . pep	LIVRKEGNLLIITHP				

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g523 LIVRKEGNLLIIANPX
130

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1487>:

a523.seq
1 ATGACTGTAT GGTTTGTTCG CGCTGTTGCC GTCTTAATCA TCGAATTATT
51 GACGGGAACG GTTTATCTTT TGGTTGTCAG CGCGGCTTTG GCGGGTTCGG
101 GCATTGCTTA CGGGCTGACC GGCAGCACGC CTGCCGCCGT CTGACCGCC
151 GCTCTGCTTT CCGCGCTGGG TATTGTTTC GTACACGCCA AAACCGCCGT
201 GGGAAAAGTT GAAACGGATT CATATCAGGA TTTGGATGCC GSGCAATATG
251 CCGAATCCT CCGGCACGCA GCGGCAACC GTTACGAAGT TTTTATCGC
301 GGTACGCACT GGCAGGCTCA AAATACGGGG CAAGAAGAGC TTGAACCAGG
351 AACGCGCGCC CTAATCGTCC GCAAGGAAG CAACCTTCTT ATCATCGCAA
401 AACCTTAA

This corresponds to the amino acid sequence <SEQ ID 1488; ORF 523.a>:

a523.pep
1 MTVWFVAAVA VLIIELLTGT VYLLVVSAAAL AGSGIAYGLT GSTPAAVLTA
51 ALLSALGIWF VHAKTAVGKV ETDSYQDLDA GQYAEILRHA GGNRYEVFYR
101 GTHWQAQNTG QEELEPGTRA LIVRKEGNLL IIAKP*

m523/a523 94.4% identity in 126 aa overlap

	10	20	30	40	50
m523.pep	AVLIIELLTGTVYLLVVSAAALAGSGIAYGLTGSTPAAVLTXALLSALGIXF				
a523	MTVWFVAAVAVLIIELLTGTVYLLVVSAAALAGSGIAYGLTGSTPAAVLTAALLSALGIWF				
	10	20	30	40	50
	60	70	80	90	100
m523.pep	VHAKTAVRKVETDSYQDLDAQYVEILRHTGGNRYEVFYRGTHWQAQNTGQEELEPGTRA				
a523	VHAKTAVGKVETDSYQDLDAQYAEILRHAGGNRYEVFYRGTHWQAQNTGQEELEPGTRA				
	70	80	90	100	110
	120				
m523.pep	LIVRKEGNLLIITHPX				
a523	LIVRKEGNLLIIAKPX				
	130				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1489>:

g525.seq
1 atgaagtacg tccggttatt tttcctcggc acggcactcg ccggcactca
51 agcggcggct gccgaaatgg ttcaaactga agcggcagc taccgcccg
101 ttatctgaa aaaagatacc gccctgatta aagtcaaacc gttcaaactg
151 gataaatatc ccgttaccaa tgccgagttt gccgaatttg tcaacagcca
201 ccccaatgg caaaaaggca ggatcggttc caaacaggca gaaccgctt
251 acctgaagca ttggatgaaa aacggcagcc gcagctatgc gccgaaggcg
301 ggcgaaattga aacagccggt taccaatatt tcttggttg ccgccaacgc
351 ctattgcgcc gcacaaggca aacgcctgcc gaccatcgac gaatgggaat
401 ttgccggact tgcttcgcc acgcagaaaa aacggctcaa acgaaccgg
451 ctacaaccgc actattctcg attggtatgc cgacggcgga cggaaaaggcc
501 tgcacgatgt cggcaaagca ccgcccgaac tactggggtg tttatgatat
551 gcacgggctg a

This corresponds to the amino acid sequence <SEQ ID 1490; ORF 525.ng>:

g525.pep
1 MKYVRLFFLG TALAGTQAAA AEMVOIEGGS YRPLYLKKDT GLIKVKPFKL
51 DKYPVTNAEF AEFVNSHPQW QKGRIGSKQA EPAYLKHWMK NGSRSYAPKA
101 GELKQPVNTI SWFAANAYCA AQKRLPTID EWEFAGLASA TQKKRLKRTR
151 LQPHYSRLVC RRRTERPARC RQSTARTGV FMICTG *

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1491>:

790

```

m525.seq
1  ATGAAGTATG TCCGGTTATT TTWCCTCGGC GCGGCACTCG cCrrCACTCA
51  ArCGGCGGCT GCGGAAATGG TTCAAATCGA AGGCGGCAGC TACCGCCCrC
101 TTTATCTGAA AAAAGATACC GGCCTGATTA AAGTCAAACC GTTCAAACCTG
151 GATAAATATC CCGTTACCAA TGCCGAGTTT GCCGAATTTG TCAACAGCCA
201 CCCCCAATGG CAAAAAGGCA GGATCGGTTT CAAACAGGCA GAACCCGCTT
251 ACCTGAAGCA TTGGATGAAA AACGGCAGCC GCAGCTATGc GCCGAAGgCG
301 GgCGAATTAA AACAACCGGT AACCAATGTT TCCTGGwTTG CCGCCAAcGC
351 CTATtGCGCC GCACAAGGCA AACGCCTGCC GACCATTGAC GAATGGGAAT
401 TTGCCGGACT TGCTTCCGCC ACGCAGAAAA A.CGGCTCAA ACGAACCCGG
451 CTACAACGC ACTATTCTCG ATTGGTATGC CGACGGCGGA CGGAAAGGCC
501 TGCACGATGT CGGCA.AAGG CCGCCGAAC TACTGGGGCG TTTATGATAT
551 GCACGGGCTG A

```

This corresponds to the amino acid sequence <SEQ ID 1492; ORF 525>:

```

m525.pep
1  MKYVRLFXLG AALAXTOXAA AEMVQIEGGS YRPLYLKDDT GLIKVKPFKL
51  DKYPVTNAEF AEFVNSHPQW QKGRIGSKQA EPAYLKHWK NGSRSYAPKA
101 GELKQPVTNV SWXAANAYCA AQGKRLPTID EWEFAGLASA TQKXRLKRTR
151 LQPHYSRLVC RRRTERPARC RXKAARTTGA FMICTG*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 525 shows 94.1% identity over a 186 aa overlap with a predicted ORF (ORF 525.ng) from *N. gonorrhoeae*:

```

m525/g525
10      20      30      40      50      60
m525.pep  MKYVRLFXLGAALAXTOXAAAEMVQIEGGSYRPLYLKDDTGLIKVKPFKLDKYPVTNAEF
g525      MKYVRLFFLGTAAGTQAAAEMVQIEGGSYRPLYLKDDTGLIKVKPFKLDKYPVTNAEF
10      20      30      40      50      60

70      80      90      100     110     120
m525.pep  AEFVNSHPQWQKGRIGSKQAEPAYLKHWKNGSRSYAPKAGELKQPVTNVSWXAANAYCA
g525      AEFVNSHPQWQKGRIGSKQAEPAYLKHWKNGSRSYAPKAGELKQPVTNISWFAANAYCA
70      80      90      100     110     120

130     140     150     160     170     180
m525.pep  AQGKRLPTIDWEFAGLASATQKXRLKRTRLQPHYSRLVRRRTERPARCRXKAARTTGA
g525      AQGKRLPTIDWEFAGLASATQKRLKRTRLQPHYSRLVRRRTERPARCRQSTARTTGV
130     140     150     160     170     180

m525.pep  FMICTGX
g525      FMICTGX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1493>:

```

a525.seq
1  ATGAAGTTTA CCCGGTTACT CTTTCTCTGT GCGGCACTCG CCGGCACTCA
51  AGCGGCAGCT GCCGAAATGG TTCAAATCGA AGGCGGCAGC TACCGCCCGC
101 TTTATCTGAA AAAAGATACC GGCCTGATTA AAGTCAAACC GTTCAAACCTG
151 GATAAATATC CCGTTACCAA TGCCGAGTTT GCCGAATTTG TCAACAGCCA
201 CCCCCAATGG CAAAAAGGCA GGATCGGTTT CAAACAGGCA GAACCCGCTT
251 ACCTGAAGCA TTGGATGAAA AACGGCAGCC GCAGCTATGC GCCGAAGGCG
301 GCGGATTTAA AACAACCGGT AACCAATGTT TCCTGGTTTC CCGCCAAACGC
351 CTATTGCGCC GCACAAGGCA AACGCCTGCC GACCATTGAC GAATGGGAAT
401 TTGCCGGACT TGCTTCCGCC ACGCAG.AAA AACGGCTCAA ACGAACCCGG
451 CTACAACGC ACTATTCTCG ACTGGTATGC GGATGGCGAC CGGAAAGACC
501 TGCACGATGT CGGCAAAG.G TCGCCCGAAC TACTGGGGCG TTTATGATAT
551 GCACGGTCTG A

```

This corresponds to the amino acid sequence <SEQ ID 1494; ORF 525.a>:

```
a525.pep
  1 MKFTRLLEFLC AALAGTQAAA AEMVQIEGGS YRPLYLKKDT GLIKVKPFKL
 51 DKYPVTNAEF AEFVNSHPQW QKGRIGSKQA EPAYLKHWK NGSRSYAPKA
101 GDLKQPVTNV SWFAANAYCA AQGKRLPTID EWEFAGLASA TQXKRLKRTR
151 LQPHYSRLVC GWRPERPARC RQXVARTTGA FMICTV*
```

m525/a525 90.8% identity in 185 aa overlap

```

      10      20      30      40      50      60
m525.pep  MKYVRLFXLGAALAXTQXAAAEMVQIEGGSYRPLYLKKDTGLIKVKPFKLDKYPVTNAEF
a525      MKFTRLLEFLCAALAGTQAAAEMVQIEGGSYRPLYLKKDTGLIKVKPFKLDKYPVTNAEF
      10      20      30      40      50      60

      70      80      90     100     110     120
m525.pep  AEFVNSHPQWQKGRIGSKQAEPAYLKHWKNGSRSYAPKAGELKQPVTNVSWXAANAYCA
a525      AEFVNSHPQWQKGRIGSKQAEPAYLKHWKNGSRSYAPKAGDLKQPVTNVSWFAANAYCA
      70      80      90     100     110     120

      130     140     150     160     170     180
m525.pep  AQGKRLPTIDWEFAGLASATQXKRLKRTRLQPHYSRLVCRRRTERPARCRXKAARTTGA
a525      AQGKRLPTIDWEFAGLASATQXKRLKRTRLQPHYSRLVCGWRPERPARCRQXVARTTGA
      130     140     150     160     170     180

m525.pep  FMICTGX
a525      FMICTVX
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1495>:

```
g525-1.seq
  1 ATGAAGTACG TCCGGTTATT TTCTCTCGGC ACGGCACTCG CCGGCCTCA
 51 AGCGGCGGCT GCCGAAATGG TTCAAATCGA AGGCGGCAGC TACCGCCCGC
101 TTTATCTGAA AAAAGATACC GGCCTGATTA AAGTCAAACC GTTCAAACCTG
151 GATAAATATC CCGTTACCAA TSCCGAGTTT GCCGAATTG TCAACAGCCA
201 CCCCCAATGG CAAAAAGGCA GSATCGGTTT CAAACAGGCA GAACCCGCTT
251 ACCTGAAGCA TTGGATGAAA AACGGCAGCC GCAGCTATGC GCCGAAGCGG
301 GGCGAATTGA AACAGCCGGT TACCAATATT TCCTGGTTTG CCGCCAACGC
351 CTATTGCGCC GCACAAGGCA AACGCCCTGCC GACCATCGAC GAATGGGAAT
401 TTGCCGGACT TGCTTCCGCC ACGCAGAAAA ACGGCTCAAA CGAACCCTGC
451 TACAACCGCA CTATTCTCGA TTGGTATGCC GACGGCGGAC GGAAGGCCCT
501 GCACGATGTC GGCAAAGACC GCCCGAACTA CTGGGGTGT TATGATATGC
551 ACGGCTGAT TTGGGAATGG ACGGAAGATT TCAACAGCAG CCTGCTTTCT
601 TCCGGCAATG CCAACGCGCA AATGTTTGC AGCGGCGCAT CTGTCGGGGC
651 GAGCGACTCG TCCAACTATG CCGCCTTCCT CCGCTACGGC ATCCGCACCA
701 GCCTGCAATC CAAATACGTC CTGCACAACT TGGGCTTCCG CTGCGCAAGC
751 CGATAA
```

This corresponds to the amino acid sequence <SEQ ID 1496; ORF 525-1.ng>:

```
g525-1.pep
  1 MKYVRLFFLG TALAGTQAAA AEMVQIEGGS YRPLYLKKDT GLIKVKPFKL
 51 DKYPVTNAEF AEFVNSHPQW QKGRIGSKQA EPAYLKHWK NGSRSYAPKA
101 GELKQPVTNI SWFAANAYCA AQGKRLPTID EWEFAGLASA TQKNGSNEPG
151 YNRTILDWYA DGGKRLHDV GKDRPNYGV YDMHGLIEWE TEFNSLLS
201 SGNANAQMEF SGASVGASDS SNYAAFLRYG IRTSLQSKYV LHNLFRCAS
251 R*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1497>:

```
m525-1.seq
  1 ATGAAGTATG TCCGGTTATT TTCTCTCGGC GCGGCACTCG CCGGCCTCA
 51 AGCGGCGGCT GCCGAAATGG TTCAAATCGA AGGCGGCAGC TACCGCCCGC
101 TTTATCTGAA AAAAGATACC GGCCTGATTA AAGTCAAACC GTTCAAACCTG
```


m525-1.ppt

1	MKYVRLFFLG	AALAGTQAAA	AEMVQIEGGS	YRPLYLKKDT	GLIKVKPFKL
51	DKYPVPTNAEF	AEFVNSHPQW	QKGRISSKQA	EWFLKHHMK	NGSRSYAPKA
101	GELKQPVPTNV	SFWAANAQA	AQGRKLPTID	EPEYFAGLAS	TQKNGSNPEG
151	YNRTILDWYA	DGGRKGLHDV	GKGRPNYWG	YDMHGLINW	TEDFNSSLLS
201	SGNANAQMFC	SGASIGSSDS	SNYAAFLRYG	IRTSLSQSYV	LHNLGFRCTS
251	R*				

	10	20	30	40	50	60
m525-1.pep	MKYVRLFFFLGAALAGTQAAAAEMVQ	IEGGSYRPLYLKKDTGLIKVKPFLDKYPVTNAEF				
g525-1	MKYVRLFFFLGTALAGTQAAAAEMVQ	IEGGSYRPLYLKKDTGLIKVKPFLDKYPVTNAEF				
	10	20	30	40	50	60
	70	80	90	100	110	120
m525-1.pep	AEFVNSHPQWQKGRIGSKQAEPA	YLKHWMKNGSRSYAPKAGELKQPV	TNVSWFAANAYCA			
g525-1	AEFVNSHPQWQKGRIGSKQAEPA	YLKHWMKNGSRSYAPKAGELKQPV	TNISWFAANAYCA			
	70	80	90	100	110	120
	130	140	150	160	170	180
m525-1.pep	AQGKRLPTIDEWEFAGLASATQK	NGSNEPGYNRTILDWYADGGRKGLH	DVGKGRPNYGV			
g525-1	AQGKRLPTIDEWEFAGLASATQK	NGSNEPGYNRTILDWYADGGRKGLH	DVGKDRPNYGV			
	130	140	150	160	170	180
	190	200	210	220	230	240
m525-1.pep	YDMHGLIEWETEDFNSSLLSSGN	ANAMFCSGASIGSSDSSNYAAF	FLRYGIRTSLQSKYV			
g525-1	YDMHGLIEWETEDFNSSLLSSGN	ANAMFCSGASVGSDDSSNYAAF	FLRYGIRTSLQSKYV			
	190	200	210	220	230	240
	250					
m525-1.pep	LHNLGFRCTSRX					
g525-1	LHNLGFRCSRX					
	250					

a525-1.seq

1	ATGAAGTTTA	CCCGGTTACT	CTTTCTCTGT	GCGGCACTCG	CCGGCACTCA
51	AGCGGCAGCT	CGCGAAATGG	TTCAAATCGA	AGGCGCAAGC	TACCCGCCCG
101	TTGCTTCGAA	AAAAGATAAC	GGCTGTGATTA	AAGTCAACAC	GTTCCAAACTGT
151	GATAAAATATC	CCGTTACCAA	TGCCGAGTTT	GCCGAATTTG	TCAACAGCCA
201	CCCCCAATGG	CAAAAAGGCA	GGATCGGTTT	CAAAACAGGCA	GAACCCCGTT
251	ACCTGAAGCA	TGTGATGAAA	AACGCGACGC	GACGATATGC	GCCGAAGGCG
301	GGCGATTTTAA	AACAACCGGT	AACCAATGTT	TCCTGGTTTC	CCGCGAACAAC
351	CTATTGCGCC	GCAACAAGCT	AACCGCTGCC	GACGATTGAC	GAATGGGAAT
401	TTGCCGGACT	TGCTTCCGCC	ACGCAGAAAA	ACGGCTCAA	CGAACCCGGC
451	TACAACCGCA	CTATTCTCGA	CTGGTATGCG	GATGGCGCAT	GGAAGAGCTT
501	GCACGATGTC	GGCAAAAGTC	GCCCGAACTA	CTGGGGCGTT	TATGATATGC
551	ACCGCTCGAT	TGTGGGAATG	ACGGAAGATT	TCAACAGCAG	CCTGCTTTCT
601	TCCGGCAATG	CCAACGCGCA	AATGTTTTCG	AGCGGCGCGT	CTATCGGGTG
651	GAGCGACTCG	TCCAACATATG	CGCGTTCCTT	CCGCTACGCG	ATTCGCAACA
701	CGCTCGCAATC	CAAATATGTC	TTGCACAAC	TGGGCTTCGG	TTGCACAACG
751	CGATAA				

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This corresponds to the amino acid sequence <SEQ ID 1500; ORF 525-1.a>:

a525-1.pep

```

1  MKFTRLFLC AALAGTQAAA AEMVQIEGGS YRPLYLKDT GLIKVKPFKL
51  DKYPTNAEF AEFVNSHPQW QKGRIGSKQA EPAYLKHWK NGSRSYAPKA
101 GDLKQPVTV SWFAANAYCA AOGKRLPTID EWEFAGLASA TOKNGSNEPG
151 YNRTILDWYA DGDRLDHDV GKGRPNYWG VYDMHGLIEWE TEDFNSSLSS
201 SGNANAQMFC SGASIGSSDS SNYAAFLRYG IRTSLQSKYV LHNLGFRCTS
251 R*
```

m525-1/a525-1 97.2% identity in 251 aa overlap

	10	20	30	40	50	60
m525-1.pep	MKYVRLFFLGAALACTQAAA	AEMVQIEGGSYRPLYLKDTGLIKVKPFKLDKYPVTNAEF				
a525-1						
	10	20	30	40	50	60
	70	80	90	100	110	120
m525-1.pep	AEFVNSHPQWQKGRIGSKQAE	PAYLKHWKNGSRSYAPKAGELKQPV	TNVS	SWFAANAYCA		
a525-1						
	70	80	90	100	110	120
	130	140	150	160	170	180
m525-1.pep	AQGKRLPTIDWEFAGLASATQ	KNGSNEPGYNRTILDWYADGGRKGLHDV	GKGRPNYWG			
a525-1						
	130	140	150	160	170	180
	190	200	210	220	230	240
m525-1.pep	YDMHGLIEWETEDFNSSLSS	SGNANAQMFCSGASIGSSDSSNYAAFLRYG	GIRTS	LQSKYV		
a525-1						
	190	200	210	220	230	240
	250					
m525-1.pep	LHNLGFRCTSRX					
a525-1						
	250					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1501>:

g527.seq

```

1  atgggttttac cagtctcctt ttttcagcct gtccagttgg cggcgggtcgc
51  gcttggtcgg tctgccgtcg ggatgggagg aagtgatgag gctgaattgg
101 tcgagctggt tgcactcttc cctcaatgct gccgttttcg cgtcttcttc
151 atacagaagc cgcgcctcgg gtgcccggcg gcgttggtgg ttcaaacctt
201 taaccttgat tttatgggga aggggaattga gcgtcaggtc gataatatcg
251 ccgatgtcta tgggttttact gtttttgact ttcgagccgt ttacttgaac
301 cctacccagt tcgatatgct tttgcgcaag ggaacgggtc ttgaaaaaac
351 gtgccgcccc aagccatttg tccagccgca tggcggaaga atcgtgcttg
401 tctttcatat gattttggtt gaaataattg aatttgtttc gagtttagca
451 taa
```

This corresponds to the amino acid sequence <SEQ ID 1502; ORF 527.ng>:

g527.pep

```

1  MVLPVSEFFQ VQLAAVALGR SAVGMGSSDA AELVELFALF POCRRFRVFF
51  IQKPRLGCR ALVVQTFNLD FMGKGIERQV DNIADVYGFT VDFRAVYLN
101 PTQFDMLLRK GTGLEKTRCP KPFVQPHGGR IVLVFHTILF EIIEFVSSLA
151 *
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1503>:

m527.seq

```

1  ATGGTITTTAC CAGTCTCCIT TTTTCAGCCT GTCCAGTTGG CGGCGGTTCGC
51  GCTTGGTTCG TCTGCCGTCTG GATAGGCGG AAGTGATGCG GCTGAATTGG
101 TCGAGCTGTT TCGCTCTTTC CCTCAATGTT GCCGTWTCG CGTCTCTTTC
151 ATACAGAAGC CGCGCTTCG ATGCCGGGCG GCGTTGGTGG TTCAAACCTT
```

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201 TAACCKTGAT TTTATAGGGA AGGG.AATTk AgCkTCaGty GrTwATaTCG
 251 CsGATGTmTA TGGTTTTACT GTTTTTGACC TTCGAGCCGT TTACTTGAAC
 301 CCTACCCAGT TCGATGTGCT TTTGCGCAAG GGAACGGGTC TTGAAAAAAC
 351 GTGCCGCCCA AAGCCATTTG TCCAGCCGCA TGGCGGAAGA ATCGTGCTTG
 401 TCTTTCATAC GATTTTGTTC GAAATAATTG AATTTGTTTC CAGTTTAGCA
 451 TAA

This corresponds to the amino acid sequence <SEQ ID 1504; ORF 527>:

m527.pep

1 MVLPVSFQPVQLAAVALGR SAVGIGGSDA AELVELFALF PQCCRVRVLF
 51 IQKPRXGCRA ALVVQTFNND FIGKXNXASV XXIADVYGT VFDLRAVYLN
 101 PTQFDVLLRK GTGLEKTCRP KPFVQPHGGR IVLVFHTILF EIIEFVSSLA
 151 *

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 527 shows 90.0% identity over a 150 aa overlap with a predicted ORF (ORF 527.ng) from *N. gonorrhoeae*:

m527/g527

	10	20	30	40	50	60
m527.pep	MVL	PSF	FQPV	QLAA	VALGR	SAVGIGGSDA
g527	MVL	PSF	FQPV	QLAA	VALGR	SAVGIGGSDA
	10	20	30	40	50	60
	70	80	90	100	110	120
m527.pep	ALV	VQTF	NXDF	IGKXN	XASVXXI	ADVYGT
g527	ALV	VQTF	NLDF	MGKGI	ERQVDN	IADVYGT
	70	80	90	100	110	120
	130	140	150			
m527.pep	KPF	VQPH	GGRIV	LVFHT	ILFEI	IEFVSSLA
g527	KPF	VQPH	GGRIV	LVFHT	ILFEI	IEFVSSLA
	130	140	150			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1505>:

a527.seq

1 ATGTTTAC CAGTCTCCTT TTTTCAGCCT GTCCAGTTGG CGGCGGTGCG
 51 GCTTGGTCGG TCTGCCGTCG GGATAGGCGG AAGTGATGCG GCTGAATTGG
 101 TCGAGCTGTT TCGCTCTCTC CCTCAATGTT GCCGTTTTCG CGTCCTCTTC
 151 ATACAGAAGC CGCGCCTCGG ATGCCGGGCG CGCTTGGTGG TTCAAACCTT
 201 TAACCTTGAT TTTATAGGGA AGGGAATTGA GCGTCAGGTC GATAATATCG
 251 CCGATGTCTA TGGTTTTACT GTTTTTGACC TTCGAGCCGT TTACTTGAAC
 301 CCTACCCAGT TCGATGTGCT TTTGCGCAAG GGAACGGGTC TTGAAAAAAC
 351 GTGCCGCCCA AAGCCATTTG TCCAGCCGCA TGGCGGAAGA ATCGTGCTTG
 401 TCTTTCATAC GATTTTGTTC GAAATAATTG AATTTGTTTC GAGTTTAGCA
 451 TAA

This corresponds to the amino acid sequence <SEQ ID 1506; ORF 527.a>:

a527.pep

1 MVLPVSFQPVQLAAVALGR SAVGIGGSDA AELVELFALF PQCCRFRVLF
 51 IQKPRXGCRA ALVVQTFNLD FIGKGIERQV DNIADVYGT VFDLRAVYLN
 101 PTQFDVLLRK GTGLEKTCRP KPFVQPHGGR IVLVFHTILF EIIEFVSSLA
 151 *

m527/a527 93.3% identity in 150 aa overlap

	10	20	30	40	50	60
m527.pep	MVL	PSF	FQPV	QLAA	VALGR	SAVGIGGSDA
a527	MVL	PSF	FQPV	QLAA	VALGR	SAVGIGGSDA
	10	20	30	40	50	60

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	70	80	90	100	110	120
m527.pep	ALVVQTFNKF	IGKXNXASV	XXIADVYG	FTVFDLRA	VYLNPTQ	FDVLLRKG
			:			
a527	ALVVQTFN	LDFIGKIER	QVDNIADV	YGFTVFD	LRAVYLN	PTQFDVLL
	70	80	90	100	110	120
	130	140	150			
m527.pep	KPFVQPHG	GRIVLVFH	TILFEIIE	FVSSLAX		
a527	KPFVQPHG	GRIVLVFH	TILFEIIE	FVSSLAX		
	130	140	150			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1507>:

```

g528.seq
1  atggaattc gggtaataaa atatacggca acggtcgcgt tgtttgcatt
51  tacggttgca ggctgccggc tggcggggtg gtatgagtgt ttgtccttgt
101 ccggctggtg taagccgaga aaacctgccg ccatcgattt ttgggatatt
151 ggccgagaga gtccgctgtc tttagaggac tacgagatac cgctttcaga
201 cggcaatcgt tccgtcaggg caaacgaata tgaatccgcg caaaaatctt
251 acttttatag gaaaataggg aagtttgaag cctgcggggt ggattggcgt
301 acgcgtgacg gcaaaccttt gggtgagagg ttcaaacagg aaggtttcga
351 ctgtttgtaa aagcaggggt tgcggcgcaa cggcctgtcc gagcgcgtcc
401 gatggtaa

```

This corresponds to the amino acid sequence <SEQ ID 1508; ORF 528.ng>:

```

g528.pep
1  MEIRVIKYTA TAALFAFTVA GCRLAGWYEC LSLSGWCKPR KPAAIDFWDI
51  GGESPLSLED YEIPLSDGNR SVRANEYESA QKSYFYRKIG KFEACGLDWR
101 TRDGKPLVER FKQGGFDCLE KQGLRRNGLS ERVRW*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1509>:

```

m528.seq (partial)
1  ATGGAATTC GGGCAATAAA ATATACGGCA ATGGCTGCGT TGCTTGCATT
51  TACGTTGCA GGCTGCCGGC TGGCGGGGTG GTATGAGTGT TCGTCCCTCA
101 CCGGTGTGTG TAAGCCGAGA AAACCGGCTG CCATCGATT TTTGGATATT
151 GGCGGCGAGA GTCCGCCGTC TTTAGGGGAC TACGAGATAC CGCTTTCAGA
201 CGGCAATAGT TCCGTCAGGG CAAACGAATA TGAATCCGCA CAACAATCTT
251 ACTTTTACAG GAAAATAGGG AAGTTTGAAG C.TGCGGGCT GGATTGGCGT
301 ACGCGTGACG GCAAACCTTT GATTGAGACG TTCAAACAGG GAGGATTTGA
351 CTGCTTGGAA AAG....

```

This corresponds to the amino acid sequence <SEQ ID 1510; ORF 528>:

```

m528.pep (partial)
1  MEIRAIKYTA MAALLAFTVA GCRLAGWYEC SSLTGWCKPR KPAAIDFWDI
51  GGESPPSLGD YEIPLSDGNS SVRANEYESA QKSYFYRKIG KFEXCGLDWR
101 TRDGKPLIET FKQGGFDCLE K....

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 528 shows 89.3% identity over a 121 aa overlap with a predicted ORF (ORF 528.ng) from *N. gonorrhoeae*:

	10	20	30	40	50	60
m528.pep	MEIRAIKYTA	MAALLAFTV	AGCRLAGW	YECSSLTG	WCKPRKPA	AIDFWDIG
g528	MEIRVIKYT	AALFAFTV	AGCRLAGW	YECSSLTG	WCKPRKPA	AIDFWDIG
	10	20	30	40	50	60
	70	80	90	100	110	120
m528.pep	YEIPLSDGN	SSVRANEY	ESAQKSYF	YRKIGKF	EXCGLDWR	TRDGKPLI
g528	YEIPLSDGN	RSVRANEY	ESAQKSYF	YRKIGKF	EACGLDWR	TROGKPLV
	70	80	90	100	110	120

a528.seq

```
1 ATGGAATTC GGGCAATAAA ATATACGGCA ATGGCTGCGT TGCTTGCAAT
51 TACGGTTGCA GGCTGCCGGT T3GCAAGTTG GTATGAGTGT TCGTCCCTGT
101 CCGGCTGGTG TAAGCCGAGA AAACCTGCCG CCATCGATT TTGGGATATT
151 GCGCGCCAGA GTCCTCCGTC TTTAGAGGAC TACGAGATAC CGCTTTCAG
201 CGGCAATCGT TCCGTCAGGG CAAACGAATA TGAATCCGCA CAACAATCTT
251 ACTTTTACAG GAAAATAGGG AAGTTGAAG CCTGCGGGTT GGATTGCGGT
301 ACGCGTGACG GCAAACCTTT GATTGAGACG TTCAAACAGG AAGGTTTTGA
351 TTGTTTGAAG AAGCAGGGGT TCGCGCGCAA CGGTCTGTCC GAGCGCGTCC
401 GATGGTAA
```

```
a528.pep
1  MEIRAIKYTA MAALLAFTVA GCLRGWYEC SSSLGWCKPR KPAAIDFWDI
51  GGESPPSLED YEIPLSDGNR SVRANEYESA QQSYFYRKIG KFEACGLDWR
101 TRDGKPLIET FKOEGFDCLK KOGLERNGLS ERVRW*
```

	10	20	30	40	50	60
m528.pep	MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLTGWCKPRKPAAIDFWDIGGESPPSLGD					
	:					
a528	MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLSGWCKPRKPAAIDFWDIGGESPPSLED					
	10	20	30	40	50	60
	70	80	90	100	110	120
m528.pep	YEIPLSDGNSSVRANEYESAQQSYFYRKIGKFEXCGLDWRTRDGKPLIETFKQGGFDCLE					
	:					
a528	YEIPLSDGNSRVRANEYESAQQSYFYRKIGKFEACGLDWRTRDGKPLIETFKQEGFDCLE					
	70	80	90	100	110	120

g528-1.seq

```
1  ATGGA AATTC GGGTAATAAA ATATACGGCA ACGGCTGCGT TGTTTGCATT
51  TACGGTGTGA GGTGCTCCGGC TTGGCGGGTG GTATGAGTGT TCGTCCCTGT
101 TCCGGCTGGTG TARGCCGAGA AAACCTGCCG CCATCGATTG TTGGGATATT
151 GCGCGCGAGA GTCCGCTGTC TTTAGAGATA TACGAGATAC CGCTTTCAGA
201 CGGCAATCGT TCCGTCAGGG CAACACGAAT TGAATCCGCG CAAAAATCTT
251 ACTTTTATAG GAAATATAGG AAGTTTGAAG CCTCGGGGTT GGATTGGCGT
301 ACGCGTGACG GCAAACCTTT GGTGAGAGG TTCAAACAGG AAGGTTTCGA
351 CTGTTTGGAA AAGCAGGGGT TCGCGCGCAA CGGCGTGTC GAGCGCGTCC
401 GATGGTAA
```

g528-1.pep

1	MEIRVIKYTA	TAALFAFTVA	GCRLAGWYEC	SSLSGWCKPR	KPAAIDFWDI
51	GGESPLSLD	YEIPLSDGNR	SVRANEYESA	QKSYFYRKIG	KFEACGLDWR
101	TRDGKPLVER	FKOEGFDCLE	KOGLRRNGLS	ERVVR*	

m528-1.seq
1 ATGGAAATTC GGGCAATAAA ATATACGGCA ATGGCTGCGT TGCTTGCATT

797

```

51  TACGCTTGCA  GGCTGCCGGC  TGGCGGGGTG  GTATGAGTGT  TCGTCCCTCA
101 CCGGCTGGTG  TAAGCCGAGA  AAACCGGCTG  CCATCGATTT  TTGGGATATT
151 GCGGCGCAGA  GTCGCCCGTC  TTTAGGGGAC  TACGAGATAC  CGCTTTCAGA
201 CGGCAATCGT  TCCGTCAGGG  CAAACGAATA  TGAATCCGCA  CAACAATCTT
251 ACTTTTACAG  GAAAATAGGG  AAGTTTGAAG  CCTGCGGGCT  GGATTGGCGT
301 ACGCGTGACG  GCAAACCTTT  GATTGAGACG  TTCAAACAGG  GAGGATTTGA
351 CTGCTTGGA  AAGCAGGGGT  TGCGGCGCAA  CGGTCTGTCC  GAGCGCGTCC
401 GATGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1516; ORF 528-1>:

m528-1.pep..

```

1  MEIRAIKYTA  MAALLAFTVA  GCRLAGWYEC  SSLTGWCKPR  KPAAIDFWDI
51  GGESPPSLGD  YEIPLSDGNR  SVRANEYESA  QQSYFYRKIG  KFEACGLDNR
101 TRDGKPLIET  FKQGGFDCLE  KQGLRRNGLS  ERVRW*

```

g528-1/m528-1 92.6% identity in 135 aa overlap

```

               10      20      30      40      50      60
g528-1.pep  MEIRVIKYTATAALFAFTVAGCRLAGWYECSSLSGWCKPRKPAAIDFWDIGGESPLSLED
               |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||
m528-1       MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLTGWCKPRKPAAIDFWDIGGESPPSLGD
               10      20      30      40      50      60

               70      80      90     100     110     120
g528-1.pep  YEIPLSDGNRSVRANEYESAQKSYFYRKIGKFEACGLDWRTRDGKPLVERFKQEGFDCLE
               |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||
m528-1       YEIPLSDGNRSVRANEYESAQKSYFYRKIGKFEACGLDWRTRDGKPLIETFKQGGFDCLE
               70      80      90     100     110     120

               130
g528-1.pep  KQGLRRNGLSERVRWX
               |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||
m528-1       KQGLRRNGLSERVRWX
               130

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1517>:

a528-1.seq

```

1  ATGGAATTC  GGGCAATAAA  ATATACGGCA  ATGGCTGCGT  TGCTTGCAAT
51  TACGGTTGCA  GGCTGCCGGT  TGGCAGGTTG  GTATGAGTGT  TCGTCCCTGT
101 CCGGCTGGTG  TAAGCCGAGA  AAACCTGCCG  CCATCGATTT  TTGGGATATT
151 GCGGCGCAGA  GTCCTCCGTC  TTTAGAGGAC  TACGAGATAC  CGCTTTCAGA
201 CGGCAATCGT  TCCGTCAGGG  CAAACGAATA  TGAATCCGCA  CAACAATCTT
251 ACTTTTACAG  GAAAATAGGG  AAGTTTGAAG  CCTGCGGGTT  GGATTGGCGT
301 ACGCGTGACG  GCAAACCTTT  GATTGAGACG  TTCAAACAGG  AAGGTTTGA
351 TTGTTTGAAA  AAGCAGGGGT  TGCGGCGCAA  CGGTCTGTCC  GAGCGCGTCC
401 GATGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1518; ORF 528-1.a>:

a528-1.pep

```

1  MEIRAIKYTA  MAALLAFTVA  GCRLAGWYEC  SSLSGWCKPR  KPAAIDFWDI
51  GGESPPSLED  YEIPLSDGNR  SVRANEYESA  QQSYFYRKIG  KFEACGLDWR
101 TRDGKPLIET  FKQEGFDCLE  KQGLRRNGLS  ERVRW*

```

a528-1/m528-1 97.0% identity in 135 aa overlap

```

               10      20      30      40      50      60
a528-1.pep  MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLSGWCKPRKPAAIDFWDIGGESPPSLED
               |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||
m528-1       MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLTGWCKPRKPAAIDFWDIGGESPPSLGD
               10      20      30      40      50      60

               70      80      90     100     110     120
a528-1.pep  YEIPLSDGNRSVRANEYESAQKSYFYRKIGKFEACGLDWRTRDGKPLIETFKQEGFDCLE
               |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||
m528-1       YEIPLSDGNRSVRANEYESAQKSYFYRKIGKFEACGLDWRTRDGKPLIETFKQGGFDCLE
               70      80      90     100     110     120

               130
a528-1.pep  KQGLRRNGLSERVRWX
               |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||
m528-1       KQGLRRNGLSERVRWX
               130

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1519>:

```
g529.seq (partial)
  1  atgacccata tcaaaccggt cattgccgcg ctgcactca tcgggcttgc
 51  cgcctgctcc ggcagcaaaa ccgaacagcc caagctcgac taccaaagcc
101  ggtcgacccg cctgatcaaa ctggaagtcc cgcctgattt gaacaacccc
151  gaccaaggca acctctaccg cctgcctgcc ggttcgggag ccgtccgcgc
201  cggggatttg gaaaaacgcc gcacaccgca cgtccaacag ccagcggatg
251  ccggaagtat tgaaaagcgt caaaggcgct cgttcgagc ggcgacggca
301  gccaacgcct ggcttgctgt tgacggcaaa tcccccgccg aaatctccgc
351  cgctttctg.
```

This corresponds to the amino acid sequence <SEQ ID 1520; ORF 529.ng>:

```
g529.pep (partial)
  1  MTHIKPVIAA LALIGLAACS GSKTEQPKLD YQSRSHRLIK LEVPPDLNNP
 51  DQGNLYRLPA GSGAVRAGDL EKRRTPAVQQ PADAGSIEKR QRRPLRAATA
101  ANAWLVVDGK SPAEISAAF.
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1521>:

```
m529.seq
  1  ATGACCCATA TCAAACCCGT CATTGCCGCG CTCGACTCA TCGGGCTTGC
 51  CGCCTGCTCC GGCAGCAAAA CCGAACAGCC CAAGCTCGAC TACCAAAGCC
101  GGTCGCACCG CCGATCAAAA CTTGAAGTCC CACCTGATTT GAACAACCCC
151  GACCAAGGCA ACCTCTACCG CCTGCCTGCC GGTTCGGGCG CCGTCCGCGC
201  CAGCGATTTC GAAAAACGCC GCACACCCGC CGTCCAACAG CCTGCCGATG
251  CCGAAGTATT GAAAAGCGTC AAAGGTGTCC GCCTCGAGCG CGACGGCAGC
301  CAACGCTGGC TCGTTGTCTGA CGGCAAGTCT CCTGCCGAAA TCTGGCCGCT
351  CCTGAAAGCC TTTTGGCAGG AAAACGGCTT CGACATCAAA TCCGAAGAAC
401  CCGCCATCGG ACAAATGGAA ACCGAGTGGG CGGAAAACCG CGCCAAAATC
451  CCCCAGACA GCTTGCGCCG CCTCTTCGAC AAAGTCGGCT TGGGCGGCAT
501  CTACTCCACC GGCAGCGCGG ACAAATTCAT CGTCCGTATC GAACAGGGCA
551  AAAACGGCGT TTCGACATC TTCTTCGCC ACAAAGCCAT GAAAGAAGTG
601  TACGGCGGCA AAGACAAAGA CACGACCGTA TGGCAGCCCT CCCCCTCCGA
651  TCCCAACCTC GAAGCCGCTT TCCTGACGCG CTTATGCAA TATTTGGGCG
701  TTGACGGACA GCAGGCGGAA AACGCATCGG CAAAAAACC TACCCTTCCC
751  GCCGCCAACG AATGGCGCG TATCGAAGGC AAAAGCCTGA TTGTCTTTGG
801  CACTACGGC AGAAACTGCG GCGCACCGT GCTCGCCCTC GACCGCATCG
851  GGCTGACCGT CGTCGGTCAA AACACCGAAC GCCACGCTT CCTGGTTCAA
901  AAAGCCCCGA ACGAAAGCAA TGCAATTACC GAACAAAAC CCGGCCTGTT
951  CAAACGCTG CTGGGCAAAG GCAAAGCGGA GAAACCTGCC GAACAGCCGG
1001 AACTGATTGT CTATGCAGAA CCTGTCGCCA ACGGCTCGCG CATCGTCCTG
1051 CTCAACAAAG ACGGCAGCGC ATATGCCGCG AAAGACGCAT CGCATTATT
1101 GGGCAAATC CATTCCGAAC TCGGTAA
```

This corresponds to the amino acid sequence <SEQ ID 1522; ORF 529>:

```
m529.pep
  1  MTHIKPVIAA LALIGLAACS GSKTEQPKLD YQSRSHRLIK LEVPPDLNNP
 51  DQGNLYRLPA GSGAVRASDL EKRRTPAVQQ PADAELVLSV KGVRLERDGS
101  QRWLVVDGKS PAEIWPLLKA FWQENGFDIK SEEPALGQME TEWAENRAKI
151  PQDSLRLRLFD KVLGGIYST GERDKFIVRI EQKNGVSDI PFAHKAMKEV
201  YGGKDKDTTV WQPSPSDPNL EAAFLTRFMQ YLGVDGQQAE NASAKKPTLP
251  AANEMARIEG KSLIVFGDYG RNWRRTVLAL DRIGLTVVGQ NTERHAFIVQ
301  KAPNESNAVT EQKPLFKRL LGKGKAEKPA EQPELIVYAE PVANGSRIVL
351  LNKDGSAYAG KDASALLGKL HSELR*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 529 shows 83.5% identity over a 115 aa overlap with a predicted ORF (ORF 529.ng) from *N. gonorrhoeae*:

g529/m529

	10	20	30	40	50	60
g529.pep	MTHIKPVIAALALIGLAACSGSKTEQPKLDYQSRSHRLIKLEVPPDLNNPDQGNLYRLPA					

799

```

|||||
m529      MTHIKPVIAALALIGLAACSGSKTEQPKLDYQSRSHRLIKLEVPPDLNPDQGNLYRLPA
           10      20      30      40      50      60

           70      80      90      100     110     120
g529. pep  GSGAVRAGDLEKRRTPAVQQPADAGSIEKRQRRLRAATAANAWLVVDGKSPAEISAAFX
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m529      GSGAVRASDLEKRRTPAVQQPADA EVLKS VKGVRLER-DGSQRWLVDGKSPAEIWPLLK
           70      80      90      100     110

m529      AFWQENGFDIKSEEP AIGQMETEWAENRAKIPQDSLRLR LFDKVGLGGIYSTGERDKFIVR
120      130      140      150     160     170

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1523>:

```

a529. seq
1  ATGACCCATA TCAAACCCGT CATTGCCGCG CTCGCACTCA TCGGGCTTGC
51  CGCCTGCTCC GGCAGCAAAA CCGAACAGCC CAAGCTCGAC TACCAAAGCC
101 GGTTCGCACCG CCTGATCAAA CTCGAAGTCC CACCTGATT GAACAACCCC
151 GACCAAGGCA ACCTCTACCG CCTGCCTGCC GGTTCGGGCG CCGTCCGCGC
201 CAGCGATTTG GAAAAACGCC GCACACCCGC CGTCCAACAG CCTGCCGATG
251 CCGAAGTATT GAAAAGCGTC AAAGGTGTCC GCCTCGAGCG CGACGGCAGC
301 CAACGCTGGC TCGTTGTGCA CGGCAAGTCT CATGCCGAAA TCTGGCCGCT
351 CCTGAAAGCC TTTTGGCAGG AAAACGGCTT CGACATCAAA TCCGAAGAAC
401 CCGCCATCGG ACAATGGAA ACCGAGTGGG CGGAAAACCG TGCCAAAATC
451 CCCCAGACA GCTTGCGCCG CCTATTCGAC ACAGTCGGTT TGGGCGGCAT
501 CTACTCCACC GGCAGCGCGG ACAATTTCAT CGTCGTATC GAACAGGGCA
551 AAAACGGCGT TTCCGACATC TTCTTCGCCC ACAAGGCCAT GAAAGAAGTG
601 TACGGCGGCA AAGACAAAGA CACGACCGTA TGGCAGCCCT CCCCGTCCGA
651 TCCCAACCTC GAAGCCGCTT TCCTGACGCG CTTTATGCAA TATTGGGCG
701 TTGACGACA GCAGGCGGAA AACGCATCGG CAAAAAACC TACCCTTCCC
751 CCGCCCAACG AAATGGCGCG TATCGAAGGC AAAAGCCTGA TTGTCTTTGG
801 CGACTACGGC AGAAACTGGC GCGCACCGC GCTCGCCCTC GACCGCATCG
851 GGCTGACCGT CGTCGGTCAA AACACCGAAC GCCACGCTTT CTTGGTTCAA
901 AAAGCCCCGA ACGAAAGCAA TGCAGTTACC GAACAAAAAC CCGGCCTGTT
951 CAACGCCTG CTGGGCAAAG GCAAAGCGGA GAAACCTGCC GAACAGCCGG
1001 AACTGATTGT CTATGCCGAG CCTGTCGCCA ACGGCTCGCG CATCGTCTTG
1051 CTCAACAAAG ACGGCAGCGC ATATGCCGGC AAAGACGCAT CCGCATTATT
1101 GGGCAAATC CATTCCGAAC TGC GTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1524; ORF 529.a>:

```

a529. pep
1  MTHIKPVIAA LALIGLAACS GSKTEQPKLD YQSRSHRLIK LEVPPDLNPDQGNLYRLPA
51  DQGNLYRLPA GSGAVRASDL EKRRTPAVQQ PADA EVLKS VKGVRLERDGS
101 QRWLVVDGKS HAEIWPLLKA FWQENGFDIK SEEP AIGQME TEWAENRAKI
151 PQDSLRLR LFD TVGLGGIYST GERDKFIVRI EQGKNGVSDI FFAHKAMKEV
201 YGGDKD TTV WQPSDPN L EAAFLTRFMQ YLGVDGQQA E NASAKKPTLP
251 AANEMARIEG KSLIVFGDYG RNWRRTALAL DRIGLTVVGQ NTERHAFIVQ
301 KAPNESNAVT EQKPLFKRL LGKGKAEKPA EQPELIVYAE PVANGSRIVL
351 LNKDGSAYAG KDASALLGKL HSEL R*

```

m529/a529 99.2% identity in 375 aa overlap

```

           10      20      30      40      50      60
m529. pep  MTHIKPVIAALALIGLAACSGSKTEQPKLDYQSRSHRLIKLEVPPDLNPDQGNLYRLPA
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a529      MTHIKPVIAALALIGLAACSGSKTEQPKLDYQSRSHRLIKLEVPPDLNPDQGNLYRLPA
           10      20      30      40      50      60

           70      80      90      100     110     120
m529. pep  GSGAVRASDLEKRRTPAVQQPADA EVLKS VKGVRLERDGSQRWLVDGKSPAEIWPLLKA
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a529      GSGAVRASDLEKRRTPAVQQPADA EVLKS VKGVRLERDGSQRWLVDGKSHAEIWPLLKA
           70      80      90      100     110     120

           130     140     150     160     170     180

```


800

```

m529.pep  FWQENGFDIKSEEPaIGQMETEWaENRAKIPQDSLRRlFDKVGlgGIYSTGERDKFIVRI
a529      FWQENGFDIKSEEPaIGQMETEWaENRAKIPQDSLRRlFDTVGlGGIYSTGERDKFIVRI
          130      140      150      160      170      180

          190      200      210      220      230      240
m529.pep  EQGKNGVSDIFFaHKAMKEVYGGKDKDTTVWQPSpSDPNLEAAFLTRFMQYlGVdGQQAe
a529      EQGKNGVSDIFFaHKAMKEVYGGKDKDTTVWQPSpSDPNLEAAFLTRFMQYlGVdGQQAe
          190      200      210      220      230      240

          250      260      270      280      290      300
m529.pep  NASAKKPTLPaANEMARIEGKSLIVFGDYGRNWRRTVLaLDRIGlTVVGQNTeRHaFLVQ
a529      NASAKKPTLPaANEMARIEGKSLIVFGDYGRNWRRTaLaLDRIGlTVVGQNTeRHaFLVQ
          250      260      270      280      290      300

          310      320      330      340      350      360
m529.pep  KAPNEsNAVTEQKPGlFKRllGKGKAEKPAEQPElIVYAEpVANGSRIVllNKdGSAYAG
a529      KAPNEsNAVTEQKPGlFKRllGKGKAEKPAEQPElIVYAEpVANGSRIVllNKdGSAYAG
          310      320      330      340      350      360

          370
m529.pep  KDASAlLGKLHSELRX
a529      KDASAlLGKLHSELRX
          370

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1525>:

```

g530.seq
1  atgagtgcga ggcgggcaat gacgggtttg atatgggtca tcgtgtcatc
51  ctgtgtgatg gatattaaag tgtttgtcat gttatgccgt ccgaacgggt
101 cagacggcat ggctatatatt aaagtgtgcc tgaggcttcc agggcggcgc
151 ggacttttgc ctgtccgcct tccgtcagcg gaacgagcgg caggcgcacg
201 tgcggtccgc atccgcccaa ggcggatacc gccatttcg gtgcggcggg
251 actgggttcg cagaacatgg tgtcgtaaat cggaatcagc cggtcgttga

```

This corresponds to the amino acid sequence <SEQ ID 1526; ORF 530.ng>:

```

g530.pep
1  MSASAAMTGL IWVIVSSCVm DIKVFVMLCR PNGSDGMAIF KVVLRlLSGRR
51  GLLPVRLPSA ERAAGARAVR IRPRRIPPIS VRRDWVRRTW CRKSESAGR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1527>:

```

m530.seq
1  wTGAGTGCGA GCGCGGCAAT GACGGGTyTG ATATGGGTCA TCGTGTcATC
51  sTGtGTGATG GATATTAAAG TGtYtGTTGC GwTATGCCGT cCGAACGGtT
101 CGGACGGCAT GGMtATATTT AAAGTTGTCC TGAGGCTTTC AGGGCGGCGC
151 GGACTkTTGC WTGTCCGTTT yCCGTcAGCG GAACGAGCGG cAGGCGGACG
201 TGCGGTTCGC ATCTGCCCAg GCGGATACC GCCATTTCG STGCGGCGGG
251 GCTGGGTTCG CAGAACATGG TGTCGTAAAT CGGAATCAGT cGGTCGTtGA

```

This corresponds to the amino acid sequence <SEQ ID 1528; ORF 530>:

```

m530.pep
1  XSASAAMTGL IWVIVSSCVm DIKVXVAXCR PNGSDGMXIF KVVLRlLSGRR
51  GLLXVRFPSA ERAAGGRAVR ICPGRIPPIS VRRGWVRRTW CRKSESVGR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 530 shows 88.8% identity over a 98 aa overlap with a predicted ORF (ORF 530.ng) from *N. gonorrhoeae*:

```

m530/g530

m530.pep  XSASAAMTGLIWVIVSSCVMDIKVXVAXCRPNGSDGMXIFKVVLRlLSGRRGLLXVRFPSA  60
          |||

```

g530	MSASAAMTGLIWWIVSSCVMDIKVFVMLCRPNGSDGMAIFKVVLRLSGRRGLLPVRLPSA	60
	10 20 30 40 50 60	
m530.pep	ERAAGGRAVRICPGRIIPPISVRRGWVRTWCRKSESVGR	99
	: : : :	
a530	ERAAAGARAVRIRPRRIIPPISVRRDWVRTWCRKSESAGR	99

a530.seq

```
1 ATGAGTGCGA GCGCGCAAT GACGGGTTTG ATATGGGTCA TCGTGTCACT
51 CTGTGTGATG GATATTAAAG TGTTTGTTGC GTTAGCCGCT CCGAACGGTT
101 CCGACGCGCAT GGCTATATTT AAAGTTGTCC TGAGGCTTTC AGGGCGCGCG
151 GGACTTTTTC CTGTCGCGCT TCCGTCAGCG GAACAGCGCG CAGGCGGACG
201 TGCGGTTTCG ATCTGCCCCAG GCGCGATAAC GCCCATTTTC GTGCGGCGGG
251 SCTGGGTTTC CAGAACATGG TGTGCTAAAT CGGAATCAGC CGGCGTGTGA
```

a530.pep
1. MSASAAMTGL IWVIVGSCVM DIKVEVALCR PNGSDGMAIF KVLRLSGRR
51. GLLPVRLPSA ERAAGGRAVR ICPGRIPPII VRRGQVRRTW CRKSESAGR*

	10	20	30	40	50	60
m530.pep	XSASAAMTGLIWVIVSSCVM DIKVVXVAXCRPN SGDMXIFKVVLRLSGRRGLLXVRFPSA					
	:					
a530	MSASAAMTGLIWVIVSSCVM DIKFVVALCRPN SGDMAIFKVVLRLSGRRGLLPVRLPSA					
	10	20	30	40	50	60
	70	80	90	100		
m530.pep	ERAAGGRAV RICPGRIP PISVRRGWVRRTWCRKSES SVGRX					
	:					
a530	ERAAGGRAV RICPGRIP PISVRRGWVRRTWCRKSES AGRX					
	70	80	90	100		

```

g531.seq
1  ATGACCGCCC  TACTCGTCAT  CCTCGCCCTC  GCCCTGATAG  CCGTCGGCAC
51  GGCAGGCATC  GTCTATCCCG  CCCTGCCCGG  CTTGGCATTG  ATGTTTGCCG
101  GAACATGGCT  GCTTGCCTAT  GCGGGCGGCT  ATCAAATCTA  CGGCGCAGGC
151  ATCTTGTGGA  CGGTCGGACT  CATCAGCCTT  GCGCGCATAC  TGCGGACTA
201  TATGGCAGGC  ATGTTGGGGG  TAAATACAC  TGGGGCAGGC  AAACTCGCCG
251  TCCGAGGTGC  ATTGGCCGGC  AGCATCATCG  GCATATTTT  CTCCTTCCC
301  GGACTAATAC  TCGGCCCTT  TATCGGCGCG  GCGGCAGGCG  AACTGATCGA
351  TCGGCACAAT  ATGCTTCAGG  CAGGTAAAGC  GGGCTTGGGT  ACGCTGTTGG
401  GGTATTGTCG  TCGCACGGCG  TTCAAATCG  GTGTGCGCGT  ATCCACTTGG
451  TTATCTCTGT  TGGTGAAATA  CATCGCATAC  CTGTTTTAA

```

g531.ppe
1 MTALLVILAL ALIavgTAGI VYPALPGLAL MfagTWLLay AGGYQIYGag
51 ILWTVGLISL GGILADYMag MLGvKYTGAG KLAVRGALag SIIGIFFSLP
101 GLILGPFIGa AAGELIDRRN MLQAGKAGLG TLLGLVVGTA FKIGCAVSIL
151 FILLVKYIAY LF

```
m531.seq
1  ATGACCGTAC  TGACCGTCAT  CCTCGCCCTC  GCCCTGATAG  CCGTCGGCAC
51  GGCGGGCATC  GTTTaCCCCG  CCTGCGCCGG  ATTGGCATTG  ATGCTTTGCCG
101 GAACATGGECT  GCTTGCCATG  CCGCGCGGCT  ACCAAATCTA  CGCGCGGGC
151 GTTTTGTGGA  CGGTCGGACT  CATCAGCCTT  GCGGCGATAC  TGGCGGACTA
201 TGTGGCAGGC  ATATGGGGGA  CAAATATAC  CGGAGCGGGC  AAGCTCCCC
251 TTGCGGCGCG  ATTGSCCGCG  AGCATCATCG  GCATATTTT  CTCCCTTCCC
301 GGACTAATAC  TCGGTCCCTT  TATCGGCGCG  GCGGCGAGCG  CACTGATCGA
```

in531.pcp

1 MTVLTVILAL ALIavgTAGI VYPALPGLAL MfAGTWLLAY AGGYQIYGAG
51 VLWTVGLISL AGILADYVAG IWGTYKTGAG KLAVRGALAG SIIGIFFSLP
101 GLILGPFIGA AAGEIERRN MLQAGKAGLG TLGLGVGTA FKIGCAVSIL
151 FILLVKYIAY LF*

Homology with a predicted ORF from *N. gonorrhoeae*

from *N. gonorrhoeae*:

m531/q531

[illegible]

a531.seq

1	ATGACCGCCT	TGCTCGTCAT	CCTCGCCCTC	GCCTGATAG	CCGCCGGTAC
51	GGCGGGCATC	GTTTACCCCG	CCCTGCCCGG	ATTGGCATTG	ATGTTTGGCG
101	GAACCTGGCT	GCTCGCCTAC	TCCGGCGGCT	ACCAAACTCA	CGCGCGGGGC
151	GTTTGTGTGA	CGGTGGACT	CATCAGCCCT	CGCGGCATAC	TGGCGGACTA
201	TGTGGCAGGC	ATATGGGGGA	CAAAATATAC	CGGAGCGGCG	AGGCTCGCGC
251	TTCGCGGCGC	ATTGGCGGCG	AGCATCATCG	GCATATTTTT	CTCCCTTCCC
301	GGACTAATAC	TCGTTCCCTT	TATCGGCGCG	CGGCAGGCG	AACTGATCGA
351	ACGGCGCAAT	ATGCTTACGG	CAGGTAAGCG	GGGCTTGGGT	ACGCTGTTGG
401	GGCTTATCGT	CGGTACGGCG	TTCAAAATCG	GCTGCGCCGT	ATCCACTTTG
451	TTTATCCTGT	TGGTGAAATA	CATCGCCTAC	CTGTTTTTAA	

a531.pep

1 MTALLVILAL ALIAAGTAGI VYPALPGLAL MFAGTWLLAY SGGYQIYGAG
51 VLWTVGLISL AGILADYVAG IWGTKYTGAG KLAVRGALAG SIIGIFFSLP
101 GLILGPFGIAG AAGELIERN MLQAGKAGLG TLGLIVGTA FKIGCAVSIL
151 FILLVKYIAY LF*

m531/a531 96.9% identity in 162 aa overlap

	10	20	30	40	50	60
m531.pep	MTVLT	VILALALIA	AVGTAGIV	PALPGLALM	FAGTWLLAY	AGGYQIYGAGVLWTVGLISL
	:	:	:	:	:	:
a531	MTALLV	LALALIAA	STAGIV	PALPGLALM	FAGTWLLAY	SGGYQIYGAGVLWTVGLISL
	10	20	30	40	50	60
	70	80	90	100	110	120
m531.pep	AGILADY	VAGIWG	TGTYTGACK	LAVRGALAG	SIIGIFFSL	PGLILGPF
						FGIAAAGELIERRN

803

```

|||||
a531  AGILADYVAGIWGTYKTGAGKLAVRGALAGSIIGIFFSLPGLILGPFFIGAAAGELIERN
      70      80      90      100     110     120

      130      140      150      160
m531.p  MLQAGKAGLGTLGLVVGTAFAKIGCAVSILFILLVKYIAYLFX
      |||||
a531    MLQAGKAGLGTLGLVVGTAFAKIGCAVSILFILLVKYIAYLFX
      130      140      150      160

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1537>:

g532.seq (partial)

```

1  atggctgaaa caatgaaaa acaggcggat tcgcctgatt tgggtgtacgg
51  ttgggaagac aggcgcgctg tcggtaatgc gctcttgagc gcggttaccc
101 atcttttggc gattttcgtg ccgatgatta cgcgcgctg gattgtgggc
151 ggcgcgctgg aattgccggt ggagatgacg gcgtatctgg tgctgatggc
201 gatggttgcg tcgggtgctg gcacttattt gcaggtaaac cgcttcgggt
251 cggtcggtgc ggggatgctg tccatccagc gttaccgtca tgattgcgct
301 cggcgcgggg atgaaagagg gcggtttgag ...

```

This corresponds to the amino acid sequence <SEQ ID 1538; ORF 532.ng>:

g532.pep (partial)

```

1  MAETMKKQAD SPDLVYGLED RPPFGNALLS AVTHLLAIFV PMITPALIVG
51  GALELPVEMT AYLVSAMMVA SGVGTYLQVN RFGSVGSGML SIORYRHDCA
101 RRGDERGRFE ...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1539>:

m532.seq

```

1  ATGAGCGGTC AGTTGGGCAA AGGTGCGGAT GCGCCTGATT TGGTGTACGG
51  TTGGGAAGAC AGGCCGCGGT TCGGTAATGC GCTCTTGAGC GCGGTACCC
101 ATCTTTTGGC GATTTTGTG CCGATGATTA CGCCCGCGCT GATTGTGGGC
151 GGCGCGCTGG AATTGCCGCT GGAGATGACG GCGTATCTCG TGTCGATGGC
201 GATGGTTGCG TCGGGTGTG GCACTTATTT GCAGGTCAAC CGCTTCGGGC
251 CGGTCGGTTC GGGGATGCTG TCCATCCAGT CCGTGAATTT TTCGTTCTGTT
301 ACCGTGATGA TTGCGCTGGG CGCGGGGATG AAAGAGGCGG GTTTGACTAA
351 GGATGCGATG ATTTCGACGC TCTTGGGCGT ATCGTTTGTC GGCGCGTTTT
401 TGGTGTGTTT CTCGGCTGG CTTCTGCCGT ATTTGAAAAA AGTGATTACG
451 CCGACGCTCA GCGGCGTGGT CGTGATGCTC ATTGGTTTGA GTTTGGTACA
501 CGTCGGCATT ACCGATTTCG GCGGCGGCTT CCGCGCAAG GCGGACGGCA
551 CGTTCGGCTC GATGAAAAC TTGGGGCTGG CATCGCTGGT GTTGCTGATT
601 GTGTTGTTGT TCAACTGCAT GAAAAACCCG CTGTTGCGCA TGAGCGGCAT
651 TGCGGTCGGG CTGATTGCCG GCTATATCGT CGCGCTGTTT TTGGGCAAGG
701 TGGATTTTTC CGCGCTGCAA AACCTGCCGC TGGTTACGCT GCCCGTACCG
751 TTAAATACG GTTTTGCTTT CGACTGGCAC GCGTTTATTG TGGCGGGCGC
801 GATTTTCTTG TTGAGCGTGT TTGAGGCGGT CCGCGATTTA ACCGCGACGG
851 CAATGGTGTC CGACCAGCCG ATTGAAGGCG AGGAATACAC CAAACGCCTG
901 CGCGGCGGCG TGTGCTGTA CCGCTTGGTG TCGGTGATTG CGACGGCTTT
951 GGGTTCGCTG CCGCTGACGA CGTTTGCGCA AAACAACGGC GTGATTCAGA
1001 TGACCGCGCT GGCTTCGCGC CATGTGGGCA AATATATTGC CGTGATTTTG
1051 GTGCTGTTGG GTCTGTCCC CGTTGTGCGT CGCGCGTTTA CGACGATTCC
1101 GAGTCCGGTG TTGGGCGGCG CGATGGTTTT GATGTTGCGC TTAATTGCGA
1151 TTGCGGGCGT GCGGATTTTG GTCAGTCAAG GCATCCGAG GCGCGAAGCG
1201 GTGATTGCGG CAACGTCGGT CGGTTTGGGC TTGGGTGTCG CGTTTGAGCC
1251 GGAAGTGTTC AAAAACTGC CCGTCTGTTC CCAAACTCT ATTTCCGCCG
1301 GCGGCATTAC GGCAGTCTTG CTGAATTGTT TCTTGCCCGA AGATAAAACC
1351 GAGGCGGCGG TCAAGTTTGA TACCGACCAC TTGGAACACT GA

```

This corresponds to the amino acid sequence <SEQ ID 1540; ORF 532>:

m532.pep

```

1  MSGQLKGAD APDLVYGLED RPPFGNALLS AVTHLLAIFV PMITPALIVG
51  GALELPVEMT AYLVSAMMVA SGVGTYLQVN RFGPVGSGML SIQSVNFSFV
101 TVMIALGAGM KEGGLTKDAM ISTLLGVSPV GAFLVCFSAW LLPYLKKVIT
151 PTVSGVVVML IGLSLVHVI TDFGGGFGAK ADGTFGSMEN IGLASLVLLI

```

201	VLVFNCKMKN	LLRMSGIAVG	LIAGVIAVLF	LGKVDFSALQ	NLPLVTLPPV
251	FKGYFADFWDH	AFIVAGAIFFL	LSVFEAVGDL	TATAMVDSQP	IEEGEYTKRL
301	RGGVGLADGLV	SVIATALGSL	PLTTFAQNNG	VIQMTGVSAR	HGKYIAIVL
351	VLLGLFPVVG	RAGFTTIPSPV	LGGAMVLMFG	LIAIAGVRIL	VSHGIRRREA
401	VIATASVGLG	LGVAFEPEVF	KNLPVLFQNS	ISAGGITAVL	IANVIPEDKT
451	EAAVKFDTDH	LEH*			

Homology with a predicted ORF from *N. gonorrhoeae*

q532/m532

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1541>:

```
a532.seq
1 ATGAGCGGTC AGTTGGGCAA AGGTGCGGAT GCGCCTGATT TGGTGTACGG
51 TTTGGAGGAT AGGCCGCCGT TCGGTATATG GCTCTTGAGC GCGGTTACCC
101 ATCTTTTGGC GATTTTGTGT CCGATGATTA CGCCCGCGCT GATTGTGGGC
151 GGCAGCTGAG GATTGGCGTG GGAGATGACG CGGTATCTCG TGTCGATGGC
201 GATGGTTGCG TCGGGTGTCT GCACTTATTT GCAGGTCAAC CGCTTCGGGC
251 CGGTCGGTTC GGGGATGCTG TCCATCCAGT CGGTGAATTT CTCGTTCTGT
301 ACCGTCATGA TTGCGCTCGG CGCGGGGATG AAAGAGGGCG GTTTGACTAA
351 GGATGCGATG ATTTGACAGC TCTTGGGCGT ATCGTTTGTC GGCCCGTTTT
401 TGGTGTTGTT TTCCGCGTGG TCTCTGCCGT ATTTGAAAAA AGTGATTACG
451 CCGACGGTCA GCGGTGTGGT GGTGATGCTG ATTCGCTTGA GTTTGGTACA
501 CGTCGGTATT ACCGATTTCT GCGGCGGCTT CGGCGCAAGG GCGGACGGCA
551 CGTTCGGCTC GATGAAAAAC TTGGGGCTGG CATCGCTGGT GCTGCTGATT
601 GTGCTGGTGT TCAATTGCAT GAAAAACCCG CTGCTGCGGA TGAGCGGCAT
651 TGCGGTCGGT CTGATTGCCG GCTATATCGT CGCGCTGTTT TTGGGCAAGG
701 TGGATTTTTC GGCATTGCAA AACCTGCCCG TGTTTACGCT GCCCGTACCG
751 TTTAAATATG GTTTTGTCTT TGACTGGCAC GCATTATTAT GTCGCGGTGC
801 GATTTTCTTG TTGAGCGTGT TTGAGGCGGT CGGCGATTTG ACGGCGACGG
851 CAATGGTGTC CGACCAGCCG ATTGAAGGCG AGGAATACAC CAAACGCTTG
901 CGCGGCGGGC GTTTGGCGGA CGGCTTGGTG TCGGTGATTG CGACGGCTTT
951 GGGTTCCGCT CCGCTGACGA CGTTTGACA AAACAACGGC GTGATTGAGA
1001 TGACCGCGTG GGCTTCGCGC CATGTGGGCA AATATAATGC CGTATTTTTG
1051 GTGCTGTTGT GTCTGTTTCC CGTTGTCGGA CGGCGCTTAT GCACGATTCC
1101 GAGTCCGGTG TTGGGCGGCG CGATGGTTTT GATGTTGCGC TTGATTGCGA
1151 TTGCGGGCGT GCGGATTTTG GTCAGCCACG GCATCCGCAG GCGCGAAGCG
1201 GTAATTGCCG CAACGTCGGT CGGTTTGGGC TTGGGTGTCT CGTTTGAGCC
1251 GGAAGTGTTT AAAAACCTGC CCGTCTTGTT CCAAACCTCT ATTTCCGCCG
1301 GCGGATTTAC GGCAGTCTTG CTGAATTTGG TCTTGCCCGA AGATAAAACC
1351 GAGGCGGGCG TCAAGTTTGA TACCGACCAC TCTTGAACACT GA
```

a532.pep

1	MSGQLGKGAD	APDLVYGLED	RPPFGNALLS	AVTHLLAIFV	PMITPALIVG
51	GALELPVEMT	AYLVSMAMVA	SGVGTYLQVN	RFGPVGSGML	SIQSVNFSFV

```

101 TVMIALGAGM KEGGLTKDAM ISTLLGVSFV GAFLVCFSAW LLPYLKKVIT
151 PTVSGVVVMI IGLSLVHVGI TDFGGGFGAK ADGTFGSMEN LGLASLVLLI
201 VLVFNCMKNP LLRMSGIavg LIAGYIVALF LGKVDFSALQ NLPLVTLVPV
251 FKYGFADFWDH AFIVAGAIFL LSVFEAVGDL TATAMVSDQP IEGEYTKRL
301 RGGVLADGLV SVIATAGSL PLTTFAQNNG VIQMTGVASR HVGKYIAVIL
351 VLLGLFPVVG RAFTTIPSPV LGGAMVLMFG LIAIAGVRIL VSHGIRREA
401 VIAATSVGLG LGVAFEPFV KNLPVLFQNS ISAGGITAVL LNLVLPEDKT
451 EAAVKFDTDH LEH*

```

m532/a532 100.0% identity in 463 aa overlap

	10	20	30	40	50	60
m532.pep	MSGQLGKGADAPDLVYGLEDPRPPFGNALLSAVTHLLAIFVPMITPALIVGGALELPVEMT					
a532	MSGQLGKGADAPDLVYGLEDPRPPFGNALLSAVTHLLAIFVPMITPALIVGGALELPVEMT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m532.pep	AYLVSMAMVASGVGTYLQVNRFGPVGSGMLSIQSVNFSFVTVMIALGAGMKEGGLTKDAM					
a532	AYLVSMAMVASGVGTYLQVNRFGPVGSGMLSIQSVNFSFVTVMIALGAGMKEGGLTKDAM					
	70	80	90	100	110	120
	130	140	150	160	170	180
m532.pep	ISTLLGVSFVGAFLVCFSAWLLPYLKKVITPTVSGVVVMIIGLSLVHVGITDFGGGFGAK					
a532	ISTLLGVSFVGAFLVCFSAWLLPYLKKVITPTVSGVVVMIIGLSLVHVGITDFGGGFGAK					
	130	140	150	160	170	180
	190	200	210	220	230	240
m532.pep	ADGTFGSMENLGLASLVLLIVLVFNCMKNP LLRMSGIavgLIAGYIVALFLGKVDFSALQ					
a532	ADGTFGSMENLGLASLVLLIVLVFNCMKNP LLRMSGIavgLIAGYIVALFLGKVDFSALQ					
	190	200	210	220	230	240
	250	260	270	280	290	300
m532.pep	NLPLVTLVPVPFKYGFADFWDHAFIVAGAI FLLSVFEAVGDLTATAMVSDQPIEGEYTKRL					
a532	NLPLVTLVPVPFKYGFADFWDHAFIVAGAI FLLSVFEAVGDLTATAMVSDQPIEGEYTKRL					
	250	260	270	280	290	300
	310	320	330	340	350	360
m532.pep	RGGVLADGLSVIATAGSLPLTTFAQNNGVIQMTGVASRHHVGKYIAVILVLLGLFPVVG					
a532	RGGVLADGLSVIATAGSLPLTTFAQNNGVIQMTGVASRHHVGKYIAVILVLLGLFPVVG					
	310	320	330	340	350	360
	370	380	390	400	410	420
m532.pep	RAFTTIPSPVLGGAMVLMFGLIAIAGVRILVSHGIRREAVIAATSVGLGLGVAFEPFV					
a532	RAFTTIPSPVLGGAMVLMFGLIAIAGVRILVSHGIRREAVIAATSVGLGLGVAFEPFV					
	370	380	390	400	410	420
	430	440	450	460		
m532.pep	KNLPVLFQNSISAGGITAVLLNLVLPEDKTEAAVKFDTDHLEHX					
a532	KNLPVLFQNSISAGGITAVLLNLVLPEDKTEAAVKFDTDHLEHX					
	430	440	450	460		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1543>:

```

g535.seq
1  atgccctttc ccggttttcag acaantatth gcttngtcct tgctacgggt
51  ttttgccgta ggtcggattc tcgaatccga catttccaac agcgggtttt
101 cggaaacgat aaacgcgtca aatgtttttt ttgtcggata cgaatatccg
151 gcctgcattt caaatattaca tcgcttccaa ttctgcaaac ttggtatcca
201 gttctttcac gccctgtttg ccgaagtga tggtcagtcg ggcggattcg
251 cctttgtctg cggcatcgat aatcacgccg gtgccgaatt tggcgtgacg
301 gacgttttgt ccgatgcgga agcctgcgta gggttcggc tggttgaagt

```

806

```

351 catcgatgat tttgtcccggt tgtacgggtgg tttggcgcggt gttgcccgtag
401 ctgtcgaagg cgggttttttt gacggacagg tagtgcaata cttctggcgg
451 gatttcttcg acgaagcggg atgcgatgcc gaattgggtt tgtccgtgca
501 gcatgcgttg ctgtgccatg gtgatgtaga ggcgtttgct ggcgcgggtg
551 atggcgacgt acatgaggcg gcgttcttct tcgagggcgc cgcgctcggc
601 aaggetcatt tcgctgggga aacgcccctc ttccataccg gtgaggaaga
651 cggcggtgaa ttccaagcct ttggcgcggt ggacgggtcat cagttggacg
701 gctttttcgc ctgcccctgc ttggttttcg ccggattcga gggcggcggt
751 gctcaagaag gcgaggatgg ggaaggcggg atcgtctga

```

This corresponds to the amino acid sequence <SEQ ID 1544; ORF 535.ng>:

g535.pep

```

1 MPFPVFRQXF AXSLLRFFAV GRILESDISN SGFSETINAS NVFVGYEYPT
51 ACISNLHFRFQ FRKLGIQFFH ALFAEVDGQS GGFAFVCGID NHAGAEFGVT
101 DVLSDAEACV GLRLFVIDD FVPLYGGLAR VAVAVEGGFF DGQVVQYFWR
151 DFFDEAGCDA ELGLSVQHAL LCHGDVEAFA GAGDGDVHEA AFFFEAAALG
201 KAHFAGETPL FHTGEEDGVE QAFGGVDGH QLDGFFACPC LVFAGFEGGV
251 AQEGEDGEGG IV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1545>:

m535.seq

```

1 aTGCCCTTtC CCGTTTTcAG ACGGCCTTTT GCTTTGTCCT TACTtACGTT
51 TTTTGCCGTA AGTCAGATTC TTGTATCCGA CATTTCCAAC AGCGGTGTTT
101 CGGAAACAAT AGACGCGTCA AATGTTTTTG TCGGATACGA ATATCCGACC
151 TACATTTCAA ATTTACATCT CTTCCAATTT CGCAAACCTG GTGTCCAAC
201 CTTTCACGCC CTGTTTGCCG AAATTGATGG TCAGTCGGGC GGATTGCGCT
251 TTATCTGCGG CATCGATAAT CACGCCCGTG CCGAATTGG CGTGGCGGAC
301 GTTTTGTCGG ATACGGAAAC CTGCGTAGGT TTGGGGCTGT TTGTAGTCGT
351 CGATGATTTT ATCTTTGGAT GCGGCGGTTT GCGCGGTGTT GCCGTAACTG
401 TCGTAGGCAG GCTTTTGTAG GGACAGGTAG TGCAATACTT CGGGTGGGAT
451 CTCTTCGACG AAGCGGGAGA CGATGCCGAA TTGGGTTTGT CCGTGCAGCA
501 TCGGTTGTTG CGCCATGGTG ATGTAGAGGC GTTTGCGGGC GCGGGTGATG
551 GCGACGTACA TGAGGCGGCG TTCTTCTTCG AGGCCCGCGC GTTCGGCAAG
601 GCTCATTTTC CTGGGGGAAG GGCCTTCTTC CATGCCGGTG AGGAAGACGG
651 CGTTAAATTC CAAGCCTTTG GCGGCGTGGA CGGTCATGAG TTGGACGGCC
701 TTTTCGCCCTG CGCTGCCTG GTTTTCAACG GATTGAGGG CGGCATTGCT
751 TAGGAAGGCG AGAATGGGGA AGGCGGGGTC GTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1546; ORF 535>:

m535.pep

```

1 MPFPVFRFPF ALSLLTFFAV SQILVSDISN SGVSETIDAS NVFVGYEYPT
51 YISNLHLFQF RKLGVQLFHA LFAEIDGQSG GFAPICGIDN HAGAEFGVAD
101 VLSDETETCVG LGLFVVDDF IFGCGGLARV AVTVVCRFLD GQVVQYFGWD
151 LFDEAGDDAE LGLSVQHALL RHGDVEAFAG AGDGDVHEAA FFFEAAAFGK
201 AHFAGEAAFF HAGEEDGVKF QAFGGVDGHE LDGLFACACL VFTGFEGGIA
251 XEGENEGGV V*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 535 shows 80.9% identity over a 262 aa overlap with a predicted ORF (ORF 535.ng) from *N. gonorrhoeae*:

m535/g535

```

          10      20      30      40      50      59
m535.pep  MPFPVFRFPFALSLLTFFAVSQILVSDISNSGVSETIDASNVF-VGYEYPTYISNLHLFQ
          |||||: || ||| ||||: || ||||| ||||: ||||| |||||: ||||| ||
g535      MPFPVFRQXFAXSLLRFFAVGRILESDISNSGFSETINASNVFVGYEYPACISNLHFRFQ
          10      20      30      40      50      60

          60      70      80      90      100     110     119
m535.pep  FRKLGVLFLHALFAEIDGQSGGFAPICGIDNHAGAEFGVADVLSDETETCVGLGLFVVDD
          ||||: ||: |||||: ||||| |||||: ||||| |||||: ||||| ||: ||
g535      FRKLGIQFFHALFAEVDGQSGGFAPVCGIDNHAGAEFGVTDVLSDAEACVGLRLFVIDD
          70      80      90      100     110     120

```

	120	130	140	150	160	170	179
m535.pep	FIFGCGGLARVAVTVVGRLFDDGQVVQYFGWDLFDEAGDDAELGLSVQHALLRRHGDVEAFA						
	: : : :						
g535	FVPLYGGLARVAVAVEGGFFDGGQVVQYFWRDFFDEAGCDAELGLSVQHALLCHGDVEAFA						
	130	140	150	160	170	180	
	180	190	200	210	220	230	239
m535.pep	GAGDGDVHEAAFFFEAAAFGKAHFAGEAAFFHAGEEDGVKFQAFGGVDGHELDGLFACAC						
	: : : : :						
g535	GAGDGDVHEAAFFFEAAALGKAHFAGETPLFHTGEEDGVVEFQAFGGVDGHLQDGGFACPC						
	190	200	210	220	230	240	
	240	250	260				
m535.pep	LVFTGFEGGIAXEGENGEVGVV						
	: : : :						
g535	LVFAGFEGGVAQEGEDGEGGIV						
	250	260					

a535.seq (partial)

1	TTCAGACGGC	CTTTTGCCCTT	GTCCTTGCTA	CAGTTTTTTG	CCATAGGTCG
51	GATTTCGCAA	TCCGACATTT	CCAACAGCGG	TTTTTCGGAA	ACGATAGACG
101	CGTCAAATAT	TTTTGCTGGA	TACGAGTATC	CAGCCTGCAT	TTCAAATTTA
151	CATCGCTTCC	AATTTGCGAA	ACTTGGTGTC	CAACTCTTTC	AGCCCGTGTT
201	TGCCGAAATT	GATGGTCAGT	CGGGCGGATT	CGCCTTTATC	TGCGGCATCG
251	ATAATCAGCG	CGGTGCCGAA	TTTGGCGTGG	CGGACGTTT	GTCGCGATACG
301	GAACCTCGC	TAGGTTTGGG	GCTGTTTGTA	GTCGTGATG	ATTTTGTCTT
351	TGGGCGCGCG	GGTTTGGGCG	GGTGTTGCCAT	AGCGGTCGTA	GCGGGGTTTT
401	TTGACGGACA	GGTAGTGCAA	TACTTCGGGC	GGGATTCTT	CGACGAAGCG
451	GGAGACGATG	CCGAATTGGG	TTTGTCCGTG	CAGCATTCGT	TGTTTGGGCCA
501	TGGTGATGTA	GAGGCGTTTG	CGGGCGCGGG	TGATGGCGAC	GTACATCAGG
551	CGCGGTTCTT	CTTCGAGGCC	CGCGCGTTCG	GCAAGGCTTA	TTTCGTGGG
601	GAAGCGGCCT	TCTTCCATGC	C3GTGAGGAA	TACGGCGTTA	AATTCCAAGC
651	CTTTGCGCGG	GTGCACGGTC	ATAGATTGTA	CGGCTTTTTC	GCCCGCGCCT
701	GCTTGGTTTT	CGCCGGATTG	GAGAGCAGCA	TTGCTTAGGA	AAGCGAGGAT
751	GGGGAAGCGC	GGGTCGTCTG	A		

```

a535.pep (partial)
1 FRRPFALSLQ QFFAIGRLLE SDISNSGFSE TIDASNI FVG YEYPACISNL
51 HRFQFRKLGV QLFHALFAEI DGQSGGFAFI CGIDNHAGAE YFGRADVLSDT
101 ETCVGLGLFV VDDFVFGRG GLARVAIAVV GGGFDGGVVQ FGGADVDFDEA
151 GDDAELGLSV QHALLRHGDV EAFAGAGDGD VHQAFFFEA AAFGKAHFAG
201 EAAFFHAGEE YGVKQFAFGG VHGHELYGFF ARACLVFAGF ESSIA*ESED
251 EGGVV*

```

	10	20	30	40	50	60
m535.pep	MPFPVFRPPFALSLLTFFAVSQILVSDISNSGVSETIDASNVFVGYEPTYISNLHLFQF					
a535	FRPPFALSLLOFFAIGRILESDISNSGFSETIDASNIFVGYEYPACISNLHRFQF					
	10	20	30	40	50	
	70	80	90	100	110	120
m535.pep	RKLGVLQFHALFAEIDGQSGGFAFICGIDNHAGAEFGVADVLSDTETCVGLGLFVVVDDF					
a535	RKLGVLQFHALFAEIDGQSGGFAFICGIDNHAGAEFGVADVLSDTETCVGLGLFVVVDDF					
	60	70	80	90	100	110
	130	140	150	160	170	180
m535.pep	IFGCGGLARVAVTVVGRFLFDGQVVQYFGWDLFDEAGDDAELGLSVQHALLRHGDVEAFAG					
	:		:			
a535	VFGRGLLARVAIVGGFFDGQVVQYFGRDFFDEAGDDAELGLSVQHALLRHGDVEAFAG					
	120	130	140	150	160	170

808

	190	200	210	220	230	240
m535.pep	AGDGDVHEAAFFFEAAAFGKAHFAGEAAFFHAGEEDGVKFQAFGGVDGHELDGLFACACL					
a535	AGDGDVHQAAFFFEAAAFGKAHFAGEAAFFHAGEEYGVKFQAFGGVHGHELYGFFARACL					
	180	190	200	210	220	230
	250	260				
m535.pep	VFTGFEGGIXEGENGEGGVVX					
a535	VFAGFESSIXESEDGEGGVVX					
	240	250				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1549>:

g537.seq

```

1 atgaaatccc tttttatttg gctgcttcta ttgggctcgg cggcaggcgt
51 tttctaccat acccaaaacc aatccctgcc cgcgggcgaa cttgtctatc
101 cgtccgcacc gcaaatcagg gacggcggcg atgcgctgca ctacctcaac
151 cgcacccgca cacaaatcgg ttgacacgcg ctggcacacg cgccggtttt
201 ggaaaattcc gccgcagcgc acgcacgcta tctcacgctc aatcccgaag
251 acggacacgg cgaacaccat cccgacaatc cgcactacac cgcacaaaag
301 ctgaccgaac gcacacgcct tgccgggtat ctctacaacg gcgtgcatga
351 aaacatcagc acggaagagg aagccgccga atcgctccgac agcgacatcc
401 gcacgcagca acgccaagtg gacgctttga tgagcgcaat ctaccaccgc
451 ctttcgctgc ttgaccgcca taccgacgaa gcaggtgcgg cattttgtcg
501 cgaaaacggc aaaaccgtcc tcgtattcaa tcaggcgcaac ggcagcttcg
551 agcgcgcctg tgcaaaagga aggcggcagc cggaagcagg acggaatat
601 taccgcaacg cttgccacaa cgggtgcggc gtttatgctg acgaagccat
651 gcccgtaacg gaattgcttt ataccgccta tccggttggc ggcggcgcgc
701 tgccttattt ttacggggaa cgtcccgacc ccgtgccgga atatgaaatc
751 acaggcaatc ctgccagcat tgatttttcc gagggcgagc gcaaaattgc
801 gatgaaaagt ttcaagctgt atcagggtaa aaacgaaatc cgcccgtca
851 gggttttaac cgcggcaac gaccctaacg gcaggctgac cgcgcaccaa
901 ttgcgccctt tcccgtcaa acctttggaa tacggcacgc tttatacggc
951 ggtattcgac tatgtccgca acggacggca cgcgcaggcg aaatggcagt
1001 ttagaaccg aaaaccgat tacccttatt ttgaggtaaa cggcgcgag
1051 acacttgccg ttagaaaagg gaaaaatat ttcattccact ggcgcggagc
1101 ctgggtgtct gaagcgtgta ccggttatac ctaccggcgc cagttcggca
1151 acagcctgtc catactccgg cacgaagcgg gcggcattgt cttcagcgtc
1201 agcggaatgg cgggaagccg catcaggctt actccggaag acagcccgga
1251 acgcggtgta accctttatt tgcaggattg a

```

This corresponds to the amino acid sequence <SEQ ID 1550; ORF 537.ng>:

g537.pep

```

1 MKSLFIWLLL LGSAAGVFYH TQNQSLPAGE LVYPSAPQIR DGGDALHYLN
51 RIRTQIGLHA LAHAPVLENS ARRHARYLTL NPEDGHGEHH PDNPHYTAQK
101 LTERTRLAGY LYNGVHENIS TEEAAESSD SDIRTQQRQV DALMSAIYHR
151 LSLDRHTDE AGAAFVRENG KTVLVFNQGN GSFERACAKG RROPEAGRKY
201 YRNACHNGAA VYADEAMPVT ELLYTAYPVG GGALPYFYGE RPDVPPEYEI
251 TGNPASIDFS EAAGKIAMKS FKLYQGKNEI RPVRVLTAGN DPNGRLTAHQ
301 FALFPLKPLE YGTLYTAVFD YVRNGRHAQA KWQFRTRKPD YPYFEVNGGE
351 TLAVRKGEKY FIHWRGRWCL EACTRYTYRR QFGNSLSILR HEAGGIVFSV
401 SGMAGSRIRL TPEDSPERGV TLYLQD *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1551>:

m537.seq (partial)

```

1 ATGAAATCCC TTTTATTTCG GCTGCTCCTG TTGGGTTCGG CGGCAGGCGT
51 TTTCTACCAT ACCCAAAmCC AATCCCTGCC CGCGGGCGAA CTGTCTATC
101 CGTCCGCACC GCAAATCAGG GACGGCGGCG ATGCGCTGCA CTACCTCAAC
151 CGCATCCGAG CCCAAATCGG TTGCACAAG CTGGCACACG CGCCGTTTTT
201 GGAATACTCC GCCCGCAGGC ACGCAAGCTA CCTCACGCTC AATCCGGAAG
251 ACGGACACGG CGAACACCAT CCCGACAATC CGCACTACAC CGCACAAAAG

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301 CTGACCGAAC GCACACGCCT TGCCGGGTAT CTCTACAACG GCGTGCATGA
 351 AAACATCAGC ACGGAAGAAG AAGCCGCCGA ATCGTCCGAC AGCGACATCC
 401 GCACGCAGCA ACGCCAAGTG GACGGATTAA TGAGCGCAAT CTACCACCGC
 451 CTTTCCCTAC TTGACCGCCA TACGGATGAG TCAGGAGCGG CATT...

This corresponds to the amino acid sequence <SEQ ID 1552; ORF 537>:

m537.pep (partial)

1 MKSLFIRLLL LGSAGVFIH TXQSLPAGE LVYPSAPQIR DGGDALHYLN
 51 RIRAIQGLHK LAHAPVLENS ARRHASYLTL NPEDGHGEHH PDNPHYTAQK
 101 LTERTRLAGY LYNGVHENIS TEEEAESSD SDIRTQQRQV DGLMSAIYHR
 151 LSLDRHTDE SGAA...

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 537 shows 95.7% identity over a 164 aa overlap with a predicted ORF (ORF 537.ng) from *N. gonorrhoeae*:

m537/g537

	10	20	30	40	50	60
m537.pep	MKSLFIRLLL LGSAGVFIHTQXQSLPAGELVYPSAPQIR DGGDALHYLN RIRAIQGLHK					
g537	MKSLFIWLLL LGSAGVFIHTQXQSLPAGELVYPSAPQIR DGGDALHYLN RIRAIQGLHA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m537.pep	LAHAPVLENSARRHASYLTLNPEDGHGEHHPDNPHYTAQKLTERTRLAGYLYNGVHENIS					
g537	LAHAPVLENSARRHARYLTLNPEDGHGEHHPDNPHYTAQKLTERTRLAGYLYNGVHENIS					
	70	80	90	100	110	120
	130	140	150	160		
m537.pep	TEEEAESSDSDIRTQQRQVDGLMSAIYHRLSLDRHTDESGAA					
g537	TEEEAESSDSDIRTQQRQVDALMSAIYHRLSLDRHTDEAGAAFVRENGKTVLVFNQGN					
	130	140	150	160	170	180
	190	200	210	220	230	240
g537	GSFERACAKGRRQPEAGRKYRNACHNGAAVYADEAMPVTELLYTAYPVGGGALPYFYGE					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1553>:

a537.seq

1 * ATGAAATCCC TTTTATTTCG GCTGCTCCTG TTGGGTTCGG CGGCCGGCGT
 51 TTTCTATCAT ACCCAAACCC AATCCCTGCC CGCGGGCGAA CTTGTCTATC
 101 CGTCCGCACC GCAAATCAGG GACGGCGGCG ATGCGCTGCA CTACCTCAAC
 151 CGCATCCGCG CCCAAATCGG TTTGCACAAG CTGGCACACG CGCCGGTTTT
 201 GGAAAATTCC GCGCGCAGGC ACGCACGCTA TCTCACGCTC AATCCCGAAG
 251 ACGGACACGG CGAACACCAT CCCGACAATC CGCACTACAC CGCACAAAAG
 301 CTGACCGAAC GCACACGCCT TGCCGGGTAT CTCTACAACG GCGTGCATGA
 351 AAACATCAGC ACGGAAGAAG AAGCCGCCGA ATCGTCCGAC AGCGACATCC
 401 GCACGCAGCA ACGCCAAGTG GACGGATTAA TGAGCGCAAT CTACCACCGC
 451 CTTTCCCTAC TTGACCGCCA TACGGATGAG GCAGGAGCGG CATTGTGCG
 501 CGAAAACGGT AAAACCGTTC TCGTATTCAA TCAGGGCAAC GCGAGGTTTG
 551 AGCGGCATTG CGCCCAAGGC AGAAATCAGC CGGAAGCAGG ACGGAAATAT
 601 TACCGCAACG CCTGCCATAA CCGTGCGGTC GTGTACACCG ACGAAGCCAT
 651 GCGCGCACAG GAGCTGCTCT ATACAGCCTA TCCCGTCGGC AACGGCGCAC
 701 TGCCTTATTT CCACGGCGAG CGTCCAGACC CCGTGCCGGA ATATGAAATC
 751 ACGGGAATC CTGCCAGCAT TGATTTTTCG GAGGCGGCAG GCAAAATTAC
 801 TAGTAAAAGT TTCAAGCTGT ATCAGGGTAA AAACGAAATC CGCCCGTCA
 851 GGGTTTAAAC CGCCGGCAAC GACCCCAACG GCAGGCTGAC CGCGTACCAA
 901 TTCGCGCTTT TCCCGCTCAA GCCTTTGGAA TACGGTACGC TTTATACGGC
 951 GGTATTCGAC TATGTCCGCA ACGGACGGCG CGCGCAGGCG AAATGGCAGT
 1001 TTAGAACCAG AAAACCCGAT TACCCTTATT TTGAGGTAAA CGCGGCGGAG
 1051 AACTTTGCGG TTAGAAAAGG CGAAAAATAT TTCATCCACT GCGCGGAGCG
 1101 CTGGTGTGTTG GAAGCGTGTA CCCGTTATAC CTACCGGCAG CGACCCGGCA

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1151 GCCGCCTGTC CATAGGAAGG CACAAGGCGG GCGGCATCGT CTTACAGCGTT
 1201 GACGGGAATGG CGGGCAGCCG CATCACGCTT GCACCGGAAG GAGAAACGGA
 1251 ACGAGGCGTA ACCCTTTATT TACAGGATTG A

This corresponds to the amino acid sequence <SEQ ID 1554; ORF 537.a>:

a537.pep
 1 MKSLFIRLLL LGSAAGVFYH TQNQSLPAGE LVYPSAPQIR DGGDALHYLN
 51 RIRAQIGLHK LAHAPVLENS ARRHARYLTL NPEDGHGEHH PDNPHYTAQK
 101 LTERTRLAGY LYNGVHENIS TEEEAESSD SDIRTQQRQV DGLMSAIYHR
 151 LSLDRHTDE AGAAVRENG KTVLVFNQGN GRFERHCAQG RNOPEAGRKY
 201 YRNACHNGAV VYTDEAMPAQ ELLYTAYPVG NGALPYFHGE RPDVPYEYEI
 251 TGNPASIDFS EAAGKITMKS FKLYQGKNEI RPVRVLTAGN DPNGRLTAYQ
 301 FALFPLKPLE YGTLYTAVFD YVRNGRRAQA KWQFRTRKPD YPFYEVNGGE
 351 TLAVRKGEKY FIHWRGRWCL EACTRYTYRQ RFGSRLSISR HKAGGIVFSV
 401 DGMAGSRITL APEGETERGV TLYLQD*

m537/a537 98.2% identity in 164 aa overlap

	10	20	30	40	50	60
m537.pep	MKSLFIRLLL	LGSAAGVFYHTQXQSLPAGELVYPSAPQIR	DGGDALHYLN	RIRAQIGLHK		
a537	MKSLFIRLLL	LGSAAGVFYHTQXQSLPAGELVYPSAPQIR	DGGDALHYLN	RIRAQIGLHK		
	10	20	30	40	50	60
m537.pep	LAHAPVLENSARRHAS	YLTLPEDGHGEHHPDNPHYTAQK	LTERTRLAGY	LYNGVHENIS		
a537	LAHAPVLENSARRHAS	YLTLPEDGHGEHHPDNPHYTAQK	LTERTRLAGY	LYNGVHENIS		
	70	80	90	100	110	120
m537.pep	TEEEAESSDSDIRTQQRQVDGLMSAIYHRLSLDRHTDESGAA					
a537	TEEEAESSDSDIRTQQRQVDGLMSAIYHRLSLDRHTDESGAA					
	130	140	150	160		
m537.pep	GRFERHCAQGRN	QPEAGRKYR	NACHNGAVVYTDEAMPAQ	ELLYTAYPVG	NGALPYFHGE	
a537	GRFERHCAQGRN	QPEAGRKYR	NACHNGAVVYTDEAMPAQ	ELLYTAYPVG	NGALPYFHGE	
	190	200	210	220	230	240

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1555>:

g538.seq
 1 atgtcaggta gaacaggacg gaacagtgc actcaggcgc aaccggaacg
 51 cgtcatgctg gtgggcgtaa tgttgataa agatgatac ggcagcaatg
 101 ccgcccgctc gaacggtttt cagacggcat tggcggaagc cgtcgagctg
 151 gtcaaagcgg cgggcggcga ttccgtacgc gtggagactg ccaaagcgga
 201 ccgcccgcac actgcgctgt ttgtcggcac gggcaaggcg gcggagctgt
 251 cggaagcagt tgccgcagac ggcattgatt tggctgtatt caaccacgaa
 301 cttactccca cgcaggaacg caatttgaa aaaatctcc aatgccgcgt
 351 attggacaga gtggggctga ttctggcgat ttccgccgc cgcgcccgca
 401 cgcaggaagg caggctgcaa gtcgagttgg cgcaattgag ccatttggcg
 451 ggacgcttga tacgcggtta cggacattg caaagccagc gcggcggtat
 501 cggcatgaaa gggccgggcg aaaccaaact ggaaaccgac cgccgattaa
 551 ccgcccatcg gatcaacgcc ttgaaaaaac agcttgccaa cctcaaaaaa
 601 cagecgcccc tgcgcgcgaa gtcccgcgag tcgggcagaa tcaaacggtt
 651 tgcgctggtc ggctatacca atgtcggcaa atccagcctg ttcaaccggc
 701 tgaccaagtc gggcatatat gcgaaagacc agcttttcgc cactctcgac
 751 acgacggcgc ggcggctgta catcagtcgc gcatcgagca ttatcctgac
 801 cgataccgtc ggattcgtca gcgatctgcc gcacaaactg atttccgcct
 851 tttccgccac cttggaagaa accgtgcaag ccgatgtgct gctgcacgtc
 901 gtcgatgctg ccgccgggaa cagcgggcag cagattgaag acgtggaaaa
 951 cgtactgcaa gaaatccatg cccacgatat tccgtgcac aaggtgtaca
 1001 acaaaaccga cctgctgccg tctgaagaac aaaacacggg catatggcgc
 1051 gacgctgcgg gaaaaattgc cgccgtccgc atttccggtt ctgaaaatac

This corresponds to the amino acid sequence <SEQ ID 1556; ORF 538.ng>:

g538.pep

```

1  MSGRTGRNSA TQAQPERVML VGVMLDKDDT GSNAARLNGF QTALAEAVEL
51  VKAAGGDSVR VETAKRDRPH TALFVGTGKA AELSEAVAAD GIDLVPFNHE
101 LPTPTQERNLE KILQCRVLDR VGLILAIFAR RARTQEGRLQ VELAQLSHLA
151 GRLIRGYGHL QSQRGGIGMK GPGETKLETD RRLTAHRINA LKKQLANLKK
201 QRALRRKSRE SGRIKTFALV GYTNVGKSSL FNRLTKSGIY AKDOLFATLD
251 TTARRLYISP ACSIIITDTV GFVSDLPKHL ISAFSATLEE TVQADVLLHV
301 VDAAARNSGQ QIEDVENVLQ EIIAHDIPICI KVNKTDLLP SEEQNTGIWR
351 DAAGKIAAVR ISVAENTGID ALREAIAEYC AAPNTDETE MP*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1557>:

m538.seq

```

1  ATGACAGGCA GAACAGGCGG CAACGGCAGT ACCCAAGCGC AACCCGAACG
51  CGTCATGCTG GTGGGCGTAA TGTGGACAA AGATGGTACG GCAGTAGTGT
101 CCGCCCGTCT GAACGGTTTT CAGACGGCAT TGGCGGAAGC TGTCGAGCTG
151 GTCAAAGCGG CGGGCGGCGA TTCCGTGCGC GTGGAGACTG CCAAACGCGA
201 CCGTCCGCAC ACCGCGCTGT TTGTCGGCAC GGGCAAGGCG GCGGAGCTGT
251 CAGAAGCAGT TGCCGCAGAC GGCATCGATT TGGTCGTATT CAACCACGAA
301 CTCACGCCCA CGCAGGAACG CAACCTTGAA AAAGAACTsA AATGCCGCGT
351 ATTGGACAGG GTAGGGCTGA TTCTGGCGAT TTTCGCTCGC CGCGCCCGCA
401 CGCAGGAAGG CAGGCTGCAA GTCGAGTTGG CGCAATTGAG CCATTTGGCG
451 GGACGCTTGA TACGCGGTTA CGGCCATCTG CAGAGCCAGC GCGGCGGTAT
501 CCGCATGAAA GGCCCCGGCG AAACCAAACCT GGAAACCGAC CGCCGATTGA
551 TCGCCCATCG GATCAATGCC TTGATAAAAC AGCTTGCCAA CCTCAAAAAA
601 CAGCGCGCCC TGCGCCGCAA GTChCGCGAA TCGGGCACAA TCAAAACGTT
651 TGCCTGGTGC GGCTATACAA ATGTCGGAAA ATCCAGCCTG TTCAACCGGC
701 TGACAAAGTC GGGCATATAT GCAAAGGACA AGCTTAGTCC CGAATGCAGC
751 ATTATCCTGA CCGATACCGT CGGATTCGTn AGCGATCTGC CGCacAAACT
801 GATTTCGCGC TTTTCgCC.A CGCTGGAAGA AACCGCGCAA GCCGATGTGC
851 TGCTGCACGT CGTCGATGCC GCCGCTCCGA ACAGCGGACA GCAGATTGAA
901 GACGTGGAAA ACGTACTGCA AGAAATCCAT GCCGGCGATA TTCCGTGCAT
951 cAAGGTGTAC AACAAAACCG ACCTGCTGCC GTCTGAAGAA CAAAACACGG
1001 GCATATGGCG CGACGCTGCG GGAAAAATTG CCGCCGTCCG CATTTCGTT
1051 GCTGAAAATA CCGGTATAGA CGCACTGCGC GAAGCcATTG CCGAGTCTIG
1101 TCGCGCCGCA CCAAACACAG ACGAAACCGA AATGCCATGA
```

This corresponds to the amino acid sequence <SEQ ID 1558; ORF 538>:

m538.pep

```

1  MTGRTGGNGS TQAQPERVML VGVMLDKDGT GSSAARLNGF QTALAEAVEL
51  VKAAGGDSVR VETAKRDRPH TALFVGTGKA AELSEAVAAD GIDLVPFNHE
101 LPTPTQERNLE KELKCRVLDR VGLILAIFAR RARTQEGRLQ VELAQLSHLA
151 GRLIRGYGHL QSQRGGIGMK GPGETKLETD RRLIAHRINA LKQLANLKK
201 QRALRRKSRE SGTIKTFALV GYTNVGKSSL FNRLTKSGIY AKDKLSPECS
251 IILTDTGVGFV SLDLPHKLISA FSXTLEETAQ ADVLLHVVDAA AAPNSGQQIE
301 DVENVLQEIH AGDIPCIKVY NKTDLLPSEE QNTGIWRDAA GKIAAVRISV
351 AENTGIDALR EAIAESCAA PNTDETEMP*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 538 shows 92.1% identity over a 392 aa overlap with a predicted ORF (ORF 538.ng) from *N. gonorrhoeae*:

m538/g538

	10	20	30	40	50	60
m538.pep	MTGRTGGNGSTQAQPERVMLVGVMLDKDGTGSSAARLNGFQTALAEAVELVKAAGGDSVR					
	: : :					
g538	MSGRTGRNSATQAQPERVMLVGVMLDKDDTGSNAARLNGFQTALAEAVELVKAAGGDSVR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m538.pep	VETAKRDRPHALTALFVGTGKAAELSEAVAADGIDLVPFNHELTPPTQERNLEKELKCRVLDR					
	:					
g538	VETAKRDRPHALTALFVGTGKAAELSEAVAADGIDLVPFNHELTPPTQERNLEKILQCRVLDR					

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	70	80	90	100	110	120
	130	140	150	160	170	180
m538.pep	VGLILAI FARRARTQ EGR LQVELAQLSHLAGRLIRGYGHLQSQRRGGIGMKGPGETKLETD					
g538	VGLILAI FARRARTQ EGR LQVELAQLSHLAGRLIRGYGHLQSQRRGGIGMKGPGETKLETD					
	130	140	150	160	170	180
	190	200	210	220	230	240
m538.pep	RRLIAHRINALIKQLANLKKQALRRKSRESGTIKTFALVG YTNVGKSSLFNRLTKSGIY					
g538	RRLTAHRINALKKQLANLKKQALRRKSRESGRITKTFALVG YTNVGKSSLFNRLTKSGIY					
	190	200	210	220	230	240
	250	260	270	280		
m538.pep	AKDKL-----SPEC SII LTDTVGFVSDLP HKLISAFSXTLEETAQADVLLHV					
	:					
g538	AKDQLFATLDTTARRLYISPAC SII LTDTVGFVSDLP HKLISAFSATLEETVQADVLLHV					
	250	260	270	280	290	300
	290	300	310	320	330	340
m538.pep	VDAAAPNSGQQIEDVENVLQEIHA GDIPCIKVYNKTDLLPSEEQNTGIWRDAAGKIAAVR					
g538	VDAAARNSGQQIEDVENVLQEIHA GDIPCIKVYNKTDLLPSEEQNTGIWRDAAGKIAAVR					
	310	320	330	340	350	360
	350	360	370	380		
m538.pep	ISVAENTGIDALREIAIESCAAAPNTDETEMPX					
g538	ISVAENTGIDALREIAIEYCAAAPNTDETEMPX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1559>:

```

a538.seq
1  ATGACAGGCA GAACAGGCCG CAACGGCAGT ACCCAAGCGC AACCCGAACG
51  CGTCATGCTG GTGGGCGTAA TGTGTGACAA AGATGGTACG GGCAGCAGTG
101 CCACCCGTCT GAACGGTTTT CAGACGGCAT TGGCGGAAGC TGTCGAGCTG
151 GTCAAAGCGG CGGGCGGCGA TTCCGTGCGC GTGGAGACTG CCAAACGCGA
201 CCGTCCGCAC ACCGCGCTGT TTGTCCGCAC GGGCAAGGCG GCGGAGCTGT
251 CGGAAGCAGT TGCCGCAGAC GGCATCGATT TGGTCGTATT CAACCACGAA
301 CTTACGCCCA CGCAGGAACG CAATTGGGAA AAAATCCTCC AATGCCCGCT
351 ATTGGACAGA GTGGGGCTGA TTCTGGCGAT TTTCCGCCCG CGCGCCCGCA
401 CGCAGGAAGG CAGGCTGCAA GTCGAGTTGG CACAATTGAG CCATTGGCG
451 GGACGCTTGA TACGCGGTTA CGGCCATCTG CAGAGCCAGC GCGGCGGTAT
501 CGGCATGAAA GGCCCCGCGC AAACCAAACT GGAAACCGAC CGCCGATTGA
551 TCGCCCATCG GATCAATGCC TTGAAAAAAC AGCTTGCCAA CCTCAAAAAA
601 CAGCGCGCCC TCGCGCGCAA GTCCCGCGAA TCGGGCACAA TCAAAACGTT
651 TCGCGTGGTC GGCTATACCA ATGTCGGCAA ATCCAGTCTG TTCAACCGGC
701 TGACCAAGTC CGGCATATAT GCGAAAGACC AGCTTTTCGC CACACTCGAC
751 ACGACGGCGC GCGGCTGTA CATCAGTCCC GAATGCAGCA TTATCCTGAC
801 CGATACCGTC GGATTCTGCA GCGATCTGCC GCACAACTG ATTTCCGCCT
851 TTTCCGCCAC GCTGGAAGAA ACCGCGCAAG CCGATGTGCT GCTGCACGTC
901 GTCGATGCCG CCGCTCCGAA CAGCGGACAG CAGATTGAAG ACGTGGAAAA
951 CGTACTGCAA GAAATCCATG CCGCGCATAT TCCGTGCATC AAGGTGTACA
1001 ACAAAACCGA CCTGCTGCCG TCTGAAGAAC AAAACACGGG CATATGGCGC
1051 GACGCTGCGG GAAAAATTGC CGCCGTCCGC ATTTCCGTTG CTGAAAATAC
1101 CGGTATAGAC GCACTGCGCG AAGCCATTGC CGAGTATTGT GCCGCCGCAC
1151 CAAACACAGA CGAAACCGAA ATGCCATGA

```

This corresponds to the amino acid sequence <SEQ ID 1560; ORF 538.a>:

```

a538.pep
1  MTGRTGRNGS TQAQPERVML VGVMLDKDGT GSSATRLNGF QTALAEAVEL
51  VKAAGGDSVR VETAKRDRPH TALFVGTGKA AELSEAVALD GIDLVVFNHE
101 LPTPTQERNLE KILQCRVLDR VGLILAI FAR RTQEGRLQ VELAQLSLHA
151 GRLIRGYGHL QSQRGGIGMK GPGETKLETD RRLIAHRINA LKKQLANLKK

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201 QRALRRKSRE SGTIKTFALV GYTNVGKSSL FNRLTKSGIY AKDQLFATLD
 251 TTARRLYISP ECSIILTDTV GFVSDLPKLI SAFSATLEE TAQADVLHV
 301 VDAAAPNSGQ QIEDVENVLQ EIHAGDIPCI KVYNKTDLLP SEEQNTGIWR
 351 DAAGKIAAVR ISVAENTGID ALREAIAEYC AAPNTDETE MP*

m538/a538 94.6% identity in 392 aa overlap

	10	20	30	40	50	60
m538.pep	MTGRTGGNGSTQAQPERVMLVGVM	LDKDG	TGSSAARLNGFQTALAEAVELVKAAGGDSVR			
a538	MTGRTGRNGSTQAQPERVMLVGVM	LDKDG	TGSSATRLNGFQTALAEAVELVKAAGGDSVR			
	70	80	90	100	110	120
m538.pep	VETAKRDRPHTALFVGTGKAAELSEAVAADGIDL	VFNH	ELTPTQERNLEKELKCRVLD			
a538	VETAKRDRPHTALFVGTGKAAELSEAVAADGIDL	VFNH	ELTPTQERNLEKILQCRVLD			
	130	140	150	160	170	180
m538.pep	VGLILAI	FARRARTQ	EGRLQVELAQLSHLAGRLIRGYGHLQ	SQRGGIGMKGPGETKLETD		
a538	VGLILAI	FARRARTQ	EGRLQVELAQLSHLAGRLIRGYGHLQ	SQRGGIGMKGPGETKLETD		
	190	200	210	220	230	240
m538.pep	RRLIAHRINALIKQLANLKKQ	RALRRKSRES	GTIKTFALVGYTNVGKSSLEFNRLTKSGIY			
a538	RRLIAHRINALIKQLANLKKQ	RALRRKSRES	GTIKTFALVGYTNVGKSSLEFNRLTKSGIY			
	250	260	270	280		
m538.pep	AKDKL-----	SPECSII	LTDTVGFVSDLPKLI	SAFSXTLEETAQADVLHV		
a538	AKDQLFATLDTTARRLYIS	SPECSII	LTDTVGFVSDLPKLI	SAFSATLEETAQADVLHV		
	290	300	310	320	330	340
m538.pep	VDAAAPNSGQ	QIEDVENVLQ	EIHAGDIPCIKVYNKTDLLP	SEEQNTGIWRDAAGKIAAVR		
a538	VDAAAPNSGQ	QIEDVENVLQ	EIHAGDIPCIKVYNKTDLLP	SEEQNTGIWRDAAGKIAAVR		
	350	360	370	380		
m538.pep	ISVAENTGID	ALREAIAES	CAAPNTDETEMPX			
a538	ISVAENTGID	ALREAIAEY	CAAPNTDETEMPX			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1561>:

g539.seq
 1 atggaggatc tgcaggaaat cgggttcgat gtcgcccgcg taaaggtagg
 51 tcggcagcgc gaacatcatc gtctgcatca taccaggtcc ggcaacggca
 101 aggcggacga tgtattgttt gcgttctttt tgggtggcgg cttcgatttt
 151 ttgcgcgtca taggggtcgg cgggttagcc tgtctgccgg attttcaaca
 201 gaatgtcggg gaggcggatt ttgccgtcgt cccagacgac gcggcagcgg
 251 tgcgtgctgt aattgaggtc gatgcggacg atgccgtctg tgcgcaaaag
 301 ctgctgttcg atcagccaga cgcaggcggc gcaggtaatg ccgctgagca
 351 tcagcactgc ttcgtgcgtg ccattatggg tttccacaaa gtcggatttg
 401 acttcgggca ggtcgtacag gcggatttgg tgcaggattt cttggggcgg
 451 cagttcggtt tttttcgcgt cggcgggtgc tggttgttaa taactgccca
 501 agccggaatc gatgatgctt tgtgcgactg cctgacagcc gacgcagcag
 551 gtttcgcggg cttcgccttc gtagcggacg gtcagatgca gggtttcggg
 601 aacgtccagc ccgcagtggg aacaggtttt tttcatggca tttcgggttc

814

```

651 gtctgtgttt ggtgcgggcg cacaatactc ggcaatggct tcgcgagtg
701 cgtctatacc ggtattttca gcaacggaaa tgcggacggc ggcaattttt
751 cccgcagcgt cgcgccatat gcccggtgtt tggtcttcag acggcagcag
801 gtcgggtttg ttgtacacct tgatgcacgg aatatcgtag gcatcgattt
851 cttgcagtac gttttccacg tcttcaatct gctgcccgct gttccggcg
901 gcagcatcga cgacgtgcag cagcacatcg gcttgacggg tttcttccaa
951 ggtggcgga aaggcgga aacgtttgtg cggcagatcg ctgacgaatc
1001 cgacggatc ggtcaggata atgctgcatg cgggactgat gtacagccgc
1051 cgcgcgctg tgctgagagt ggcgaaaagc tgggtctttc catatatgcc
1101 cgacttggtc agccggttga acaggctgga tttgccgaca ttggtatag

```

This corresponds to the amino acid sequence <SEQ ID 1562; ORF 539.ng>:

g539.pep

```

1 MEDLQEIGFD VAAVKVGRQR EHHRLHHTQS GNGKADDVLF AFFLVGGFDF
51 LRVIGCGGVA CLPDFQQNVG EADFAVVPDD AAARAVIEV DADDAVCAQK
101 LLFDQPDAGG AGNAAEHQHC FVRAIMGFHK VGLDFGQVQV ADLVEDFLGR
151 QFGFFRVGGA SFVITAQAGI DDALCDCLTA DAAGFAVFAF VADGQMVFV
201 NVQPAVETGF FHGISVSSVF GAAQYSAMA SRSASIPVFS ATEMRTAAIF
251 PAASRHMPVF CSSDGSRSVL LYTLMHGISW AWISCSTFST SSICCLPFR
301 AASTTCSSTS ACTVSSKVAE KAEISLCGRS LTNPTVSVRI MLHAGLMYSR
351 RAVVSRVAKS WSFAYMPDLV SRLNRLDLPT LV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1563>:

m539.seq (partial)

```

1 ATGGAGGATT TGCAGGAAAT CGGGTTCGAT GTCGCCGCCG TAAAGGTAGG
51 TCGGCAGCGC GAACATCATC GTCTGCATCA TCCCCAGCCC GGCAACGGCG
101 AGGCGGACGA TGTATTGTTT GCGTTCCTTT TGGTTGGCGG CTTCGATTTT
151 TTGCGCGTCA TAGGGTGCAG CCGTGTAGCC TATCTGCCTG ATTTTCAACA
201 GAATGTCGGA AAGGCGGATT TTGCCGTCGT CCCAGACGAC GCGGCaGCGg
251 TGCGTGCTGT AATTGAGGTC GATGCGGACG ATGCCGTCGT TACGCAAAAG
301 CTGCTGTTTC ATCAGCCAGA CGCAGGCGGC GCAGGTGATG CCGCCGAGCA
351 TTTAAACCGC CTCGCGCGTG CCGCCGTGGG TTTCCACAAA GTCGGACTGG
401 ACTTCGGGCA GGTCTGTACG GCGGATTGCG TCGAGGATTT CTGCGGCGG
451 CAGCTCGGTT TTTTGCCTGT CCGCGGTGCG TTGTTGTGTA TAACTGCCCA
501 AGCCCCGCTC AATAATGCTT TGTGCGACCG CCTGACAGCC GGCGCaAGg
551 GTTTCGCGGT CTTGTTTTC GTAACGGACA GTCAGGTGGA GGTGTTGCGG
601 AACATCCAGA CCGCAGTGGA AACAGGTTTT TTTTCATGGA TTTGCGTTTC
651 GTCTGTGTTT GGTGCGGCGG CACAAGACTC GGCAATgGCT TCGCGCAGTG
701 CGTCTATACC GGTATTTTCA GCAACGGAAA TCGCGACGGC GGCAATTTTT
751 CCCGCAGCGT CCGCCCATAT GCCCGTGTTC TGTCTTTCAG ACGGCAGCAG
801 TCGCGTTTTC TTGTACACCT TgATGCACGG AATATCGCCG GCATGGATTT
851 CTTGCAGTAC GTTTTCCACG TCTTCAATCT GCTGTCCGCT GTTCGGAGCG
901 GCGGCATCGA CGACGTGCAG CAGCACATCG GCTTGCAGCG TTTCTTCCAG
951 CGTGGcG.AA AAGGCGGAAA TCAGTTTgTG CGGCAGATCG CTnACGAATC
1001 CGACGGTATC GGTCAGGATA ATGCTGCATT CGGGAC...

```

This corresponds to the amino acid sequence <SEQ ID 1564; ORF 539>:

m539.pep (partial)

```

1 MEDLQEIGFD VAAVKVGRQR EHHRLHHPQP GNGEADDVLF AFFLVGGFDF
51 LRVIGCGGVA YLPDFQQNVG KADFAVVPDD AAARAVIEV DADDAVCTQK
101 LLFDQPDAGG AGDAAEH*NR LARAAGVGFHK VGLDFGQVQV ADLVEDFLGR
151 QLGFRLVGGA LFVITAQARV NNALCDRLTA GAQGFVAVFV VTDSQVEVFG
201 NIQTAVETGF FHGISVSSVF GAAQDSAMA SRSASIPVFS ATEMRTAAIF
251 PAASRHMPVF CSSDGSRSVL LYTLMHGISP AWISCSTFST SSICCLPFGA
301 AASTTCSSTS ACAVSSSVAX KAEISLCGRS LTNPTVSVRI MLHSG...

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 539 shows 89% identity over a 345 aa overlap with a predicted ORF (ORF 539.ng) from *N. gonorrhoeae*:

m539/g539

	10	20	30	40	50	60
m539.pep	MEDLQEIGFDVAAVKVGRQR	EHHRLHHPQPGNGEADDVLF	FAFFLVGGFDFL	LRVIGCGGVA		
g539	MEDLQEIGFDVAAVKVGRQR	EHHRLHHTQSGNGKADDVLF	FAFFLVGGFDFL	LRVIGCGGVA		

815

	10	20	30	40	50	60
	70	80	90	100	110	120
m539.pep	YLPDFQQNVGKADF	FAVVPDDAAAVRAVIEVD	ADDAVCTQKLLFDQ	PDAGGAGDAAEHXNR		
g539	CLPDFQQNVGEADF	FAVVPDDAAAVRAVIEVD	ADDAVCAQKLLFDQ	PDAGGAGNAAEHQHC		
	70	80	90	100	110	120
	130	140	150	160	170	180
m539.pep	LARA	AVGFHKVGLDFGQV	QADLVEDFLGRQLG	FLRVGGALFVITAQ	ARVNNALCDRLTA	
g539	FVRA	IMGFHKVGLDFGQV	QADLVEDFLGRQFG	FRVGGASFVITAQ	AGIDDALCDCLTA	
	130	140	150	160	170	180
	190	200	210	220	230	240
m539.pep	GAQGF	AVFVFTDSQVEV	FGNIQTAVETGFF	HGISVSSVFGAAQ	DSAMASRSASIPVFS	
g539	DAAGF	AVEAFVADGQM	QVFGNVQPAVETG	FFHGISVSSVFGAA	QYSAMASRSASIPVFS	
	190	200	210	220	230	240
	250	260	270	280	290	300
m539.pep	ATEMRTAAI	FPAASRHM	PFVFCSSDGS	RSVLLYTLMHGIS	PAWISCSTFSTSSIC	CPLEFA
g539	ATEMRTAAI	FPAASRHM	PFVFCSSDGS	RSVLLYTLMHGIS	WAWISCSTFSTSSIC	CPLEFRA
	250	260	270	280	290	300
	310	320	330	340		
m539.pep	AASTTCSSTS	SACAVSSSVAXKAE	ISLCGRSLTNPTV	SVRIMLHSG		
g539	AASTTCSSTS	SACTVSSKVAEKAE	ISLCGRSLTNPTV	SVRIMLHAGLMYS	RRRAVVSRAVKS	
	310	320	330	340	350	360
g539	WSFAYMFDL	VSRLNRLDLPTLV				
	370	380				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1565>:

```

a539.seq
1  ATGGAGGATT TGCAGGAAAT CGGGTTTCGAT GTCGCCGCCG TAAAGGTAGG
51  TCGGCAGCGC GAACATCATC GTCTGCATCA TCCCCAGCCC GGCAACGGCG
101 AGGCGGACGA TGTATTGTTT GCGTTCCTTT TGGTTGGCGG CTTCGATTTT
151 TTGCGCGTCA TAGGGTGC GG GTAGCC TATCTGCCTG ATTTTCAACA
201 GAATGTCGGA AAGGCGGATT TTGCCGTCGT CCCAGACGAC GCGGCAGCGG
251 TGGCTGCTGT AATTGAGGTC GATGCGGACG ATGCCGCTCTG TACGCCAAAAG
301 CTGCTGTTTCG ATCAGCCAGA CGCAGGCGGC GCAGGTGATG CCGCCGAGCA
351 TTAAAACCGC CTCGCGCGTG CCGCCGTGGG TTTCCACAAA GTCGGACTGG
401 ACTTCGGGCA GGTGCTACAG GCGGATTGG TCGAGGATTT CTGGGGCGG
451 CAGCTCGGTT TTTGCGCGT CGGCGGTGCG TTGTTGTAA TAACTGCCCA
501 AGCCCGCGTC AATAATGCTT TGTGCGACTG CCTGACAACC GGCGCAGCAG
551 GTTTCGCGGT CTTCGTTTTC GTAACGGACG GTCAGATGCA GGTTTTCGGG
601 AACGTCCAGC CCGCAGTGGA AACAGGTTTT TTTCATGGCA TTTCGGTTTC
651 GTCTGTGTTT GGTGCGGCGG CACAATACTC GGCAATGGCT TCGCGCAGTG
701 CGCTATACCC GGTATTTTCA GCAACGGAAA TCGCGACGGC GGCAATTTTT
751 CCCGCAGCGT CCGGCCATAT GCCCGTGTTT TGTTCTTCAG ACGGCAGCAG
801 GTCGGTTTTG TTGTACACCT TGATGCACGG AATATCGCCG GCATGGATTT
851 CTTGCAGTAC GTTTTCCACG TCTTCAATCT GCTGTCCGCT GTTCGGAGCG
901 GCGGCATCGA CGACGTGCAG CAGCACATCG GCTTGC GCGG TTTCTTCCAG
951 CGTGGCGGAA AAGGCGGAAA TCAGTTTGTG CGGCAGATCG CTGACGAATC
1001 CGACGGTATC GGTGAGGATA ATGCTGCATT CGGGACTGAT GTACAGCCGC
1051 CGCGCCGTCG TGTCGAGTGT GCGGAAAAGC TGGTCTTTCG CATATATGCC
1101 CGACTTGGTC AGCCGTTGA ACAGACTGGA TTTGCCGACA TTGGTATAG

```

This corresponds to the amino acid sequence <SEQ ID 1566; ORF 539.a>:

```

a539.pep
1  MEDLQEIGFD VAAVKVGRQR EHHRLHHPQP GNGEADDVLF AFFLVGGFDF

```


816

```

51  LRVIGCGGVA YLPDFQQNVG KADFAVVPDD AAVRAVIEV DADDAVCTQK
101 LLFDQPDAGG AGDAAEH*NR LARAAGVFHK VGLDFGQVVQ ADLVEDFLGR
151 QLGFLRVGGA LFVITAAQARV NNALCDCLTT GAAGFAVEVF VTDGQMVFVG
201 NVQPAVETGF FHGISVSSVF GAAQYSAMA SRSASIPVFS ATEMRTAAIF
251 PAASRHMPVF CSSDGSRSVL LYTLMHGISP AWISCSTFST SSICCPFLGA
301 AASTCSSTS ACAVSSVAE KAEISLCGRS LTNPVSVRI MLHSGLMYSR
351 RAVVSSVAKS WSFAYMPDLV SRLNRLDLPT LV*

```

m539/a539 97.1% identity in 345 aa overlap

	10	20	30	40	50	60
m539.pep	MEDLQEIGFDVA	AVKVGRQREHRLHHP	QPGNGEADDVL	FAFFLVGGFD	FLRVIGCGGVA	
a539	MEDLQEIGFDVA	AVKVGRQREHRLHHP	QPGNGEADDVL	FAFFLVGGFD	FLRVIGCGGVA	
	10	20	30	40	50	60
	70	80	90	100	110	120
m539.pep	YLPDFQQNVGKAD	FAVVPDAAAVRAVIEV	DADDAVCTQKLL	FDQPDAGGAGD	AAEHXNR	
a539	YLPDFQQNVGKAD	FAVVPDAAAVRAVIEV	DADDAVCTQKLL	FDQPDAGGAGD	AAEHXNR	
	70	80	90	100	110	120
	130	140	150	160	170	180
m539.pep	LARAAGVFHKVGL	DFGQVVQADLVED	FLGRQLGFLRV	GGALFVITAQARV	NNALCDRLTA	
a539	LARAAGVFHKVGL	DFGQVVQADLVED	FLGRQLGFLRV	GGALFVITAQARV	NNALCDCLTT	
	130	140	150	160	170	180
	190	200	210	220	230	240
m539.pep	GAQGFVAVFVTD	SQVEVFGNIQTAV	ETGFFHGISVSS	VFGAAQDSAMAS	SRSASIPVFS	
a539	GAQGFVAVFVTD	SQVEVFGNIQTAV	ETGFFHGISVSS	VFGAAQYSAMAS	SRSASIPVFS	
	190	200	210	220	230	240
	250	260	270	280	290	300
m539.pep	ATEMRTAAIFPA	ASRHMPVFCSSDGS	RSVLLYTLMHG	ISPAWISCSTF	STSSICCPFLGA	
a539	ATEMRTAAIFPA	ASRHMPVFCSSDGS	RSVLLYTLMHG	ISPAWISCSTF	STSSICCPFLGA	
	250	260	270	280	290	300
	310	320	330	340		
m539.pep	AASTCSSTSACA	VSSSVAXKAEISL	CGRSLTNPTVSV	RIMLHSG		
a539	AASTCSSTSACA	VSSSVAXKAEISL	CGRSLTNPTVSV	RIMLHSGLMYSR	RAVVSSVAKS	
	310	320	330	340	350	360
a539	WSFAYMPDLVSR	LNRLDLPTLVX				
	370	380				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1567>:

```

g540.seq
1  atgccgccct cccgacgcgg caacggggtg tttatcaaa acggcaaaact
51  tgccaatgcg gtttccgctt gccgattgcc aaaccggcaa acctttcccg
101  tgccggtgcc gaaccgatg ccgtctgaac cttcagacgg catcggtgtg
151  ttatttgtcc actcggacgg gtgcaggttc gtattgtgtc gattcgtcgc
201  cgtaatacag cacgccgagt ttgacgggga tgcgtccctg cgatttgccg
251  tgggcgttgg aatcgcgcaa ggaatgcgag cagccgcagt attcctgctg
301  gtagaagttt tcgcgtttgc tgatttcaat catacgcgcg ccgccccgcg
351  ctttgcgcca gttgaagtc caataggcca catcatcgta aggcgcgcgcg
401  gcacggtgtc cgcagtcgtt gatttgcgcc atatttttcc agcgtga

```

This corresponds to the amino acid sequence <SEQ ID 1568; ORF 540.ng>:

```

g540.pep
1  MPFSRRNGNV FYQNGKLANA VSACRLPNRQ TFPVPVNP M FSEPSDGIGC

```

817

51 L FVHSDGCRF VLCRFVAVIQ HAEFDGDASL RFAVGVGIAQ GIRAAAVFLL
 101 VEVFAFADFN HTRAAAFAP VEVPIGHIIV RRGTVSAVV DLRHIFPA *

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1569>:

m540.seq (partial)
 1 ..CCGAACCCGA TGCCGTCTGA ACCTTCAGAC GGCATCGGGT GTTATTGTG
 51 CCACCCGGAT GGGGCGAGGT TCGTATTGTG TCGATTCTGC GCCGTAATAC
 101 AGCACGCCGA GTTTGATGGG GATTCTGCCC TGTGATTTCG GGTGGGCATT
 151 GGAATCCCTC AGGGAATAGG CACAACCGCA ATATTCTGTC TGGTAGAAGT
 201 TTTACGTTT GCTGATTCA ATCATGCGCG CGCTGCCGCC GCCTTTGCGC
 251 CAGTTGAAAT CCCAATACAC CACATCATCG TAAGGCGCGG CGGCGCGGTG
 301 TCCGCAGTCG TTGATTGCG CCATATTTT CCAGCGTGA

This corresponds to the amino acid sequence <SEQ ID 1570; ORF 540>:

m540.pep (partial)
 1 ..PNMPSEPSD GIGCLFVHPD GGRFVLCRFV AVIQHAEFDG DSAL*FAVGI
 51 GIPOGIGTTA IFLLVEVFTF ADFNHARAAA AFAPVEIPIH HIIVRRGGAV
 101 SAVDLRHIF PA*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 540 shows 85.7% identity over a 112 aa overlap with a predicted ORF (ORF 540.ng) from *N. gonorrhoeae*:

m540/g540

m540.pep				10	20	30
				PNMPSEPSDGIGCLFVHPD	GGRFVLCRFV	
g540	GNGVFYQNGKLANAVSACRLPNRQTFPV	PVNPMPSEPSDGIGCLFVHSDGCRFV	L			
	10	20	30	40	50	60

m540.pep	40	50	60	70	80	90
	AVIQHAEFDGDSALXFAVGIGIPQIGT	TAIFLLVEVFTFADFNHARAAA	AFAPVEIPIH			
g540	AVIQHAEFDGDASLRF	FAVGVGIAQGIRAAAVFLLVEVFAFADFNHTRAAAFAPVEVPIG				
	70	80	90	100	110	120

m540.pep	100	110
	HIIVRRGGAVSAVVDLRHIFPAX	
g540	HIIVRRGGTVSAVVDLRHIFPAX	
	130	140

L' estremita' N-terminale di meningococco e' assente perche' interviene la fine del contig

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1571>:

a540.seq
 1 ATGCCGTCCT CCCGACGCGG CAACGGGGTG TTTTATCAAA ACGGCAAACT
 51 TGCCAATGCG GTTTCGATT GCAGATTGCC AAACCGGCAA ACCTTCCCG
 101 TGCCGATGCC GAACCCGATG CCGTCTGAAC CTTACAGCGG CATCGGGTGT
 151 TTATTGTGCC ACCCGATGG GTGCAGGTTT GTATTGTGTC GATTGTCGCG
 201 CGTAATACAG CACGCCGAGT TTGATGGGGA TTCTGCCCTG TGATTGCGG
 251 TGGGCGTTGG AATCCCTCAG GGAATAGGCA CAACCGCAAT ATTCCTGCTG
 301 GTAGAAGTTT TCACGTTTGC TGATTCAAT CATACGCGCG CTGCCGCCGC
 351 CTTTGCGCCA GTTGAAATCC CAATACACCA CATCATCGTA AGGCGCGGCG
 401 GCGCGGCGGC CGCAGTCGTT AATCTGGTTC ATGTTTTC A

This corresponds to the amino acid sequence <SEQ ID 1572; ORF 540.a>:

a540.pep (partial)
 1 MPSSRRGNV FYQNGKLANA VSDCLPNRQ TFPVPMNPM PSEPSDGIGC
 51 L FVHPDGRF VLCRFVAVIQ HAEFDGDASL *FAVGVGIPQ GIGTTAIFLL
 101 VEFTFADFN HTRAAAFAP VEIPIHHIIV RRGAAAVV NLVHVFP

818

m540/a540 92.8% identity in 111 aa overlap

```

                                10      20      30
m540.pep                      PNPMPSEPSDGIGCLFVHPDGGRFVLCRFV
                                |||
a540      GNGVFYQNGKLANAVSDCRLPNRQTFPVPMPNPMPSEPSDGIGCLFVHPDGGRFVLCRFV
              10      20      30      40      50      60

                                40      50      60      70      80      90
m540.pep      AVIQHAEFDGDSALXFAVGIGIPQIGITTAIFLLVEVFTFADFNHARAAAFAPVEIPIH
              |||
a540      AVIQHAEFDGDSALXFAVGIGIPQIGITTAIFLLVEVFTFADFNHTRAAAFAPVEIPIH
              70      80      90      100     110     120

                                100     110
m540.pep      HIIIVRRGGAVSAVVDLRHIFPAX
              |||
a540      HIIIVRRGGAAAVVNLVHVFP
              130     140

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1573>:

```

g542.seq
1  atgccgaaat ggtcgcgcac acggcggttc agcgctcctt cgctgatgtt
51 cagcgcggtt gtcagccggt tgacttggtg tgcgcccgcg tcgaacgcgg
101 cattcagggt gcggctgaag tcttcagacg gcatagcgtc tgcttcgcgc
151 gtttgccccc ccgcccgcgc gatgccgtct gaaaccgtgt cccacaaatc
201 cgacagcagc cgcaaacagt ccgcctcgcg gcgcaatgtt tcgcccacaa
251 gcccttttgg gacgggttgc aggcaggatg ccgccaagcc gcgcaggttt
301 gggggcaaat cccatatact gaccggttcg cggttaa

```

This corresponds to the amino acid sequence <SEQ ID 1574; ORF 542.ng>:

```

g542.pep
1  MPKWSRIRRC SVLSLMFSAA VSRLTWCAPP SNAAFRVLK SSDGIASASA
51  VCPAAGSMPS ETVSHKSDSS RNTSASRRNV SPKCPFGTVC RQDAAKPRRF
101 GGKSHILTGS R*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1575>:

```

m542.seq
1  ATGCCGAAAT GGTCGCGCAT ACGGCGTTGC AGCGTCCTTT CACTGATGTT
51  CAGCGCGTCT GTCAGCCGGT TGAATTGGTG TCGCCGTCG GCAAACGCGG
101 CATTTAGGGT GCGGCTGAAG TCTTCAGACG GCATAGCGTC TGCTTCGCGC
151 GTTTGCCCCG CCGCCGCCCC GATGCCGTCT GAAACCGTGT CCCACAAGTC
201 CGACAGCAGC CGCAACACGT CCGCCTCGCG .CGCAATGTT TCGCCCAAAT
251 GCCCCTTTGG GACGGCTTTC AGGCAGGATG CCGCCAAGCC GCGCAGGTTT
301 GGGGGCAAAT CCGATATCCT GACCGGTTTC CGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1576; ORF 542>:

```

m542.pep
1  MPKWSRIRRC SVLSLMFSAS VSRLTWCAPS ANAAFRVLK SSDGIASASA
51  VCPAAGSMPS ETVSHKSDSS RNTSASRAMF RNPAPLGRNV SPKCPFGTAF
101 RQDAAKPRRF GGKSHILTGS R*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 542 shows 93.7% identity over a 111 aa overlap with a predicted ORF (ORF 542.ng) from *N. gonorrhoeae*:

```

m542/g542

              10      20      30      40      50      60
m542.pep      MPKWSRIRRC SVLSLMFSASVSRLTWCAPSANAAFRVLKSSDGIASASAVCPAAGPMPS
              |||
g542      MPKWSRIRRC SVLSLMFSAAVSRLTWCAPP SNAAFRVLKSSDGIASASAVCPAAGSMPS
              10      20      30      40      50      60

              70      80      90      100     110
m542.pep      ETVSHKSDSSRNTSASXRNVS PKCPFGTAF RQDAAKPRRF GGKSHILTGSRX

```

819

```

|||||
g542  ETVSHKSDSSRNTSASRRNVSPKCPFGTVCRQDAAKPRRFGGKSHILTGSRX
              70      80      90      100     110

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1577>:

```

a542.seq
1  ATGCCGAAAT GGTCGCGCAT ACGGCGTTGC AGCGTCCTTT CGCTGATGTT
51  CAGCGTGTCT GCCAGCCGGT TGAATTGATG TGCGCCGCCG GCAAACGCGG
101 CATTCAAGAT GCGGCTGAAG TCTTCAGACG GCATAGCGTC TGCTTCCGCC
151 GTTTGCCCCG CCGCCGGCCC GATGCCGTCT GAAACCGTGT CCCACAAGTC
201 CGACAGCAGC CGCAACACGT CCGCCTCGCG GCGCAATGTT TCGCCCAAAT
251 GCCCCTTTGG GACGGCTTTC AGGCAGGATG CCGCCAAGCC GCGCAGGTTC
301 GGGGGCAAAT CCCATATCCT GACCGGTTTC CGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1578; ORF 542.a>:

```

a542.pep
1  MPKWSRIRRC SVLSLMFSVS ASRLT*CAPP ANAAFRMLK SSDGIASASA
51  VCPAAGPMPS ETVSHKSDSS RNTSASRRNV SPKCPFGTAF RQDAAKPRRF
101 GGKSHILTGS R*

```

m542/a542 94.6% identity in 111 aa overlap

```

              10      20      30      40      50      60
m542.pep  MPKWSRIRRC SVLSLMFSVSASRLTWCAPSANAAFRVRLKSSDGIASASAVCPAAGPMPS
          |||||
a542      MPKWSRIRRC SVLSLMFSVSASRLTXCAPPANAAFRMLKSSDGIASASAVCPAAGPMPS
              10      20      30      40      50      60

              70      80      90      100     110
m542.pep  ETVSHKSDSSRNTSASRRNVSPKCPFGTAFRQDAAKPRRFGGKSHILTGSRX
          |||||
a542      ETVSHKSDSSRNTSASRRNVSPKCPFGTAFRQDAAKPRRFGGKSHILTGSRX
              70      80      90      100     110

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1579>:

```

g543.seq
1  atggtttgtc gggtatttgc cgcgcttttt ggctttcaac tcggcaatca
51  gcccgctgat gcctttggct ttgatgattt cgcgcaattg gttgcggtac
101 acggtaacca ggctcgtgcc ttcatgagcg acgttgtagg tacggatttt
151 gccgcccgtt tggtaggtgg taaagtccat attgacgggc ttctgaccgg
201 ggatgccgac ttccgacacg acgacgattt ccttgccgcc cttattgacg
251 atgggattgt ctttgacggt gacggtcgcg tttttgaatt tcagcatcgt
301 gccggaatag gtgcggatca gcagggtttg aaattctttg gccaacgctt
351 gtttttgcgc ytcggacgcy gtacgccaaag ggttgccgac cgccaatgcy
401 gtcatacgtt ggaaatcgaa atagggaacc gcataggctt cggcttttgg
451 gcgtgcagaa gccgcgtcgc cgcttttgag gatggtcaaa acctgtgtgg
501 cgttttggcg gatttgctcc actgcgtcgg ccggggaggc aaatgccatg
551 ccgatgctca aaataccgat gcccaatgcy ctgatgaagg aggatttttt
601 cacgatgtct ttccctgaaa tggatgtgta tgtttattct gcggcttttt
651 ccgcattgcc gccctcagcg tttttctcgg cgaagctggt catgaattta
701 ccgatcaggt tttccagaa cattgcagaa ctggttacgg agatggtgct
751 gccggcagca aggttttccg tatcgccgcc ctgctgcagc ccgatgtact
801 gttcgcctaa aagtcccga gtcaggattt gcgcggaacc gtcactgctg
851 aactgatact tgccgtccaa atcaaggcgc accctcgcct gataggattt
901 cgggtcaagc ccgatagcgc cgacgcgccc gaccaatacg cctgcggatt
951 tgacgggggc attgaccttc aaacgcgcga tgcgcgcgaa atcggcataa
1001 acggcgtaag ttttgctcga accgccgaac gccgcgcccgc ccgccacgcg
1051 gaaagcgaga aaggcaaccg ccgcccgcgc gatcaagacg aacagtccga
1101 cccaaaattc caatatgttc tttttcatta a

```

This corresponds to the amino acid sequence <SEQ ID 1580; ORF 543.ng>:

```

g543.pep
1  MVCRLFAAVF GFQLGNQVPD AFGFDDFAEL VAVHGNQARA FDGDVVGTVF

```

820

```

51  AAALVGKVVH IDGLLTGDAD FGTDDDFLAA LIDDGIVFDV DGRVFEFQHR
101 AGIGADQQGL KFFGQRLFLR VGRGTPRVAD RQCGHTLEIE IGNRIGFGFW
151 ACRSRVAAFE DGQNLGVL A DLSHCVGRGG KCHADAQNTD AQCADEGGFF
201 HDVFPENGCV CLFCGFFRIA ALSVFLGEAG HEFTDQVFON HCRTGYGDGV
251 AGSKVFRIAA LLQPDVLFQA KRSRQDLRGN VTAEILAVQ IKAHPRLIGF
301 RVKPDSDADAP DQYACGFDGG IDLQTADVAE IGINGVSFVR TAERRAARHA
351 ESEKGNRRRA DQDEQSDPKF QYVLFH*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1581>:

```

m543.seq
1  ATGGTTTGTC GGTATTGTC CGCCGTTTTT GGCTTTCAAC TCGGCAATCA
51  GTCCGTCACG GCCTTTTCGCT TTGATAATTT CGCCGAATTG GTTGCGGTAC
101 ACCGTAACCA GGCTCGCGCC TTCGATGGCG ACGTTGTAGG TACGGTATTT
151 ACCGCCGCTT TGGTAGGTGG TGAAGTCCAT GTTGACGGGT TTTTGCCCGG
201 GTACGCCGAC TTCGGCGCGG ACGATGATTT CTTTGCCGCC TTTATTGACG
251 ATGGGATGTG CTTTGACGTT GACGTTGGCG TTTTTTAATT TCAGCATCGT
301 GCCGGAATAG GTGCGGATCA GCAGGTTTG AAATCTTTG GCCAACGCTT
351 GTTTTTCGCG GTCGGACGCG GTGCGCCAAG GGTTGCCGAC CGCCAATGCG
401 GTCATACGTT GGAAATCGAA ATAGGGAATC GCATAGGCTT CGGCTTTTTG
451 GCGAGCGGTG TTGGCATCGC CGTTTTTTAA GATGCTCAAT ACTTGAGTGG
501 CGTTTTGACG GATTTGGCTT ACCGCGTCGG CAGGGGCGGC AAATGCCATG
551 CCGATGCTCA AAATACCGAT GCCCAATGCG CTGATGAGGG AGGATTTTTT
601 CATGATTAAG TGTCTAGTT TGAATATGAT GGCATACGTT TATTCGGCGG
651 CTTTTTCGCG ATTGCCGCG TCGGCATTTT TCTCGGCAA ACTCGTCATG
701 AATTTGCCGA TAAGGTTTTC CAGAACCATT GCAGAACTGG TTACGGAGAT
751 GGTGTCGCCG GCAGCAAGGT TTTCCGTGTC GCCGCCCTGC TGCAGCCCGA
801 TGTACTGCTC GCCCAAAAGT CCCGAAGTCA GGATTGCGC GGAAACGTCG
851 CTGCTGAACT GATACTTGCC GTCCAAATCG AGGCGCACCC TCGCCTGATA
901 GGATTTTCGG TCAAGTCCGA TAGCGCCGAC GCGCCGACC AATACGCCTG
951 CGGATTGAC GGGGGCATTG ACCTTCAAAC CGCCGATGTC GCCGAAATCG
1001 GCATAACCG CGTAAGTTTT GTCCGAACCG CCGAACGCC CACCGCCGGC
1051 CACGCGGAAA GCGAGAAAGG CAACCGCCGC CGCGCCAATC AGGACGAACA
1101 GTCCGACCCA AAATTCCAAT ATGTTCTTCT TCATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1582; ORF 543>:

```

m543.pep
1  MVCRLFAAVF GFQLGNQSVH AFRFDNFAEL VAVHGNQARA FDGDVVGTVF
51  TAALVGGEVH VDGFLPGYAD FGADDDFFAA FIDDGIVFDV DVGVFQFQHR
101 AGIGADQQGL KFFGQRLFLR VGRGAPRVAD RQCGHTLEIE IGNRIGFGFL
151 ASGVGIAVFX DAQYLSGVL T DLAYRVGRGG KCHADAQNTD AQCADEGGFF
201 HDXVSXFEYD GIRLFGGFFR IAAVGIFL GK TRHEFADKVF QNHCR'GYGD
251 GVAGSKVFRV AALLQPDVLL AQKRSQDLR GNVAELILA VQIEAHPRLI
301 GFRVKSDSAD APDQYACGFD GGIDLQADV AEINGVSF VRTAERRTAG
351 HAESEKGNRR RANQDEQSDP KFQYVLLH*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 543 shows 84.2% identity over a 379 aa overlap with a predicted ORF (ORF 543.ng) from *N. gonorrhoeae*:

```

m543/g543
10 20 30 40 50 60
m543.pep MVCRLFAAVFGFQLGNQSVHAFRFDNFAELVAVHGNQARAFDGDVVGTVFTAALVGGEVH
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g543 MVCRLFAAVFGFQLGNQPVDAFGFDDFAELVAVHGNQARAFDGDVVGTVFAALVGKVVH
10 20 30 40 50 60

70 80 90 100 110 120
m543.pep VDGFLPGYADFGADDDFFAAFIIDDGIVFDVDVGVFQFQHRAGIGADQQGLKFFGQRLFLR
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g543 IDGLLTGDADFGTDDDFLAALIDDGIVFDVDGRVFEFQHRAGIGADQQGLKFFGQRLFLR
70 80 90 100 110 120

130 140 150 160 170 180

```

821

```

m543 . pep      VGRGAPRVADRQCGHTLEIEIGNRIGFGFLASGVGIAVFXDAQYLSGVLTDLAYRVGRGG
                |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g543            VGRGTPRVADRQCGHTLEIEIGNRIGFGFWACRSRVAAFEDGQNLCGVLADLSHCVGRGG
                130      140      150      160      170      180

                190      200      210      220      230      239
m543 . pep      KCHADAQNTDAQCADEGGFFHDVXVSXFEYDG-IRLFGGFFRIAAGVIFLGKTRHEFADKV
                |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g543            KCHADAQNTDAQCADEGGFFHDV---FPENGCVCLFCGFFRIAALSVFLGEAGHEFTDQV
                190      200      210      220      230

                240      250      260      270      280      290      299
m543 . pep      FQNHCRITGYDGVAGSKVFRVAALLQPDVLLAQKRSQDLRGNVAAELILAVQIEAHPRL
                |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g543            FQNHCRITGYDGVAGSKVFRVAALLQPDVLLFAQKRSQDLRGNVTAEILAVQIKAHPR
                240      250      260      270      280      290

                300      310      320      330      340      350      359
m543 . pep      IGFRVKSDSADAPDQYACGFDGGIDLQADVAEIGINGVSFVRTAERRTAGHAESEKGNR
                |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g543            IGFRVKPDSADAPDQYACGFDGGIDLQADVAEIGINGVSFVRTAERRAARHAESEKGNR
                300      310      320      330      340      350

                360      370      379
m543 . pep      RRANQDEQSDPKFQYVLLHX
                |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g543            RRADQDEQSDPKFQYVLFHX
                360      370

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1583>:

```

a543 . seq
1  ATGGCTTATG GATTACTTGC TGCCGTTTNT AGCCTTCAAC TCGNCAATCA
51  GTCCGTCAC GCCTTTCGCT TTGATAATTT CGCCGAATTG GTTGCGGTAC
101 ACGGTAACCA GGCTCGCGCC TTCGATGGCG ACGTTGTAGG TACGGTATTT
151 ACCGCCGCTT TGGTAGGTGG TGAAGTCCAT GTTGACGGGT TTTTGCCCGG
201 NNACGCCGAC TTCGGCGCGG ACGATGATTT CTTTGCCGCC TTTATTGACG
251 ATNGGATTGT CTTTGACGTT GACGTTGGCG TTTTAAATT TCAGCATCGT
301 GCCGGAATAG GTGCGGATCA GCAGGGTTTG AAATCTTTG GCCAACGCTT
351 GTTTTTCGCG GTCCGACGCG GTGCCCAAG GGTGCCGAC CGCCAATGCG
401 GTCATACGTT GGAATCGAA ATAGGGAATC GCATAGCCTT CGGCTTTTGT
451 GCGGGCGGTG TTGGCATCAC CGCTTTTAA GATGCTCAAT ACTGAGTGG
501 CGTTTTGACG GATTGTTT ACCGCGTCGG CAGGGCGGCG AAATGCCATG
551 CCGATGCTCA AAATACGAT GCCCAATGCG CTGATGAAGG AGGATTTTTT
601 CATGATTAAG TGTCCTAGTT TGAATATGAT GGCATACGTT TATTCGGCGG
651 CTTTTTCGCG ATTGCGCGCG TCGGCATTTT TCTCGGCAA ACTCGTCATG
701 AATTTGCCGA TAAGTTTTT CAGAACCATT GCAGAACTGG TTACGGAGAT
751 GGTGTCGCCG GCAGCAAGGT TTTCCGTGTC GCCGCCCTGC TGCAGCCCGA
801 TGTACTGCTC GCCCAAAAGT CCCGAAGTCA GGATTTCGCG GGAACGTCG
851 CTGCTGAAC TACTTTGCC GTCCAAATCG AGGCGCACC TCGCCTGATA
901 GGATTTCGGG TCAAGTCCGA TAGCGCCGAC GCGCCCGACC AATACGCCTG
951 CGGATTGAC GGGGGCATTG ACCTTCAAAC CGCCGATGTC GCCGAAATCG
1001 GCATAAACGG CGTAAGTTT GTCCGAACCG CCGAACGCCG CACCGCCGGC
1051 CACGCGGAAA GCGAGAAAG CAACGCCCGC CGCGCCAATC AGGACGAACA
1101 GTCCGACCCA AAATTCCAAT ATGTTCTTTT TCATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1584; ORF 543.a>:

```

a543 . pep
1  MAYGLLAAXV SLQLXNOSVH AFRFDNFAEL VAVHGNQARA FDGDVVGTVF
51  TAALVGGEVH VDGFLPGXAD FGADDDFFAA FIDDXIVFDV DVGVF*FQHR
101 AGIGADQOGL KFFGQRLFLR VGRGAPRVAD RQCGHTLEIE IGNRIGFGFL
151 AGGVGITAF* DAQYLSGVLT DLVYRVGRGG KCHADAQNTD AQCADEGGFF
201 HD*VS*FEYD GIRLFGGFFR IAAVGIFLGK TRHEFADKVF QNHCRITGYD
251 GVAGSKVFRV AALLQPDVLL AQKRSQDLR GNVAAELILA VQIEAHPRI
301 GFRVKSDSAD APDQYACGFD GGIDLQADV AEIGINGVSF VRTAERRTAG

```

351 HAESEKGNRR RANQDEQSDP KFQYVLFH*

m543/a543 96.0% identity in 378 aa overlap

	10	20	30	40	50	60
m543.pep	MVCRLFAAVFGFQ	LGNSVHAFRDNFAELVAVHGNQARAFDGDVVGTVFTAALVGGEVH				
a543	MAYGLLAAVXSLQLXNQSVHAFRDNFAELVAVHGNQARAFDGDVVGTVFTAALVGGEVH					
	10	20	30	40	50	60
m543.pep	VDGFLPGYADFGADDDFFAAFI	DDGIVFDVVGVEFXFH	RAGIGADQQGLKFFGQRLFLR			
a543	VDGFLPGXADFGADDDFFAAFI	DDXIVFDVVGVEFXFH	RAGIGADQQGLKFFGQRLFLR			
	70	80	90	100	110	120
m543.pep	VGRGAPRVADRQCGHTLEIEIGNRIGFGFLASGVGIAVFXDAQYLSGVLTDLAYRVGRGG					
a543	VGRGAPRVADRQCGHTLEIEIGNRIGFGFLAGGVGITAFXDAQYLSGVLTDLVYRVGRGG					
	130	140	150	160	170	180
m543.pep	KCHADAQNTDAQCADEGGFFHDXVSXFEYDGIRLFGGFFRIA	AVGIFLGKTRHEFADKVF				
a543	KCHADAQNTDAQCADEGGFFHDXVSXFEYDGIRLFGGFFRIA	AVGIFLGKTRHEFADKVF				
	190	200	210	220	230	240
m543.pep	QNHCR	TGYGDGVAGSKVFRVAALLQPDVLLAQKSR	SQDLRGNVAAELILAVQIEAHPRLI			
a543	QNHCR	TGYGDGVAGSKVFRVAALLQPDVLLAQKSR	SQDLRGNVAAELILAVQIEAHPRLI			
	250	260	270	280	290	300
m543.pep	GFRVKSDSADAPDQYACGFDGGIDLQ	TADVAEIGINGVSEFVRTAERRTAGHAESEKGNRR				
a543	GFRVKSDSADAPDQYACGFDGGIDLQ	TADVAEIGINGVSEFVRTAERRTAGHAESEKGNRR				
	310	320	330	340	350	360
m543.pep	RANQDEQSDPKFQYVLLHX					
a543	RANQDEQSDPKFQYVLFHX					
	370	379				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1585>:

g544.seq

```

1  atgaaaaaaa tactcaccgc cgcgcgcgtc gcactgatcg gcatectcct
51  cgccaccgtc ctcacccccg acagtaaaac cgcgcccgcc ttctccctgc
101 cgcacctgca cggaaaaaac gtttccaacg ccgacctgca aggcaaagtc
151 asccctgatta atttttggtt tccctcctgt ccgggttggtg tgagcgaaat
201 gcccaaagtc accaaaacgg caaacgacta caaaaataaa gatttccaag
251 tcctcgccgt tgcccagccc atcgatccga tagaaagcgt ccgccaatac
301 gtcaaaagact acggactgcc gtttaccgtc atttatgatg cggacaaagc
351 cgtcggacag gcattcggca cacagggtta tccgacttcc gtccttatcg
401 gcaaaaaagg cgaaatcctc aaaacttatg tcggcggaacc cgatttcggc
451 aaactctacc aagaaatcga taccgcgctg gcgcaatag

```

This corresponds to the amino acid sequence <SEQ ID 1586; ORF 544.ng>:

g544.pep

```

1  MKKILTAAAV ALIGILLATV LIPDSKTAPA FSLPDLHGKT VSNADLQGV
51  TLINFWFPSC PGCVSEMPKV TKTANDYKNK DFQVLAVAQP IDPIESVRQY
101 VKDYGLPFTV IYDADKAVGQ AFGTQVYPTS VLIKKGEIL KTYVGEPDFG

```

m544 . seq

1	ATGAwAAAAA	TACTCACCGC	CGCCGTCGTC	GCACTGATCG	GCATCCTCCT
51	TGCCATCGTC	CTCmTCCCG	ACAGCAAAC	CGCGCCCGCC	TTCTCmTGC
101	CCGACCTGCA	CGGAaaaaaac	TGTTCCAACG	CCGACCTGCA	AGGCAAAAGTA
151	ACCCTGATTA	ATTTTtGGTT	TCTCTCCTGT	CGCGGTTGTG	TGAGCGAwAT
201	GCCCAAAATC	ATTAaaaacg	CAATGACTA	TAAaaCAAA	AACTTCCAAG
251	TACTTGCCGT	CGCCcAGCCC	ATCGATCCGA	TAGAAAGCGT	CCGCCAATAT
301	GTCAAAGACT	ACGgTTTGCC	GTTTACCGTC	ATGTATGATG	CGGACAAAGC
351	TGTCGGACAG	CGGtTTCGGCA	CACAGGTTTA	TCCGACTTCC	GTCTTATTCG
401	GCAAAATAAG	GCGAAATCTTc	AAAACCTTAC	TCGGCGCAAC	CGATTTCCGC
451	AAACTCTACC	AAGAAATCGA	TACGCGCGTG	GCcCAATAG	

m544 . pep

MS11_PEP

1 MKXILTAADV ALIGILLAIV LXPDSKTAPA FSXPDLHGKT VSNADLQGVV
51 TLINFWFPSC PGCVSXMPKI IKTANDYKXK NFQVLAVAQP IDPIESVRQY
101 VKDYGLPFTV MYDADKAVGQ AFGTQVYPTS VLIQ*GEIF KTVVGEPDFG
151 KLYOEIDTRV AO*

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 544 shows 90.7% identity over a 162 aa overlap with a predicted ORF (ORF 544.ng) from *N. gonorrhoeae*:

m544/g544

	10	20	30	40	50	60
m544 . pep	MXKILTA	AAVVALIGILLAI	VLXPDSKTAPAFS	XPDLHGKTVSNADL	QGKVTLINFW	FPSC
	:					
g544	MKKILTA	AAVVALIGILLAT	VLIPDSKTAPAFS	LPDLHGKTVSNADL	QGKVTLINFW	FPSC
	10	20	30	40	50	60
	70	80	90	100	110	120
m544 . pep	PGCVS	XMPIKI	IKTANDYKX	KNFQVLAVAQ	PIDPIESVRQ	YVKDYGLPFTVMYDADKAVGQ
		:				
g544	PGCVSE	MPKVTKT	ANDYKNK	DFQVLAVAQ	PIDPIESVRQ	YVKDYGLPFTVIYDADKAVGQ
	70	80	90	100	110	120
	130	140	150	160		
m544 . pep	AFGTQ	VYPTSVL	IGKKGEI	FKTYVGEP	DFGKLYQE	IDTRVAQX
			:			
g544	AFGTQ	VYPTSVL	IGKKGEI	LKTYVGEP	DFGKLYQE	IDTALAQX
	130	140	150	160		

a544.seq

```

1  ATGAAAAAAA TACTCACCGC CGCGCTCGTC GCACTGATCG GCATCCTCCT
51  TGCCATCGTC CTCATCCCGC ACAGCAAAAC CGCGCCCGCT TTCTCCCTGT
101 CCGANGTCGA CGGAAAAANC GTTTNCAACG CCGACCTGCA AGGCNAAGTT
151 ANCCTGATTA ANTTTGGTT TCCCTCCTGT CCGGGTTGTG TGAGCGCAAT
201 GNCCANAATC ATTAAAACGG TAAATGACTA TAAAAACAAA AACTTCTCAAG
251 TCCTTGCCGT CGCCAGCCG ATCGATCCGA TAGAAAGCGT CCGCCAATAT
301 GTCAAAGACT ACGGTTTGCC GTTTACCGTC ATGTATGATG CGGACAAAGC
351 TGTCGGACAG CGATTCCGCA CACAGGTTTA TCCGACTTCC GTCTTATTCG
401 GCAAAAAGG CGAATCTCT AAAACTTATG TCGGCGTACC CGATTTCCGC
451 AAACCTTACC AAGAATACGA TACCGCGCTG GCACAAATAG

```

a544.pep

1 MKKILTAADV ALIGILLAIV LIPDSKTAPA FLSXLHGKX VXNADLQGXV
51 XLIXFWFPSC PGCVSEMXXI IKTANDYKNK NFOVLAVAP IDPIESVRQY
101 VKDYGLPFTV MYDADKAVGQ AFGTQVYPTS VLIGKKGEIL KTYVGPEPFG

824

151 KLYQEIDTAL AQ*

m544/a544 88.9% identity in 162 aa overlap

	10	20	30	40	50	60
m544 . pep	MXKILTAAVVALIGILLAIVLXPDSKTAPAFSXPDLHGKTVSNADLQGKVTLINFWFPSC					
a544	MKKILTAAVVALIGILLAIVLIPDSKTAPAFSLSXLHGKXVXNADLQGXVXLIXFWFPSC					
	10	20	30	40	50	60
	70	80	90	100	110	120
m544 . pep	PGCVSXPMPKIIKTANDYKXKNFQVLAVAQPIDPIESVRQYVKDYGLPFTVMYDADKAVGQ					
a544	PGCVSEMXXIIKTANDYKXKNFQVLAVAQPIDPIESVRQYVKDYGLPFTVMYDADKAVGQ					
	70	80	90	100	110	120
	130	140	150	160		
m544 . pep	AFGTQVYPTSVLIGKXGEIFKTYVGEPDFGKLYQEIDTRVAQX					
a544	AFGTQVYPTSVLIGKKGEILKTYVGEPDFGKLYQEIDTALAQX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1591>:

g547 . seq

```

1  atgttcgtag  ataacggatt  taataaaacg  gtacgcgagtt  ttgccccaaat
51  cgtcgaaact  ttcgacgtat  tcttcttttag  gaacgattgc  gcctttttta
101 cgcagatgaa  acagcgggtgc  ggttgggtct  gctcgttggt  atatctcggt
151 gatataattta  caagatgcgg  cttcgagatt  ccgaaccgct  cctttaaaga
201 gcttgggctt  ttgatacaga  taagtctgtc  ggaacgtttt  aggactaatg
251 ccgaagtcga  gatggatgcc  cttacttcc  ccttactcag  aaaatattta
301 aaatttataa  tgttacatat  agttacaaat  attagagttt  tttgtgtgtg
351 cgtcaaggaa  ttgttgacaa  ttttagttaa  aaatttgtct  ccaaaccgaa
401 aaaagcgggt  tgtttttgt  tgtaa

```

This corresponds to the amino acid sequence <SEQ ID 1592; ORF 547.ng>:

g547 . pep

```

1  MFVDNGFNKT  VASFAQIVET  FDVFFFRNDC  AFFTQMKQRC  GWVCSLVYLV
51  DIFPRCGFEI  PNRSPKELGL  LIQISLSERF  RTNAEVEMDA  HYFPLLRKYL
101 KFIMLHIVTN  IRVFCVCVKE  LLTILVKNL  PNGKKRFVFC  C*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1593>:

m547 . seq

```

1  ATGTTTCGTAG  ATAACGGATT  TAATAAAACG  GTACCGAGTT  TTGCCCAAAT
51  CGTCGAAACT  TTCGACGTAT  TCTTCTTTAG  GAACGATTGC  GCCTTTTFTA
101 CGCAGATGAA  ACAGCGGTGC  GGTGGGTCT  GCTCGTTGTT  ATATCTCGTT
151 GATATCTTTC  CAAGATGCGG  ATTCGAGATT  CCGAACCCT  CTTTAAAGA
201 GCTTGGGCTT  TTGATACAGA  TAAGTCTGTC  GGAACGTTT  AGGACTAATG
251 CCGAAGTCGA  GATGGATGCT  CATTACTTCC  CCTTACTCAG  AAAATATTTA
301 AAATTTATAA  TGTTACATAT  ATTTACAAAT  ATTAAAGTTT  TTTTGTGTGT
351 GTGCGTCAAG  GAATTGTTGA  CAATTTTAGT  TAAAAATTG  TCTCCAAACG
401 GAAAAAGCG  GTTTGTTTT  TGTGTGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1594; ORF 547>:

m547 . pep

```

1  MFVDNGFNKT  VASFAQIVET  FDVFFFRNDC  AFFTQMKQRC  GWVCSLVYLV
51  DIFPRCGFEI  PNRSPKELGL  LIQISLSERF  RTNAEVEMDA  HYFPLLRKYL
101 KFIMLHIFTN  IKVFXCVCK  ELLTILVKNL  SPNGKKRFVF  CC*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 547 shows 97.2% identity over a 142 aa overlap with a predicted ORF (ORF 547.ng) from *N. gonorrhoeae*:

m547/g547

825

	10	20	30	40	50	60
m547.pep	MFVDNGFNKTVASFAQIVETFDVFFFRNDCAFFTQMKQRCGWVCSLVYLVDIFPRCGFEI					
g547	MFVDNGFNKTVASFAQIVETFDVFFFRNDCAFFTQMKQRCGWVCSLVYLVDIFTRCGFEI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m547.pep	PNRSFKELGLLIQISLSERFRTNAEVEMDAHYFPLLRLKYLKFIMLHIFTNIKVFXCVCVK					
g547	PNRSFKELGLLIQISLSERFRTNAEVEMDAHYFPLLRLKYLKFIMLHIVTNIRVF-CVCVK					
	70	80	90	100	110	
	130	140				
m547.pep	ELLTILVKNLSPNGKKRFVFCCX					
g547	ELLTILVKNLSPNGKKRFVFCCX					
	120	130	140			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1595>:

```
a547.seq
1  ATGTTCTAG  ATAACGGATT  TAATAAACG  GTAGCGAGTT  TTGCCCAAAT
51  CGTCGAACT  TTCGACGTAT  TCTTCTTAG  GAACAATTGC  ACCTTTTSTA
101 CGCAGATGAA  ACAGCGGTGC  GGTGGGTCT  GCTCGTTGGT  ATATCTCGT?
151 GATATCTTTC  CAGATGCGG  CTTGAGATT  CCGAACCGCT  CCTTTAAAGA
201 GCTTGGGCTT  TTGATACAGA  TAAGTCTGTC  GGAACGTTT  AGGACTAATG
251 CCGAAGTCGA  GATAGATGCT  CATTACTTCC  CCTTACTCAG  AAAATATTTA
301 AAATTTATAA  TGTACATAT  ATTACAAAT  ATTAAAGTTT  TTTT.TGTGT
351 GTGCGTCAAG  GAATTGTTGA  CAATTTTAGT  T
```

This corresponds to the amino acid sequence <SEQ ID 1596; ORF 547.a>:

```
a547.pep
1  MFVDNGFNKT  VASFAQIVET  FDVFFFRNNC  TFFTQMKQRC  GWVCSLVYLV
51  DIFPRCGFEI  PNRSFKELGL  LIQISLSERF  RTNAEVEIDA  HYFPLLRLKY
101 KFILMLHIFTN  IKVFXCVCVK  ELLTILV
```

m547/a547 97.6% identity in 127 aa overlap

	10	20	30	40	50	60
m547.pep	MFVDNGFNKTVASFAQIVETFDVFFFRNDCAFFTQMKQRCGWVCSLVYLVDIFPRCGFEI					
a547	MFVDNGFNKTVASFAQIVETFDVFFFRNCTFFTQMKQRCGWVCSLVYLVDIFPRCGFEI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m547.pep	PNRSFKELGLLIQISLSERFRTNAEVEMDAHYFPLLRLKYLKFIMLHIFTNIKVFXCVCVK					
a547	PNRSFKELGLLIQISLSERFRTNAEVEIDAHYFPLLRLKYLKFIMLHIFTNIKVFXCVCVK					
	70	80	90	100	110	120
	130	140				
m547.pep	ELLTILVKNLSPNGKKRFVFCCX					
a547	ELLTILV					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1597>:

```
g548.seq
1  atgttttccg  taccgcgttc  ctttttgccg  ggcgttttcg  tacttgccgc
51  gcttgccgcc  tgcaaacctc  aagacaacag  tgcggcgcaa  gccgcttctt
101 caagtgcac  cgcgccggtc  gcggaaaatg  cggcaaacgc  gcaaacgcgc
151 ggtacggata  tgcgtaagga  agacatcggc  ggcgatttca  cactgaccga
201 cggcgaaggc  aagcctttca  gcctgagcga  tttgaaaggc  aaggctcgtga
251 ttctgtcttt  cgcctttacg  cactgtcccc  atgtctgccc  gacagggtct
```

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```

301 ttgacgtaca gcgacacttt gaagcagttg ggcgggcagg ctaaggacgt
351 gaaagtggty ttcgtcagca tcgatccgga acgcgacacg cctgaaatca
401 tcggcaagta tgccaaacag ttcaatccgg actttatcgg tctgacggca
451 acggggcgcc aaaacctgcc ggtcatcaag cagcaatacc gcgtgggttc
501 tgccaaaatc aatcaaaaag acgacagcga aaactatttg gtcgaccact
551 cttccggtgc gtatcttata gataaaaacg gtgaggttgc cattttctcg
601 ccttacggaa gcgagccgga aacgattgct gccgatgtaa ggaccctgct
651 ctga

```

This corresponds to the amino acid sequence <SEQ ID 1598; ORF 548.ng>:

m548.pep

```

1 MFSVPRSFLP GVFVLAALAA CKPDNSAAQ AASSASAPA AENAAKPOTR
51 GTDMRKEDIG GDFLTLDGEG KPFSLDLKG KVVILSFGFT HCPDVCPTGL
101 LTYSIDLKQL GGQAKDVKVV FVSIDPERDT PEIIGKYAKQ FNPDFIGLTA
151 TGGQNLPIVK QQYRVVSAKI NQKDDSENYL VDHSSGAYLI DKNGEVAIFS
201 PYGSEPETIA ADVRTLL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1599>:

m548.seq

```

1 ATGTTTTCCTG TACCGCGTTC CTTTTTGCCG GCGGTTTTCG TACTTGCCGC
51 GCTTGCCGCC TGCAAACCTC AAGACAACAG TCGCGCGCAA GTCGCTTCTT
101 CAAGTGCATC CGCGTCGGCT GCGGAAAATG CGGCAAAGCA AnACACGCGC
151 GGTACGGATA TCGTAAGGA AGACATCGGC GCGGATTTCG CGCTGACCGA
201 CCGCGAAGGC AAGCCTTTCA ACCTGAGCGA TTTGAAAGGC AAGGTCTGTA
251 TTCTGTCTTT CGGCTTTACG CACTGTCCCG ATGTCTGCCC GACAGAGCTT
301 TTGACGTACA GCGACACGTT GAAGCAGTTG GCGGGGACAG CTAAGGACGT
351 GAAAGTGGTG TTCGTCAGCA TCGATCCGGA ACGCGACACG CCTGAAATCA
401 TCGGCAAGTA TGCCAAACAG TTCAATCCGG ACTTTATCGG TCTGACGGCA
451 ACGGGCGGCC AAAACCTGCC GGTATCAAG CAGCAATACG GCGTGGTTTC
501 TGCCAAAGTC AATCAAAAmG ACGACAGCGA AAACATTTTG GTCGACCACT
551 CTTCGGGTGC GTATCTCATC GACAAAACG GTGAGGTTGC CATTTTCTCG
601 CCTTACGGA GCGAGCCGGA AACGATTGCT GCCGATGTA GGACCCTGCT
651 CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1600; ORF 548>:

m548.pep

```

1 MFSVPRSFLP GVFVLAALAA CKPDNSAAQ VASSASASA AENAAKQXTR
51 GTDMRKEDIG GDFLTLDGEG KPFNLSDLKG KVVILSFGFT HCPDVCPTGL
101 LTYSIDLKQL GGQAKDVKVV FVSIDPERDT PEIIGKYAKQ FNPDFIXLTA
151 TGGQNLPIVK QQYRVVSAKV NQXDDSENYL VDHSSGAYLI DKNGEVAIFS
201 PYGSEPETIA ADVRTLL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 548 shows 95.9% identity over a 217 aa overlap with a predicted ORF (ORF 548.ng) from *N. gonorrhoeae*:

m548/g548

	10	20	30	40	50	60
m548.pep	MFSVPRSFLPGVFVLAALAAACKPDNSAAQVASSASASAAENAAKQXTRGTDMRKEDIG					
g548	MFSVPRSFLPGVFVLAALAAACKPDNSAAQAASSASAPAAENAAKPQTRGTDMRKEDIG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m548.pep	GDFLTLDGEGKPFNLSDLKGKVVILSFGFTHCPDVCPTGLLTYSIDLKQLGGQAKDVKVV					
g548	GDFLTLDGEGKPFSLDLKGKVVILSFGFTHCPDVCPTGLLTYSIDLKQLGGQAKDVKVV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m548.pep	FVSIDPERDTPETIIGKYAKQFNPDFIXLTATGGQNLPIVKQQYRVVSAKVNQXDDSENYL					
g548	FVSIDPERDTPETIIGKYAKQFNPDFIGLTATGGQNLPIVKQQYRVVSAKINQKDDSENYL					
	130	140	150	160	170	180

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```

                190      200      210
m548.pep      VDHSSGAYLIDKNGEVAIFSPYGSEPETIAADVRTLX
                |||||
g548          VDHSSGAYLIDKNGEVAIFSPYGSEPETIAADVRTLX
                190      200      210

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1601>:

```

a548.seq
1  ATGTTTTCCTG TACCGCGTTC CTTTTGCCG GCGTTTTTCG TACTTGCCCG
51  GCTTGCCGCC TGCAAACCTC AAGACAACAG TCGGGCGCAA GTCGCTTCTT
101 CAAGTGCATC CGCGTCGCTC GCGGAAATG CGGCAAAGCC GCAAACGCGC
151 GGTACGGATA TCGCTAAGGA AGACATCGGC GCGGATTTCG CGCTGACCGA
201 CGGCGAAGGC AAGCCTTTCG ACCTGAGCGA TTTGAAAGGC AAGGTCGTGA
251 TTCTGTCTTT CGGCTTTACG CACTGTCCCG ATGTCTGCCC GACAGAGCTT
301 TTGACGTACA GCGACACGTT GAAGCAGTTG GCGGGGCAGG CTAAGGACGT
351 GAAAGTGGTG TTCGTCAGCA TCGATCCGGA ACGCGACACG CCTGAAATCA
401 TCGGCAAGTA TGCCAAACAG TTCAATCCGG ACTTTATCGG TCTGACGGCA
451 ACGGGCGACC AAAACCTGCC GGTCAATCAAG CAGCAATACC GCGTGGTTTC
501 TGCCAAAGTC AATCAAAAAG ACGACAGCGA AAATATTGTC GTCGACCACT
551 CTTCCGGTGC GTATCTCATC GACAAAAACG GTGAGGTTGC CATTTTCTCG
601 CTTACGGAA GCGAGCCGGA AACGATTGCT GCCGATGTAA EGACCCTGCT
651 CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1602; ORF 548.a>:

```

a548.pep
1  MFSVPRSFPLGVFVLAALAA CKPQDNSAAQ VASSASASA AENAAKPQTR
51  GTDMRKEDIG GDFLTLDGEG KPFNLSDLKG KVVILSFGFT HCPDVCPTFL
101 LTYSDTLKQL GGQAKDVKV FVSIDPERDT PEIIGKYAKQ FNPDFIGLTA
151 TGDQNLPIVK QQYRVVSAKV NQKDDSENYL VDHSSGAYLI DNKEVAIFS
201 PYGSEPETIA ADVRTL*

```

m548/a548 97.7% identity in 217 aa overlap

```

                10      20      30      40      50      60
m548.pep      MFSVPRSFPLGVFVLAALAAACKPQDNSAAQVASSASASAAENAAKQXTRGTDMRKEDIG
                |||||
a548          MFSVPRSFPLGVFVLAALAAACKPQDNSAAQVASSASASAAENAAKPQTRGTDMRKEDIG
                10      20      30      40      50      60

                70      80      90      100     110     120
m548.pep      GDFLTLDGEGKPFNLSDLKGKVVILSFGFTHCPDVCPTELLTYSDTLKQLGGQAKDVKV
                |||||
a548          GDFLTLDGEGKPFNLSDLKGKVVILSFGFTHCPDVCPTELLTYSDTLKQLGGQAKDVKV
                70      80      90      100     110     120

                130     140     150     160     170     180
m548.pep      FVSIDPERDTP EIIGKYAKQFNPD F IXL TATGGQNLPIVKQYRVVSAKV NQKDDSENYL
                |||||
a548          FVSIDPERDTP EIIGKYAKQFNPD F IGL TATGDQNLPIVKQYRVVSAKV NQKDDSENYL
                130     140     150     160     170     180

                190     200     210
m548.pep      VDHSSGAYLIDKNGEVAIFSPYGSEPETIAADVRTLX
                |||||
a548          VDHSSGAYLIDKNGEVAIFSPYGSEPETIAADVRTLX
                190     200     210

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1603>:

```

g550.seq
1  atgataacgg acaggtttca tctctttcat tttccagtat ctttcattta
51  tcaatctgac aacaaaatgc cgcctgaaaa cagttcagac ggcattttaa
101 ccacaaacgg cttacagctt ccattcgccc aacttggcag cgtaagcttc

```

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151  caaatctgca atcgacgagg ttgccacgcc gctttccatc gctgctttgg
201  cggcagccgt agcgacgcga ggcagcaggc gggaaatcgaa cggagtagga
251  atcaggtatt ccgcgccgaa ttcgaatttc ttaccgtaag cggcaaccac
301  ttcttcggtt acttcttcca tcgccaaatc tgccaaagca tacacgcagg
351  cgcgtttcat ttcttcggtt atggtggttg cgcgcacatc caacgcgccc
401  cggaagatga acgggaagca caatacgttg ttcacttggt tcgggaagtc
451  ggagcggccg gtaccgataa ccacgtcccg acgggtttct ttcccgagcg
501  gcggcaggat ttccggattc gggttggcca tggcgaacac gatgggtttt
551  tcgttcatcg tgttcaacat ttcaggcgtc agcagggttg cgcggagag
601  gcccagaag atgtctttgc ctttaaccgc atcggcaagt acgcgcccgc
651  cgttgtcttc aacggcgtag aatttttttg attcgtccat gcggtctttg
701  tcttcgcggg tttggtaaat cagcctttg gagttgcaaa cgtttacgtt
751  ttcacgtttc aagcccaaat ccagcagttg gttcaggcag gcaatcgcg
801  cggcacctgc gccggagcac accaaagtcg cttcttcgat ttacggccg
851  gtataacgca gggcggttcaa tacggcgcg cggtaatga tggcgtgccc
901  gtgctggtca tcatgaaata cggggatttt gcagcggttg cgtaa

```

This corresponds to the amino acid sequence <SEQ ID 1604; ORF 550.ng>:

g550.pep

```

1  MITDRPHLFH FVVSFIYQSD NKMPPENSSD GILTTNGLQL PFAQLGVSFV
51  QICNRTGCHA AFHRCFGGSR SDARQQAGIE RSRNQVFRAE FEFLTVSGNH
101 FFGYFFHRQI CQSIHAGAFH FFVDGGCADI QRAPEDEREA QVVHLVREV
151 GAAGTDNHVR TGFFRQRQD FRIRVGHGEH DGFFVHRVQH FRRQQVCAGE
201 AQEDVFAFNR IGKYAPAVVF NGVEFFGFVH AVFVFAGLVN HAFGVANGYV
251 FTFQAQIQQL VQAGNRGGTC AGAHQSRFFD FTAGITQGVQ YGGGGNDGRA
301 VLVIMKYGDF AAFA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1605>:

m550.seq (partial)

```

1  ..GACGGCATCG GCAAGCACGC GCTGGCCGTT GTCTTCAATG GCGTAGAACT
51  GTTGGACTC GTCCATACGG TCTTTGTCTT CGCGGGTTTG GTAAATCACG
101 CCTTTGGAGT CGCAAACGGT CACGTTTTCG CGTTTCAAGC CCATATCCAG
151 CAATTGGWTC AAGCAGGCAA TCGCGGCCGC ACCTGCGCCG GAACACACCA
201 AAGTCGCTTC TTCGATTITA CGGCCGGTAA AACGCAKGGC GTTCAATACG
251 GCGGCGGCCG TAATGATGGC CGTGCCGTGC TGGTCGTCGT GGAATACGGG
301 GATTTTGCAG CGTTTGCCTA A

```

This corresponds to the amino acid sequence <SEQ ID 1606; ORF 550>:

m550.pep (partial)

```

1  ..DGIGKHALAV VFNGVBLEFL VHTVVFVAGL VNHAFGVANG HVFAFQAQIQ
51  QLXQAGNRGR TCAGTHQSRF FDFTAGKTXG VQYGGGGNDG RAVLVVVEYG
101 DFAAFA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 550 shows ___% identity over a ___ aa overlap with a predicted ORF (ORF 550.ng) from *N. gonorrhoeae*:

m550/g550

m550.pep				10	20	30	
				DGIGKHALAVVFNGVBLEFLVHTVVFVAGLVN			
				: : : : : : :			
g550	DGFFVHRVQHFR	RRQQVCAGEAQ	EDVFAFNRI	GKYAPAVVF	NGVEFFGFVH	AVFVFAGLVN	
	190	200	210	220	230	240	
m550.pep		40	50	60	70	80	90
		HAFGVANGHV	FAFQAQIQ	QLXQAGNR	GRTTCAGTH	QSRFFDFT	AGKTXGVQ
		: : : :					
g550		HAFGVANGYV	FTFQAQIQ	QLVQAGNR	GGTCAGAH	QSRFFDFT	AGITQGVQ
		250	260	270	280	290	300
m550.pep		100					
		VLVVVEYGD	FAAFAX				
		: :					
g550		VLVIMKYGD	FAAFAX				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1607>:

```
a550.seq
1  CTATATCAAT CTGACAGCAA AATGCCGCCT GAAAACAGTT CAGACGGCAT
51  TTTAACCGCA AACGGCTTAC AGCTTCCATT CGCTCAGCTT GGCAGCGTAA
101 GCTTCCAAAT CTGCAATCGG ACGGGTTGCC ACGCCGCTTT CCATCGCTGC
151 TTTGGCGGCA GCCGTAGCAA CGCGCGGCAG CAGGCGGGAA TCGAACGGAG
201 TCGGAATCAG GTATTCCGCG CCGAATTCAA ATTTCTTACC GTAAGCGGCA
251 ACCACTTCTT CGGTTACCTC TTCCATCGCC AAATCCGCCA AAGCATACAC
301 GCAGGCGCGT TTCATTCTTT CGTTGATGGT CGTCGCGCCG ACATCCAACG
351 CACCGCGGAA GATGAACGGG AAGCACAATA CATTGTTCAC TTGGTTCGGG
401 AAGTCGGAGC GGCCGGTACC GATAACCACG TCCGGACGGG TTTCTTTCGC
451 CAGCGCGGCG AGGATTTCGG GATTGCGGTT GGCCATAGCG AACACGATGG
501 GTTTTTCTGT CATGGTGTTC AGTATTTCAG GCGTCAGCAG GTTCGCGCCG
551 GAGAGGCCCA AGAAGATGTC TTTGCCTTTG ACGGCATCGG CAAGCAGCGG
601 CTGGCCGTTG TCTTCAATGG CGTAGAAGTG TTTGGACTCG TCCATACGGT
651 CTTTGTCTTC GCGGGTTTGG TAAATCACGC CTTTGGAGTC GCAAACGGTC
701 ACGTTTTTCG GTTTCAGGCC CAAATCCAGC AATTGGTTCA AGCAGGCAAT
751 CGCGGCGGCA CTTGCGCCGG AACACACCAA AGTCGCTTCT TCGATTTTAC
801 GGCCGGTAAA ACGCAGGCGG TTCAATACGG CAGCGGCGGT AATGATGGCC
851 GTGCCGTGCT GGTCTCGTGT GAATACGGGG ATTTTGCAGC GTTTCGTAA
```

This corresponds to the amino acid sequence <SEQ ID 1608; ORF 550.a>:

```
a550.pep
1  LYQSDSKMPP ENSSDGILTA NGLQLPFAQL GSVSEFQICNR TGCHAAFHRC
51  FGGSRSNARQ QAGIERSRNO VFRAEFKFLT VSGNHFFGYL FHRQIRQSIH
101 AGAFHFFVDG RRADIQRTAE DEREAYIVH LVREVGAAGT DNHVRTGFFR
151 QRRQDFRIRV GHSEHDGFFV HGVQYFRRQQ VRAGEAQEDV FAFDGIKHA
201 LAVVFNGVEL FGLVHTVFVF AGLVNHAFGV ANGHVFAFQA QIQQLVQAGN
251 RGRTCAGTHQ SRFFDFTAGK TQGVQYGS GG NDGRAVLVVV EYGDFAAFA*
```

m550/a550 97.2% identity in 106 aa overlap

```
m550.pep                                10      20      30
                                DGICKHALAVVFNGVELFGLVHTVFVFAGL
                                |||
a550      EHDGFFVHGVQYFRRQQVRAGEAQEDVFAFDGIGKHALAVVFNGVELFGLVHTVFVFAGL
                                170      180      190      200      210      220

                                40      50      60      70      80      90
m550.pep      VNHAFGVANGHVFAFQAQIQQLXQAGNRGRTCAGTHQSRFFDFTAGKTGQVQYGGGGNDG
                                |||
a550      VNHAFGVANGHVFAFQAQIQQLVQAGNRGRTCAGTHQSRFFDFTAGKTGQVQYGS GGNDG
                                230      240      250      260      270      280

                                100
m550.pep      RAVLVVVEYGDFAAFAX
                                |||
a550      RAVLVVVEYGDFAAFAX
                                290      300
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1609>:

```
g552.seq
1  atgaagctga aaaccttggt attgcccttc gccgcactgg cattgtgtgc
51  caacgcattt gccgccccgc ccggcgacgc gtcgttggca cgttggctgg
101 atacgcagaa ttctgaccgg gatatagaaa aaaatatgat tgaaggcttt
151 aatgccggat ttaaaccgta tgcggacaaa gcccttgccg aaatgccgga
201 agcgaaaaaa gatcaggcgg cagaagcctt taatcggtat cgtgagaatg
251 ttttgaaaga tttgattacg cccgaagtga aacaggctgt ccgcaatacc
301 ttattgaaga atgcccgatg aatatacagc caagaagaaa ttgacggcat
351 gattgccttt tacggttcgc ctgtcggtca gtccgtcgtt gccaaaaatc
401 cgcgcttaat caagaaatcg atgagtgaat tagcggtatc ttggactgca
```

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451 ttgtcagggg aaatcgcgcg acatcatctg cccgagttta cggaagagtt
 501 acggcgcatc atctgcggcg gtatagtga ttaa

This corresponds to the amino acid sequence <SEQ ID 1610; ORF552.ng>:

g552.pep
 1 MKLKTLLLPF AALALCANAF AAPPGDASLA RWLDTQNFDR DIEKNMIEGF
 51 NAGFKPYADK ALAEMPEAKK DQAAEFNRY RENVLKDLIT PEVKQAVRNT
 101 LLKNAREIYT QEEIDGMIAF YGSPVGQSVV AKNPRLIKKS MSEIAVSWTA
 151 LSGKIAHHHL PEFTEELRRI ICGGIVD*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1611>:

m552.seq (partial)
 1 ..ATTAACTGA AAACCTTGTT ATTGCCCTTC GCCACGCTGG CATTGTGCAC
 51 CAATGCTTTT GCCGCCCGC CCAGCGACGC GTCGTTGGCG CGTTGGCTGG
 101 ATACGCAGAA TTTTGACCGG GATATAGAAA AAAATATGAT TGAGGGCTTT
 151 AATGCCGGAT TTAACCGTA TCGGCACAAA GCCCTTGCCG AAATGCCGGA
 201 AGCGAAAAAA GATCAGGCGG CAGAAGCCTT TAACCGTTAT CGTGAGAATG
 251 TTTTGAAAGA TTTGATTACG CCCGAAGTGA AACAGGCTGT CCGCAATACT
 301 TTATTGAAGA ATGCCCGTGA GATATACACG CAAGAAGAAA TTGACGGCAT
 351 GATTGCCTTT TACGGTTCGC CTGTCGGTCA GTCCGTCGTT GCCAAAAATC
 401 CGCGCTTAAT CAAGAAATCG ATGAGTGAAA TAGCGGTATC TTGGACTGCA
 451 TTGTCAGGGA AAATCGCGCA ACATCATCTG CCCGAGTTTA CGGAAGAGTT
 501 GCGGCGCATC ATCTGCGCGG GTAAAAATCC CGATGCGGGC TGTAACAACG
 551 CCGGACAGGT TGGGAAAAGG CATCAGAAAT AA

This corresponds to the amino acid sequence <SEQ ID 1612; ORF 552>:

m552.pep (partial)
 1 ..IKLKTLLLPF ATLALCTNAF AAPPSDASLA RWLDTQNFDR DIEKNMIEGF
 51 NAGFKPYADK ALAEMPEAKK DQAAEFNRY RENVLKDLIT PEVKQAVRNT
 101 LLKNAREIYT QEEIDGMIAF YGSPVGQSVV AKNPRLIKKS MSEIAVSWTA
 151 LSGKIAHHHL PEFTEELRRI ICGKPNPDAG CKQAGQVGKR HQK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 552 shows 97.1% identity over a 174 aa overlap with a predicted ORF (ORF 552.ng) from *N. gonorrhoeae*:

m552/g552

	10	20	30	40	50	60
m552.pep	IKLKTLLLPFATLALCTNAFAAPPSDASLARWLDTQNFDRDIEKNMIEGFNAGFKPYADK					
	: : : : : :					
g552	MKLKTLLLPFAALALCANAFAPPGDASLARWLDTQNFDRDIEKNMIEGFNAGFKPYADK					
	10	20	30	40	50	60
	70	80	90	100	110	120
m552.pep	ALAEMPEAKKDQAAEFNRYRENVLKDLITPEVKQAVRNTLLKNAREIYTQEEIDGMIAF					
	: : : : :					
g552	ALAEMPEAKKDQAAEFNRYRENVLKDLITPEVKQAVRNTLLKNAREIYTQEEIDGMIAF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m552.pep	YGSPVGQSVVAKNPRLIKSMSEIAVSWTALSGKIAHHHLPEFTEELRRIICGGKPNPDAG					
	: : : : :					
g552	YGSPVGQSVVAKNPRLIKSMSEIAVSWTALSGKIAHHHLPEFTEELRRIICGGIVDX					
	130	140	150	160	170	
	190					
m552.pep	CKQAGQVGKRHQKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1613>:

a552.seq
 1 ATTAACTGA AAACCTTGTT ATTGCCCTTC GCCACGCTGG CATTGTGCAC
 51 CAATGCTTTT GCCGCCCGC CCAGCGACGC GTCGTTGGCG CGTTGGCTGG
 101 ATACGCAGAA TTTTGACCGG GATATAGAAA AAAATATGAT TGAGGGCTTT
 151 AATGCCGGAT TTAACCGTA TCGGCACAAA GCCCTTGCCG AAATGCCGGA

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```

201 AGCGAAAAAA GATCAGGCGG CAGAAGCCTT TAACCGTTAT CGTGAGAATG
251 TTTTGAAAGA TTTGATTACG CCCGAAGTGA AACAGGCTGT CCGCAATACT
301 TTATTGAAGA ATGCCCGTGA GATATACACG CAAGAAGAAA TTGACGGCAT
351 GATTGCCTTT TACGGTTCGC CTGTCGGTCA GTCCGTCGTT GCCAAAAATC
401 CGCGCTTAAT CAAGAAATCG ATGAGTGAAA TAGCGGTATC TTGGACTGCA
451 TTGTCAGGGA AAATCGCGCA ACATCATCTG CCGAGTTTA CGGAAGAGTT
501 GCGGCGCATC ATCTGCGGCG GTAAAAATCC CGATGCGGGC TGTAACAACG
551 CCGGACAGGT TGGGAAAAGG CATCAGAAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 1614; ORF 552.a>:

```

a552.pep
  1 IKLKTLLLPF ATLALCTNAF AAPPSDASLA RWLDTQNFDR DIEKNMIEGF
 51 NAGFKPYADK ALAEMPEAKK DQAAEAFNRY RENVLKDLIT PEVKQAVRNT
101 LLKNAREIYT QEEIDGMIAF YGSPVGQSVV AKNPRLIKKS MSEIAVSWTA
151 LSGKIAQHHL PEFTEELRRI ICGGKNPDAG CKQAGQVGKR HQK*

```

m552/a552 100.0% identity in 193 aa overlap

```

              10      20      30      40      50      60
m552.pep      IKLKTLLLPFATLALCTNAFAAPPSDASLARWLDTQNFDRDIEKNMIEGFNAGFKPYADK
              |||
a552           IKLKTLLLPFATLALCTNAFAAPPSDASLARWLDTQNFDRDIEKNMIEGFNAGFKPYADK
              10      20      30      40      50      60

              70      80      90      100     110     120
m552.pep      ALAEMPEAKKDQAAEAFNRYRENVLKDILITPEVKQAVRNTLLKNAREIYTQEEIDGMIAF
              |||
a552           ALAEMPEAKKDQAAEAFNRYRENVLKDILITPEVKQAVRNTLLKNAREIYTQEEIDGMIAF
              70      80      90      100     110     120

              130     140     150     160     170     180
m552.pep      YGSPVGQSVVAKNPRLIKKSMSEIAVSWTALSGKIAQHHLPEFTEELRRIICGGKNPDAG
              |||
a552           YGSPVGQSVVAKNPRLIKKSMSEIAVSWTALSGKIAQHHLPEFTEELRRIICGGKNPDAG
              130     140     150     160     170     180

              190
m552.pep      CKQAGQVGKRHQKX
              |||
a552           CKQAGQVGKRHQKX
              190

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1615>:

```

m552-1.seq
  1 TTGAATATTA AACTGAAAAC CTTGTTATTG CCCTTCGCCA CGCTGGCATT
 51 GTGCACCAAT GCTTTTGCCG CCCCGCCCAG CGACGCGTCG TTGGCGCGTT
101 GGCTGGATAC GCAGAATTTT GACCGGGATA TAGAAAAAAA TATGATTGAG
151 GGCTTTAATG CCGGATTTAA ACCGTATGCG GACAAAGCCC TTGCCGAAAT
201 GCCGGAAGCG AAAAAAGATC AGGCGGCAGA AGCCTTTAAR CGTTATCGTG
251 AGAATGTTTT GAAAGATTG ATTACGCCCG AAGTGAAACA GGCTGTCCGC
301 AATACTTTAT TGAAGAATGC CCGTGAGATA TACACGCAAG AAGAAATTGA
351 CGGCATGATT GCCTTTTACG GTTCGCTGTG CGGTCAGTCC GTCGTTGCCA
401 AAAATCCGCG CTTAATCAAG AAATCGATGA GTGAAATAGC GGTATCTTGG
451 ACTGCATTGT CAGGGAAAAT CGCGCAACAT CATCTGCCCG AGTTTACGGA
501 AGAGTTGCGG CGCATCATCT GCGGCGGTAA AAATCCCGAT GCGGGCTGTA
551 AACAGCCGGG ACAGGTTGGG AAAAGGCATC AGAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1616; ORF 552-1>:

```

m552-1.pep
  1 LNIKLKTL L PFATLALCTN AFAAPPSDAS LARWLDTQNF DRDIEKNMIE
 51 GFNAGFKPYA DKALAEMPEA KKDQAAEAFN RYRENVLKD LITPEVKQAVR
101 NTLLKNAREI YTQEEIDGMI AFYGSVPVQS VVAKNPRLIK KSMSEIAVSW
151 TALSGKIAQH HLPFTEELR RIICGGKNPD AGCKQAGQVG KRHQK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1617>:

a552-1.seq

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```

1  TTGAATATTA AACTGAAAAC CTTGTTATTG CCCTTCGCCA CGCTGGCATT
51  GTCCACCAAT GCTTTTGCCG CCCC GCCCAG CGACGCTCG TTGGCGCGTT
101 GGCTGGATAC GCAGAATTTT GACCGGGATA TAGAAAAAAA TATGATTGAG
151 GGCTTTAATG CCGGATTAA ACCGTATGCG GACAAAGCCC TTGCCGAAAT
201 GCCGGAAGCG AAAAAAGATC AGGCGGCAGA AGCCTTTAAC CGTTATCGTG
251 AGAATGTTTT GAAAGATTG ATTACGCCCG AAGTGAAACA GGCTGTCCGC
301 AATACTTTAT TGAAGAATGC CCGTGAGATA TACACGCAAG AAGAAATTGA
351 CGGCATGATT GCCTTTTACG GTTCGCCTGT CGGTCAGTCC GTCGTTGCCA
401 AAAATCCGCG CTTAATCAAG AAATCGATGA GTGAAATAGC GGTATCTTGG
451 ACTGCATTGT CAGGGAAAT CCGCAACAT CATCTGCCG AGTTTACGGA
501 AGAGTTGCGG CGCATCATCT GCGGCGGTAA AAATCCCGAT GCGGGCTGTA
551 AACAAGCCGG ACAGGTTGGG AAAAGGCATC AGAATAAA

```

This corresponds to the amino acid sequence <SEQ ID 1618; ORF 552-1.a>:

a552-1.pep

```

1  LNIKLKTL L PFATLALCTN AFAAPPSDAS LARWLDTONF DRDIEKNMIE
51  GFNAGFKPYA DKALAEMPEA KKDQAAEAFN RYRENVLKDL ITPEVKQAVR
101 NTLLKNAREI YTQEEIDGMI AFYGSVPVQS VVAKNPRIK KSMSEIAVSW
151 TALSGKIAQH HLPFTEELR RIICGKNPD AGCKQAGQVG KRHQK*

```

a552-1/m552-1 100.0% identity in 195 aa overlap

	10	20	30	40	50	60
a552-1.pep	LNIKLKTL L	PFATLALCTN	AFAAPPSDAS	LARWLDTONF	DRDIEKNMIE	GFNAGFKPYA
m552-1	LNIKLKTL L	PFATLALCTN	AFAAPPSDAS	LARWLDTONF	DRDIEKNMIE	GFNAGFKPYA
	10	20	30	40	50	60
a552-1.pep	DKALAEMPEA	KKDQAAEAFN	RYRENVLKDL	ITPEVKQAVR	NTLLKNAREI	YTQEEIDGMI
m552-1	DKALAEMPEA	KKDQAAEAFN	RYRENVLKDL	ITPEVKQAVR	NTLLKNAREI	YTQEEIDGMI
	70	80	90	100	110	120
a552-1.pep	AFYGSVPVQS	VVAKNPRIK	KSMSEIAVSW	TALSGKIAQH	HLPFTEELR	RIICGKNPD
m552-1	AFYGSVPVQS	VVAKNPRIK	KSMSEIAVSW	TALSGKIAQH	HLPFTEELR	RIICGKNPD
	130	140	150	160	170	180
a552-1.pep	AGCKQAGQVG	KRHKX				
m552-1	AGCKQAGQVG	KRHKX				
	190					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1619>:

g553.seq

```

1  atggattatc tgcaaacctt gtctttgggc ttgacaaaaa agctgcccg
51  tatactgcaa acagaagtag cggagtgttg cttggcatgt ctacggcgtg
101 tggccggatt ttatggtttc tatacggatt tgcgcgcact gcgttcaaaa
151 tactgtctgt cacttaaggg tgagaatttg gcagatattg ttcgtttg
201 tgatgatatg gggctgacgg gacgggcgtt gaggtggat ttagacgaat
251 tgggcagttt ggcctgccc tgtattctac attgggattt gaatcatttt
301 gtggtgcttg aatcggatc ttcggacggg gctgcccgtc tggatccggc
351 ttcgggacga cgaaaagtca agacggagga aatatcgccg aagtttacgg
401 gaattgcttt ggaactgttg ccaaacacgc gtttcgaggg aggggaagaa
451 aagcaggaaa tccgcatoct acccatgttg cgcgggattt ctgggctggg
501 gcggacattg tttcagcttt tggctttggc agcagcaatg gaagtgtttg
551 cttttttaca aaacgtcagc ttcaagatcg gacgtggtga atcgtttg
601 ttaatcggac gatcgggctg cggtaaatcg acacttttgg atattttaag
651 cggcaatcta cctccgaat caggcaaat catgataaat gggcacgaca
701 tttacagctt accgccacct tttattccgc aatttgagtg cgatggtcaa
751 ggcaggacga tgttttatag tggattaaat ttaaaccggt ag

```

This corresponds to the amino acid sequence <SEQ ID 1620; ORF 553.ng>:

g553.pep

```
m553.seq (partial)
  1  ATGGATTATT  TATCAAGACT  GTCCTTTGGA  TTTAACAAAA  AGCTACCTGT
 51  CATTCTGCAA  ACAGAAGTTG  CTGAATGTGG  TTTAGCATGC  CTGACATCCA
101  TCTTGTCTCA  TTATGCTTTT  CACACTGATT  TAAGAACGTT  AGCCCAAAAA
151  TACACCTGTG  CATTAAAGGG  CGCAAATCTT  GCAGACATCA  TGAGATTTGG
201  CAATGAAATG  AATTTAACGC  CACGAGCTTT  GCGTTTAGAG  TTAGATGAGC
251  TGTCAAATTT  ACAACTACCC  TGCATTCTCC  ATTGGAACIT  AAACCATTTT
301  GTTGTACTTT  GTTCCATTTT  CAAAGACAGT  ATCGTCATTA  TGACCCTTGC
351  TGTCGGTATG  CGAAAAATCA  AAATGGACGA  AGTTTCACAA  AAATTCACAG
401  GGATTGCCCT  AGAATTATTC  CCCAATACCC  ATTTTGAAGA  GAAAAAGAA
451  ACAAAAGAAA  TCAAAATATT  ATCTCTATTA  AGGGGGGG.  T  CAGGCTTAAA
501  ACGCTCTTTA  ATTCAAATGC  TTATATTAGC  TATTTCTTTG  GAAGTCTTTG
551  CATTG...
```

```
m553.pep      (partial)
  1  MDYLSRLSFG FNKKLPVILQ TEVAECGLAC LTSILSYGYF HTDLRTLROK
51  YTLSLKGANL ADIMRFGNEM NLTTPRALRL LDELSNQLP CILHWNLNHF
101 VVLCSIKSDS IVIMDPAVGM RQIKMDEVSQ KFTGIALELF PNTHFEEKKE
151 TKKIKILSLR RGXSGDKRSL IQMLILAI SL EVFAL...
```

ORF 553 shows 65.5% identity over a 185 aa overlap with a predicted ORF (ORF 553.ng) from *N. gonorrhoeae*:

	10	20	30	40	50	60
g553.pep	MDYLQNLSLGLTKKLPVILQTEVAE	CGLACLA	AVAGFYGF	YTDLR	LR	SKYCLSLK
	: : :			: : : :		
m553	MDYLSRLSFGFNKKLPVILQTEVAE	CGLACLT	SILSYYG	FHTDL	RL	LRQKYTL
	10	20	30	40	50	60
	70	80	90	100	110	120
g553.pep	ADIVRFADDMGLTGRALRLDLDEL	GSLRLPCILH	WDLNHFV	LVESV	SDGA	AVMDPASGR
	: : :	: : :	:		: : :	
m553	ADIMRFGNEMNLT	PRALRL	ELDELS	NLQLPCILH	WNLNHFV	LVCSISKDSIVIMDP
	70	80	90	100	110	120
	130	140	150	160	170	180
g553.pep	RKVKTEEISRKFTGIALELW	PNTRFE	EAGEEKQ	EIRILP	MLRGIS	GLGRTLFQ
	: : :	: :	: : :	:		: : :
m553	RKIKMDEV	SQKFTGIALEL	FPNTH	FEEKKET	KKIKIL	SLLRGXSG
	130	140	150	160	170	180
	190	200	210	220	230	240
g553.pep	EVFAFLQNV	SFKIGR	GESLALIGR	SGCGK	STLLDIL	SGNLPP
	:					
m553	EVFAL					

```
a553.seq
  1  ATGCCCCATC  TGCAAAACCT  GTCTTTGGGC  TTAAGAAAA  AGCTGCCTGT
51  TATCCTGCAA  ACAGAAATAT  CAGAATGCGG  CTTGGCATGT  CTGGCGGCTG
101 TGGCGGGATT  TCATGGTTTC  CATAACGAAT  TACGCGCACT  GCGTTCAAAA
151 TAC
```

This corresponds to the amino acid sequence <SEQ ID 1624; ORF 553.a>:

```
a553.pep
      1  MPHLQNLSLG LKKKLPVILQ TEISECGLAC LAAVAGFHGF HTNLRALRSK
     51  Y
```

m553/a553 62.7% identity in 51 aa overlap

	10	20	30	40	50	60
m553.pep	MDYLSRLSFGFNKKLPVILQTEVAECGLACLT	SILSYYGFTDLRTL	RQKYTL	SLKGANL		
	: : : : : : : : :					
a553	MPHLQNLSLG LKKKLPVILQTEISECGLACLA	AVAGFHGFHTNLRALRSKY				
	10	20	30	40	50	
	70	80	90	100	110	120
m553.pep	ADIMRFGNEMNLT	PRALRLELDELSNL	QLPCILHWNLNH	FVVLCSISKDS	SIVIMDPAVGM	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1625>:

```
g554.seq..
      1  atgacagcac ataaaatcct gcccgctcctt cttcccatca tcttaggcgt
     51  ttctcacgca acggctgcat cgcccgcgcc caacagaccg acggtacacg
    101  ccgccccac gctccaaaca ccgaaacccc tcacggcggc acacatcggt
    151  atcgaccttc aaagcaggca gactttatcc gccaaaaaca ccaatacccc
    201  tgtcgaaccg gcggcactaa cccaactgat gaccgcatat ttggttttca
    251  aaaacatgaa atcgggaaat atccaatctg aagaaaactt aaaaataccc
    301  gaatccgcat gggcttcaga aggaagcaga atgtttgtac gtcccgcgca
    351  tacggtcagc accgacaaac tcttaaaagg catgattgcc ctatgcgcaa
    401  acgatgccgc cctaaccctt gccgaccggc tgggcaacgg ctcgattgaa
    451  aattttgtgc aacaaatgaa caaagaagcc cgacgcttgg gcatgaagaa
    501  caccgtatcc aaaaaccgga caggcttggg tagagaagga caggtttcca
    551  ccgccaaga cctctccctg ctgtctgaag cattgatgcg cgactttccg
    601  gaatattacc cgctgttttc catcaaatcg ttcaagtttg aaaacataga
    651  acaaaacaac cgcaatatcc ttttatatag ggacaacaat gtaaacggcc
    701  tgaaagccgg gcacacagaa agcggcggtt acaaccttgc cgtgtcatac
    751  tccggcaacg gcaggcacat ccttgtcatc acactagggt cggaatcggc
    801  ggaaaccgc gcacgggaca acagcaagct gctgaaccgg gcattgcagg
    851  ccttcgatac gcccaaaata tatccgaaag gcaaaaccgt tgcccaaatc
    901  caaatttccg gaggcagcaa aaaaaccgtc cgcgcagggt tcctcaaaga
    951  agcctacatc actctgccac ataaagaagc gaaaatggca gaacagattt
   1001  tggaaaccat acagccgatt cccgccccgg taaaaaaagg gcagatttta
   1051  ggaaaaaatca aaatcaggca aaacggacat accattgccg aaaaagaaat
   1101  cgtcgcactg gaaaacgtag aaaaaagaag ccggtggcaa aggccttggg
   1151  cgcgtctgac agggcagtaa
```

This corresponds to the amino acid sequence <SEQ ID 1626; ORF 554.ng>:

```
g554.pep..
      1  MTAHKILPVL LPIILGVSHA TAASPAENRP TVHAAPTLOT PETLTAHIV
     51  IDLQSRQTLA AKNTNTPVEP AALTQLMTAY LVFKNMKSGN IQSEENLKIP
    101  ESAWASBGSR MFVRPGDTVS TDKLLKGMIA LCANDAALTL ADRLNGSIE
    151  NFVQQMNKEA RRLGMKNTVF KNPTGLGREG QVSTAKDLSL LSEALMRDFP
    201  EYYPLFSIKS FKFENIEONN RNILLYRDNN VNGLKAGHTE SGGYNLAVSY
    251  SGNRHLILVI TLGSESAETR ASDNSKLLNR ALQAFDTPKI YPKGKTVAQI
    301  QISGGSKKTV RAGFLKEAYI TLPHEAKMA EQILETIQPI PAPVKKGQIL
    351  GKIKIRQNGH TIAEKEIVAL ENVEKRSRWQ RLWTRLTGQ*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1627>:

```
m554.seq..
      1  ATGACAGCAC ATAAAATCCT GCCCGTCCTG CTTTCCATCA TCTTAGGCGT
     51  TTCTCACGCA ACGGCTGCAT CGCCCGCGCC CAACAGACCG ACGGTACACG
    101  CCGCCCCAC GTTCCAAACA CCCGAAACCC TCACAGCGGC ACACATCGTT
    151  ATCGACCTTC AAAGCAAACA GATTTTATCC GCCAAAAACA TCAATACCCC
    201  TGTGTAACCG GCGGCACTAA CCAACTGAT GACCGCATAT CTGGTTTTC
    251  AAAACATGAA ATCGGGCAAT ATCCAATCTG AAGAAAACCT AAAAATACCC
```

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```

301 GAATCCGCAT GGGCTTCAGA AGGAAGCAGA ATGTTTGTAC GTCCCGGCGA
351 TACGGTCAGC ACCGACAAAC TCTTAAAAGG CATGATTGCA CTATCCGCAA
401 ACGATGCCGC CCTAACCTT GCCGGCCGGC TGGGCAACGG CTCGATTGAA
451 AATTTTGTGC AACAAATGAA CAAAGAAGCC CGACGCTTGG GCATGAAGAA
501 CACTGTATTC AAAAACCAGA CAGGCTTGAG TAGAGAAGGA CAGGTTTCCA
551 CCGCCAAAGA CCTCGCCCTG CTGTCTGAAG CATTGATGCG CGACTTTCGG
601 GAATATTACC CGCTGTTTTT CATCAAATCT TTCAAATTCA AAAATATAGA
651 ACAAAACAAC CGCAATATCC TTTTATATAG GGACAACAAT GTAAACGGTC
701 TGAAAGCCGG ACACACAGAA AGCGGCGGCT ACAACCTTGC CGTGTGCATC
751 TCCGGCAACG GCAGGCACAT CCTTGTATC ACATTGGGTT CGGAATCGGC
801 GGAAACACGC GCATCAGACA ACAGCAAGCT GCTGAACTGG GCATTGCAGG
851 CCTTCGATAC GCCCAAATA TATCCGAAAG GCAAAACCGT TGCCCAAATC
901 CAAATTTCGG GAGGCAGCAA AAAAACCGTC CGCGCAGGCT TCCTCAAAGA
951 AGCCTACATC ACTCTGCCAC ATAAGGAAGC GAAATGCGA GAACAAATTC
1001 TAGAAACCAT ACAGCCGATT CCCGCCCCAG TAAAAAAGG GCAAATTTTA
1051 GGAAAAATCA AAATCAGACA AAACGGATAC ACCATTGCCG AAAAAGAAAT
1101 CGTCGCACTG GAAAATGTAA AAAAAGAAG CCGGTGGCAA AGGCTTTGGG
1151 CGTGTCTGAC AGGGCAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1628; ORF 554>:

m554 . pep . .

```

1  MTAHKILPVL LSIILGVSHA TAASPAPNRP TVHAAPTFTQ PETLTAAHIV
51  IDLSKQILS AKNINTPVEP AALTQMTAY LVFKNMKSGN IQSEENLKIP
101 ESAWASEGSR MFVRPGDIVS TDKLLKGMIA LSANDAALTL AGRNGSIE
151 NFVQMNKEA RRLGMKNTVF KNPTGLSREG QVSTAKDLAL LSEALMRDFP
201 EYYPLFSIKS FKFKNIEQNN RNILLYRDNN VNGLKAGHTE SGGYNLAVSY
251 SGNRHLVIT LGSESAETR ASDNSKLLNW ALQAFDTPKI YPKGKTVAQI
301 QISGGSKKTV RAGFLKEAYI TLPHEAKMA EQILETIQPI PAPVKKGQIL
351 GKIKIRONGY TIAEKEIVAL ENVKKRSRWQ RLWACL TGQ*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 554 shows 96.1% identity over a 389 aa overlap with a predicted ORF (ORF 554.ng)

from *N. gonorrhoeae*:

m554/g554

	10	20	30	40	50	60
m554 . pep	MTAHKILPVLLSIILGVSHATAASPAPNRP TVHAAPTFTQ PETLTAAHIV IDLSKQILS					
g554	MTAHKILPVLLPIILGVSHATAASPAPNRP TVHAAPTFTQ PETLTAAHIV IDLSKQILS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m554 . pep	AKNINTPVEPAALTQMTAYLVFKNMKSGNIQSEENLKIPESAWASEGSRMFVRPGDIVS					
g554	AKNTNTPVEPAALTQMTAYLVFKNMKSGNIQSEENLKIPESAWASEGSRMFVRPGDIVS					
	70	80	90	100	110	120
	130	140	150	160	170	180
m554 . pep	TDKLLKGMIALSANDAALTL AGRNGSIE NFVQMNKEARRLGMKNTVFNPTGLSREG					
g554	TDKLLKGMIALCANDAALTL ADRNGSIE NFVQMNKEARRLGMKNTVFNPTGLGREG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m554 . pep	QVSTAKDLALLSEALMRDFPEYYPLFSIKSFKFKNIEQNNRNILLYRDNNVNGLKAGHTE					
g554	QVSTAKDLSLLSEALMRDFPEYYPLFSIKSFKFENIEQNNRNILLYRDNNVNGLKAGHTE					
	190	200	210	220	230	240
	250	260	270	280	290	300
m554 . pep	SGGYNLAVSYSGNRHLVITLGSESAETR ASDNSKLLNWALQAFDTPKIYPKGKTVAQI					

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```

g554      SGGYNLAVSYSGNGRHILVITLGSESAETRASDNSKLLNRLAQAFDTPKIYPKGKTVAQI
           250      260      270      280      290      300

           310      320      330      340      350      360
m554 . pep QISGGSKKTVRAGFLKEAYITLPHKEAKMAEQILETIQPIAPVKKGQILGKIKIRONGY
           |||||:|||||:|||||:|||||:|||||:|||||:
g554      QISGGSKKTVRAGFLKEAYITLPHKEAKMAEQILETIQPIAPVKKGQILGKIKIRONGH
           310      320      330      340      350      360

           370      380      390
m554 . pep TIAEKEIVALENVKRSRWQRLWACLTGQX
           |||||:|||||:|||||:
g554      TIAEKEIVALENVKRSRWQRLWTRLTGQX
           370      380      390

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1629>:

```

a554 . seq
1  ATGACAGCAC ATAAATCCT GCCCGTCCTG CTTTCCATCA TCTTAGGCGT
51  TTCTCAGCA ACGGCTGCAT CGCCCGCGCC CAACAGACCG ACGGCACACG
101 CCGCCCCCAC GTTCCAAACA CCCGAAACCC TCACAGCGGC ACACATCGTT
151 ATCGACCTTC AAAGCAAACA GATTTTATCC GCCAAAAACA TCAATACCCC
201 TGTGGAACCG GCGGCACTAA CCCAACTGAT GACCGCATAT CTGGTTTCA
251 AAAACATGAA ATCGGGAAAT ATCCGATCTG AAGAAACTT AAAAATACCC
301 GAATCCGCAT GGGCTTCAGA AGGAAGCAGA ATGTTTGTAC GTCCCGGCGA
351 TACGGTCAGC ACCGACAAC TCTTAAAGG CATGATTGCA CTATCCGCAA
401 ACGATGCCGC CCTAACCTT GCGGCCGCG TGGGCAACGG CTCGATTGAA
451 AATTTTGTGC AACAAATGAA CAAAGAAGCC CGACGCTTGG GCATGAAGAA
501 CACTGTATTC AAAAATCCGA CAGGCTTGAG TAGAGAAGGA CAGGTTTCCA
551 CCGCCAAAGA CCTCGCCAG CTGTCTGAAG CATTGATGCG CGACTTTCCG
601 GAATATTACC CGCTGTTTTC CATCAAATCT TCAAATTC AAAATATAGA
651 GCAAAACAAC CGCAATATCC TTTATATAG GGACAACAAT GTAAACGGTC
701 TGAAAGCCGG ACACACAGAA AGCGGCGGCT ACAACCTGCG CGTGTATAC
751 TCCGGCAACG GCAGGCACAT CTTGTATC ACATTGGGTG CGGAATCGGC
801 GGAAACACGC GCATCAGACA ACAGCAAGCT GCTGAACGTC GCATTGCAAG
851 CCTTCGATAC GCCCAARATA TATCCGAAAG GCAAAACCGT TGCCCAATC
901 CAAATTTCCG GAGGCAGCAA AAAAACCGTC CGCGCAGGCT TCCTCAAAGA
951 AGCCTACATC ACTCTGCCAC ATAAGGAAGC GAAATGGCA GAACAAATTC
1001 TAGAAACCAT ACAGCCGATT CCGCCCGAG TAAAAAAGG GCAAATTTTA
1051 GGAAAAATCA AAATCAGACA AAACGGATAC ACCATTGCCG AAAAAGAAAT
1101 CGTCGCACTG GAAATGTAA AAAAAGAAG CCGGTGGCAA AGGCTTTGGG
1151 CGTGTCTGAC AGGCAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1630; ORF 554.a>:

```

a554 . pep
1  MTAHKILPVL LSIILGVSHA TAASPAPNRP TAHAAPTFTQ PETLTAAHIV
51  IDLQSKQILS AKNINTPVEP AALTQLMTAY LVFKNMKSNG IRSEENLKIP
101 ESAWASEGSR MFVRPGDTVS TDKLLKGMIA LSANDAALTL AGR LGNGSIE
151 NFVQMNKEA RRLGMKNTVF KNPTGLSREG QVSTAKDLAQ LSEALMRDFP
201 EYYPLFSIKS FKFKNIEQNN RNILLYRDNN VNGLKAGHTE SGGYNLAVSY
251 SNGNRHILVI TLGSESAETR ASDNSKLLNW ALQAFDTPKI YPKGKTVAQI
301 QISGGSKKTV RAGFLKEAYI LPHKEAKMA EQILETIQPI PAPVKKGQIL
351 GKIKIRONGY TIAEKEIVAL ENVKRSRWQ RLWACLTGQ*

```

m554/a554 99.2% identity in 389 aa overlap

```

           10      20      30      40      50      60
m554 . pep MTAHKILPVLLSIILGVSHATAASPAPNRPVHAAPTFTQ PETLTAAHIVIDLQSKQILS
           |||||:|||||:|||||:|||||:|||||:|||||:
a554      MTAHKILPVLLSIILGVSHATAASPAPNRPVHAAPTFTQ PETLTAAHIVIDLQSKQILS
           10      20      30      40      50      60

           70      80      90      100     110     120
m554 . pep AKNINTPVEPAALTQLMTAYLVFKNMKSNGIQSEENLKIPESAWASEGSRMFVRPGDTVS
           |||||:|||||:|||||:|||||:|||||:|||||:
a554      AKNINTPVEPAALTQLMTAYLVFKNMKSNGIRSEENLKIPESAWASEGSRMFVRPGDTVS

```

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	70	80	90	100	110	120
	130	140	150	160	170	180
m554 . pep	TDKLLKGMIALSANDAALTLAGRLNGS	SIENFVQOMNKEARRLG	MKNTVFKNPTGLSREG			
a554	TDKLLKGMIALSANDAALTLAGRLNGS	SIENFVQOMNKEARRLG	MKNTVFKNPTGLSREG			
	130	140	150	160	170	180
	190	200	210	220	230	240
m554 . pep	QVSTAKDLALLSEALMRDFPEYYPLFS	IKSFKFKNIEQNNRNILLYRDNNV	NGLKAGHTE			
a554	QVSTAKDLAQLSEALMRDFPEYYPLFS	IKSFKFKNIEQNNRNILLYRDNNV	NGLKAGHTE			
	190	200	210	220	230	240
	250	260	270	280	290	300
m554 . pep	SGGYNLAVSYSGNGRHILVITLGS	ESAETRASDNSKLLNWALQAFDTP	KIYPKGKTVAQI			
a554	SGGYNLAVSYSGNGRHILVITLGS	ESAETRASDNSKLLNWALQAFDTP	KIYPKGKTVAQI			
	250	260	270	280	290	300
	310	320	330	340	350	360
m554 . pep	QISGGSKKTVRAGFLKEAYITLPH	KEAKMAEQILETIQIPAPVKKGQIL	GKIKIRONGY			
a554	QISGGSKKTVRAGFLKEAYITLPH	KEAKMAEQILETIQIPAPVKKGQIL	GKIKIRONGY			
	310	320	330	340	350	360
	370	380	390			
m554 . pep	TIAEKEIVALENVKKRSRWQRLW	ACL	TGQX			
a554	TIAEKEIVALENVKKRSRWQRLW	ACL	TGQX			
	370	380	390			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1631>:

g556. seq..

```

1 atggacaata agaccaaact gcgcttgagg gcctgattt tactgaccac
51 cggcggttta agcctcatta tcgtattgat tgctgattcc tggccgcttg
101 ccacccctgct tggccgctgc atcgctcgccg ccgctgcccgg cggtttgtt
151 tggacatccc gccgacagca acgccaagtt atcgaacgct tgaaaaaatt
201 cgacatcgat ccgaaaaaag gcagaatcaa cgaggcaaac ctgcgccgta
251 tgtaccacag cggcgggaaa caccagaaag atgcgattac cctgatctgc
301 ctgtcgcaaa aatgttcggt ggacgaggcg cagcgtatgt tcaaaaaacg
351 cccgacacgt caggaaatca atcaaatggc ggcaaaacag tcgcgcggtc
401 agaaacgtcc gcaccgttaa

```

This corresponds to the amino acid sequence <SEQ ID 1632; ORF 556.ng>:

g556. pep.

```

1 MENKTKLRLG GLILLTTAVL SLIIVLIVDS WPLAILLAIV IVAAAAGGFV
51 WTSRRQQRQF IERLKKFDID PEKGRINEAN LRRMYHSGGQ HQKDAITLIC
101 LSOKCSVDEA HAMFKRPRTR OEINQMAAKQ SRGQKRPHR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1633>:

m556. seq..

```

1 ATGGACAATA AGACCAAAC TCGCTTGGGC GGCCTGATTT TACTGACCAC
51 CGCCGTTTGA AGCCTCATTA TCGTATTGAT TGTCGATTCC TGGCCGCTTG
101 CCATCCTGCT TGCAGCCGTC ATGTGCTGCTG CCGCTGCGGG CGGTTTGTG
151 TGGACATCCC GCCGACAGCA ACGCCAGTTT ATCGAACGCC TGAAAAAATT
201 CGACATCGAT CCCGAAAAAG GCAGAATCAA CGAGGCAAAC CTGCGCCGTA
251 TGTACCACAG CGGCGGACAA CACCAGAAAG ATGCGATTAC CCTGATCTGC
301 CTGTCGCAAA AATGTTTCGT GGACGAGGCG CAGCCTATGT TCAAAAAACG
351 CCCGACACGT CAGGAAATCA ATCAAATGGC GGCAAAACAG TCGCGCGGTC
401 AGAAACGTCC GCACCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1634; ORF 556>:

m556. pep..

```

1 MDNKTCLRLG GLILLTTAVL SLIIVLIVDS WPLAILLAIV IVAAAAGGFV
51 WTSRRQQRQF IERLKKFDID PEKGRINEAN LRRMYHSGGQ HQKDAITLIC

```

838

101 LSQKCSVDEA HAMFKKRPTR QEINQMAAKQ SRGQKRPHR*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 556 shows 100.0% identity over a 139 aa overlap with a predicted ORF (ORF 556.ng) from *N. gonorrhoeae*:

m556/g556

	10	20	30	40	50	60
m556.pep	MDNKT	KLRLG	LILLT	TAVLS	LIIVL	IVDSW
	PLAIL	LA	AVIA	AAA	AGGF	VWTS
	SRRQ	QRQF				
g556	MDNKT	KLRLG	LILLT	TAVLS	LIIVL	IVDSW
	PLAIL	LA	AVIA	AAA	AGGF	VWTS
	SRRQ	QRQF				
	70	80	90	100	110	120
m556.pep	IERLK	KFDID	PEKGR	INEAN	LRRMY	HSGGQ
	HQKDA	ITLIC	LSQK	CSVDE	AHAM	FKKRP
	TR					
g556	IERLK	KFDID	PEKGR	INEAN	LRRMY	HSGGQ
	HQKDA	ITLIC	LSQK	CSVDE	AHAM	FKKRP
	TR					
	70	80	90	100	110	120
	130	140				
m556.pep	QEINQ	MAAKQ	SRGQ	KRPHR	X	
g556	QEINQ	MAAKQ	SRGQ	KRPHR	X	
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1635>:

a556.seq

1	ATGGACAATA	AGACCAA	ACT	GCGCTTGGGC	GGCCTGATT	TACTGACCAC
51	CGCCGTTT	TAAGCCT	CATTA	TCGTATTGAT	TGTCGATTCC	TGGCCGCTTG
101	CCATCCTG	CTGCGCC	GTC	ATCGTCGCCG	CCGCTGCGGG	CGGCTTTGTT
151	TGGACATCC	CGACAGCA	ACGCCAGTT	ATCGAACGTC	TGAAAAAATT	
201	CGACATCGAT	CCCGAAA	AAG	GCAGAATCAA	CGAGGCAAAC	CTGCGCCGTA
251	TGTACCACAG	CGGCGGACAA	CACCAAAA	AAG	ATGCGATTAC	CCTGATCTGC
301	CTGTGCGCAA	AATGTT	CGGT	GGACGAGGCG	CACGCTATGT	TCAAAAAACG
351	CCCGACACGT	CAGGAA	TCA	ATCAAATGGC	GGCAAAACAG	TCGCGCGGTC
401	AGAAACGTCC	GCACCGTTAA				

This corresponds to the amino acid sequence <SEQ ID 1636; ORF 556.a>:

a556.pep

1	MDNKT	KLRLG	GLILL	TTAVL	SLIIV	LIVDS
	WPLAIL	LA	AVIA	AAA	AGGF	V
51	WTSRR	QQRQF	IERLK	KFDID	PEKGR	INEAN
	LRRMY	HSGGQ	HQKDA	ITLIC		
101	LSQK	CSVDEA	HAMFK	KRPTR	QEINQ	MAAKQ
	SRGQ	KRPHR	*			

m556/a556 100.0% identity in 139 aa overlap

	10	20	30	40	50	60
m556.pep	MDNKT	KLRLG	LILLT	TAVLS	LIIVL	IVDSW
	PLAIL	LA	AVIA	AAA	AGGF	VWTS
	SRRQ	QRQF				
a556	MDNKT	KLRLG	LILLT	TAVLS	LIIVL	IVDSW
	PLAIL	LA	AVIA	AAA	AGGF	VWTS
	SRRQ	QRQF				
	70	80	90	100	110	120
m556.pep	IERLK	KFDID	PEKGR	INEAN	LRRMY	HSGGQ
	HQKDA	ITLIC	LSQK	CSVDEA	HAMFK	KRPTR
a556	IERLK	KFDID	PEKGR	INEAN	LRRMY	HSGGQ
	HQKDA	ITLIC	LSQK	CSVDEA	HAMFK	KRPTR
	70	80	90	100	110	120
	130	140				
m556.pep	QEINQ	MAAKQ	SRGQ	KRPHR	X	
a556	QEINQ	MAAKQ	SRGQ	KRPHR	X	
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1637>:

839

g557.seq
 1 atgaacaaaa tattccttac tgccgcagcc ttggtgctgg gcgcgtgcgg
 51 tttccacctg aaaggtgcag acggcatttc tccgccgctg acctaccgga
 101 gctggcacat cgaaggcgga caggcattgc aatttccttt ggaaaccgcg
 151 ctgtatcagg cttcgggcag ggtggacgat gctgccggcg cgcagatgac
 201 cctgcgtata gacagcgttt cccaaaacaa ggaaacctat accgttacct
 251 gtgcggcagt catcaacgaa tatcttttga tattgacggt tgaagcgag
 301 gtattgaaac gcggcgagcc ggtcggcaaa ccgatgaccg tgtccgtccg
 351 ccgcattttg gattatgccg acaacgaaat ttggggcaaa caggaagaag
 401 aagaaaccct gtgggcggaa atgcggcagg atgttgccga acagattgtc
 451 cgccgcctga cttttctgaa ggcggaatga

This corresponds to the amino acid sequence <SEQ ID 1638; ORF 557.ng>:

g557.pep..
 1 MNKIFLTAAL LVLGACGFHL KGADGISPPL TYRSWHIEGG QALQFPLETA
 51 LYQASGRVDD AAGAQMTRLI DSVSQNKETY TVTRAAVINE YLLILTVEAQ
 101 VLKRGEFVGK PMTVSVRRIL DYADNEILGK QEEEEELWAE MRQDVAEQIV
 151 RRLTFLKAE*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1639>:

m557.seq..
 1 ATGAACAAAC TGTTCCTTAC TGCCGCAGTG CTGATGCTGG GCGCGTGCGG
 51 TTTCCACCTG AAAGGTGCAG ACGGCATTTC TCCGCCGCTG ACCTACCGGA
 101 GCTGGCACAT CGAAGGCGGA CAGGCATTGC GGTTCCTTTT GGAAACCGCG
 151 CTGTATCAGG CTTCCGGCAG GGTGGACGAT GCTGCCGGCG CGCAGATGAC
 201 CCTGCGTATA GACAGCGTTT CCCAAAACAA GGAAACCTAC ACCGTTACCC
 251 GTGCGGCAGT CATCAACGAA TATCTTTTGA TATTGACGGT TGAAGCGCAG
 301 GTATTGAAAC GCGGCGAGCC GGTGCGTAAA CCGATGACCG TGTCCTGCCG
 351 CCGCGTCCTT GCTTATGCCG ACAACGAGAT CTTGGGCAAA CAGGAAGAGG
 401 AAGCGGCATT GTGGGCGGAA ATGCGGCAGG ATGCCGCCGA ACAGATTGTC
 451 CGCCGCCTGA CTTTCTGAA GCGGAATGA

This corresponds to the amino acid sequence <SEQ ID 1640; ORF 557>:

m557.pep..
 1 MNKFLTAAL LMLGACGFHL KGADGISPPL TYRSWHIEGG QALRFPLETA
 51 LYQASGRVDD AAGAQMTRLI DSVSQNKETY TVTRAAVINE YLLILTVEAQ
 101 VLKRGEFVGK PMTVSVRRVL AYADNEILGK QEEEAALWAE MRQDAAEQIV
 151 RRLTFLKAE*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 557 shows 94.3% identity over a 159 aa overlap with a predicted ORF (ORF 557.ng) from *N. gonorrhoeae*:

m557/g557

	10	20	30	40	50	60
m557.pep	MNKFLTAALVLMGACGFHLKGADGISPPLTYRSWHIEGGQALRFPLETALYQASGRVDD					
	: : : :					
g557	MNKIFLTAALVLMGACGFHLKGADGISPPLTYRSWHIEGGQALQFPLETALYQASGRVDD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m557.pep	AAGAQMTRLRIDSVSQNKETYTVTRAAVINEYLLILTVEAQVLKRGEFVGKPMTVSVRRVL					
	: : : : : : : : :					
g557	AAGAQMTRLRIDSVSQNKETYTVTRAAVINEYLLILTVEAQVLKRGEFVGKPMTVSVRRIL					
	70	80	90	100	110	120
	130	140	150	160		
m557.pep	AYADNEILGKQEEEAALWAE MRQDAAEQIVRRLTFLKAE*					
	: : : : : : : :					
g557	DYADNEILGKQEEETLWAE MRQDVAEQIVRRLTFLKAE*					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1641>:

840

```

a557.seq
1  ATGAACAAAC TGTTCCTTAC TGCCGCAGTG CTGATGCTGG GCGCGTGCGG
51  TTTCACACCTG AAAGGTGCAG ACGGCATTTC TCCGCCGCTG ACCTACCGGA
101 GCTGGCACAT CGAAGGCGGA CAGGCATTGC AGTTTCCTTT GGAAACCGCG
151 CTGTATCAGG CTTCGGGTAG GGTGGACGAT GCTGCCGCGC CGCAGATGAC
201 CCTGCGTATA GACAGCGTTT CCAAAAACAA GGAAACCTAC ACCGTTACCC
251 GTGCGGCAGT CATCAACGAA TATCTTTTGA TATTGACGGT TGAAGCGCAG
301 GTATTGAAAC GCGGCGAGCC GGTCCGGCAA CCGATGACCG TGTCCGTCCTG
351 CCGCGTCCTT GCTTATGCCG ACAACGAGAT CTTGGGCAAA CAGGAAGAGG
401 AAGCGGCATT GTGGGCGGAA ATGCGGCAGG ATGCCGCCGA ACAGATTGTC
451 CGCGCCTGA CCTTCTGAA GCGGAATGA

```

This corresponds to the amino acid sequence <SEQ ID 1642; ORF 557.a>:

```

a557.pep
1  MNKLFLTA AV LMLGACGFHL KGADGISPPL TYRSWHIEGG QALQFPLETA
51  LYQASGRVDD AAGAQMTRLI DSVSQNKETY TVTRAAVINE YLLILTVEAQ
101 VLKRGE PVGK PMTVSVRRVL AYADNEILGK QEEEAALWAE MRQDAAEQIV
151 RRLTFLKAE*

```

m557/a557 99.4% identity in 159 aa overlap

	10	20	30	40	50	60
m557.pep	MNKLFLTA AV LMLGACGFHL KGADGISPPL TYRSWHIEGG QALRFPLETALYQASGRVDD					
a557	MNKLFLTA AV LMLGACGFHL KGADGISPPL TYRSWHIEGG QALQFPLETALYQASGRVDD					
	10	20	30	40	50	60
m557.pep	AAGAQMTRLIDS V SQNKETY TVTRAAVINE YLLILTVEAQ VLKRGE PVGK PMTVSVRRVL					
a557	AAGAQMTRLIDS V SQNKETY TVTRAAVINE YLLILTVEAQ VLKRGE PVGK PMTVSVRRVL					
	70	80	90	100	110	120
m557.pep	AAGAQMTRLIDS V SQNKETY TVTRAAVINE YLLILTVEAQ VLKRGE PVGK PMTVSVRRVL					
a557	AAGAQMTRLIDS V SQNKETY TVTRAAVINE YLLILTVEAQ VLKRGE PVGK PMTVSVRRVL					
	70	80	90	100	110	120
m557.pep	AYADNEILGK QEEEAALWAE MRQDAAEQIV RRLTFLKAE X					
a557	AYADNEILGK QEEEAALWAE MRQDAAEQIV RRLTFLKAE X					
	130	140	150	160		
m557.pep	AYADNEILGK QEEEAALWAE MRQDAAEQIV RRLTFLKAE X					
a557	AYADNEILGK QEEEAALWAE MRQDAAEQIV RRLTFLKAE X					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1643>:

```

g558.seq..
1  ATGGATGCTT GTTTTTTCGT CATTCCCGCA CAGGCGGGAA TTCGGAGATT
51  CGGGATTGTT TTCAAACGTT CGGGTCGGAT TCTTGCCGGT GCAGGAATGA
101 TGCCCTTATA TACTTTCTCC GAGCTTTATA TGCTTCAACA GGGGACGGCA
151 CATCAAGCAC CGCACTGCGT GTTGCCCGAA CGAGGCTGCC CTCGATTAG
201 ATTCTATCGC TATAAACAGA CGGGTTTCAA CCGAAAAGGA ATGGGGATAA
251 AGTCCATTTC CGACACCTCT CGGGCGATGC CGTCTGAAAA CCAATCTCCA
301 CTTTCAGACG GCATTGTTTA G

```

This corresponds to the amino acid sequence <SEQ ID 1644; ORF 558.ng>:

```

g558.pep..
1  MDACFFVIPA QAGIRRFQIV FKRSGRILAG AGMMPLYTFS ELYMLQQGTA
51  HQAPHCVLPE RGCPPIRFYR YKQTGFNRKG MGIKSISDTS RAMPSENQSP
101 LSDGIV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1645>:

```

m558.seq..
1  ATGAATGCTT GTTTTTTCGT CATTCCACAA CAGGCGGGAA TTCGGAGATT
51  CGGGATTGTT TTCAAACGTT CGGGTCGGAT TCTTGCCGGT GCAGGAATGA
101 TGCCCTTATA TACTTTCTCC GAGCTTTATA TGTTTCAACA GGGGACGGCA
151 CATCAAGCAC CGCACTGCGT GTTGCCCGAA CGAGACTACC CTCGATTAG
201 ATTCTATCGC CATAAACAGA CGGGTTTCAA CCGAAAAGGA ATGGGGATAA
251 AGTCCATTTC CGACATCTsT CGGGCGATGC CGTCTGAAAA CCAATCTCCA
301 CTTTCAGACG GCATTGTTTA G

```

This corresponds to the amino acid sequence <SEQ ID 1646; ORF 558>:

m558.pep.
 1 MNACFFVIPT QAGIRREGIV FKRSGRILAG AGMMPLYTFS ELYMFQQGTA
 51 HQAPHCVLPE RDYPPIRFYR HKQTGFNRKG MGIKSISDIX RAMPSENQSP
 101 LSDGIV*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 558 shows 92.5% identity over a 106 aa overlap with a predicted ORF (ORF 558.ng) from *N. gonorrhoeae*:

m558/g558

	10	20	30	40	50	60
m558.pep	MNACFFVIPTQAGIRREGIVFKRSGRILAGAGMMPLYTFSELYMFQQGTAHQAPHCVLPE					
	: :					
g558	MDACFFVIPTQAGIRREGIVFKRSGRILAGAGMMPLYTFSELYMLQQGTAHQAPHCVLPE					
	10	20	30	40	50	60
	70	80	90	100		
m558.pep	RDYPPIRFYRHKQTGFNRKGMGIKSISDIXRAMPSENQSPSLSDGIVX					
	: :					
g558	RGCPPIRFYRYKQTGFNRKGMGIKSISDTSRAMPSENQSPSLSDGIVX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1647>:

a558.seq
 1 ATGAATGCTT GTTTTTTCGT CATTCCACAC CAGGCGGGAA TTCGGAGATT
 51 CGGGATTGTT TTCAAACGTT CGGGTCGGAT TCTTGCCGGT GCGGGAATGA
 101 TGCCCTTATA TATAGTGGAT TAAATTAAA TCAGGACAAG GCGACGAAGC
 151 CGCAGACAGT ACAAATAGTA CGGCAAGGCG AGGCAACGCC GTACTGGTTT
 201 AAATTTAATC CACTATACTT TCTCCGAGCT TTATATGTTT CAACAGAGGA
 251 CGGCACATCA AGCACCGCAC TGCCTGTTGC CCGAACGAGA CTGCCCTCCG
 301 ATTAGATTCT ATCGCTATAA ACAGACGGGT TTCAACCGAA AAGGAATGGG
 351 AATGAAGTCC GTTTCGACA CCTCTCGGGC GATGCCGTCT GAAAACCAAT
 401 CTCCACTTTC AGACGGCATT GTTTAG

This corresponds to the amino acid sequence <SEQ ID 1648; ORF 558.a>:

a558.pep
 1 MNACFFVIPT QAGIRREGIV FKRSGRILAG AGMMPLYIVD *I*IRTRRRS
 51 RRQYK*YGKA RQRTGLNLI HYTFSELYMF QORTAHQAPH CVLPERDCPP
 101 IRFYRYKQTG FNRKGMGMKS VSDTSRAMPS ENQSPLSDGI V*

m558/a558 70.2% identity in 141 aa overlap

	10	20	30	
m558.pep	MNACFFVIPTQAGIRREGIVFKRSGRILAGAGMMPLY-----			
a558	MNACFFVIPTQAGIRREGIVFKRSGRILAGAGMMPLYIVDXIXIRTRRRSRQYKXYGKA			
	10	20	30	40
	50	60	70	80
m558.pep	-----TFSELYMFQQGTAHQAPHCVLPERDYPPIRFYRHKQTGFNRKGMGIKS			
a558	RQRTGLNLIHYTFSELYMFQORTAHQAPHCVLPERDCPPIRFYRYKQTGFNRKGMGMKS			
	70	80	90	100
	110	120		
	90	100		
m558.pep	ISDIXRAMPSENQSPSLSDGIVX			
	:			
a558	VSDTSRAMPSSENQSPSLSDGIVX			
	130	140		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1649>:

g560.seq
 1 atgtcatca tccgaacct gatttactgg ctgatactct g-tccagcct

842

```

51  gattttctctc tttcccttta tgetgctcgc ctgccttttc cgggacgggg
101  cgcacaagat ggcgcgggtc tgggtcgga tctcaactg gtcgctcaaa
151  cacatcgctc ggctcaaata ccgcatcatc ggcgcggaac acattccgga
201  ccgcccctcc gtcactctgcg ccaaacacca aagcggtcg gaaacgctcg
251  cgctccaaga gatttttccg ccgcaggttt acgttgcaa gcgcgagttg
301  ttcaaaatcc cctttttcgg ctggggcttg aaactggtca aaaccatagg
351  catagaccgc aacaaccgcc gcgaagccaa cgaacagctc ataaaacagg
401  gtttgccgcy caaaaacgaa ggttattgga ttaccatttt ccccgaaggc
451  acgcgccttg cgcccggaac acgcggcaaa taaaactcg gcggcgcgcy
501  catggcgaaa atgtttgaga tggacatcgt ccccgctgcc ctcaacagcg
551  gcgaattttg gccgaaaaat tcctttctga aatatccggg ggaaatcacc
601  gtcacatctc gtccgaccat cccgcacgca agcggcagcg aagccgaatt
651  gatggaaaaa tgcaaacacc tcattgaaac gcaacaaccg cttatttccg
701  gcgcaggccc gtttgccgcc gaaatgccgt ctgaaaccgc atga

```

This corresponds to the amino acid sequence <SEQ ID 1650; ORF 560.ng>:

g560.pep..

```

1  MLIIRNLIYW LILCSSLIFL FPFMLLASPF RDGAHKMARV WVGILNWSLK
51  HIVGLKYRII GAEHIPDRPS VICAKHQSGW ETLALQEIFP PQVYVAKREL
101  FKIPFFGWGL KLVKTIGIDR NNRREANEQL IKQGLARKNE GYWITIFPEG
151  TRLAPGKRK YKLGGARMAK MFEMDIVPVA LNSGEFWPKN SFLKYPGEIT
201  VIICPTIPHA SGSEAELEMEK CEHLIETQQP LISGAGPFAA EMPSET*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1651>:

m560.seq

```

1  ATGCTCATCA TCCGCAACCT GATTACTGCG CTGATACTCT GTTCCACCCT
51  GATTTCCTCT TTTCCCTTTA TGCTGCTCGC CTCGCCTTTC CGGGACGGGG
101  CGCACAAGAT GGCGCGGGTC TGGGTGCGCA TTCTCAACTG GTCGCTCAAA
151  CACATCGTCG GGCTCAAATA CCGCATCATC GGCGCGGAAA ACATCCCCGA
201  CCGCCCCGCC GTCATCTGCG CCAAACACCA AAGCGGCTGG GAAACGCTCG
251  CCTTCAGGGA CATTTTCCG CCGCAGGTTT ACCTTGCCAA ACGCGAGTTG
301  TTCAAATCC CTTTTTTCGG CTGGGGCTTG AAACGGTCA AAACCATAGG
351  CATAGACCGC AACAAACGCC GCGAAGCCAA CGAGCAGCTC ATAAACAGG
401  GGTGGTGCG CAAAACGAA GGCTATTGGA TTACCATTTT CCCCAGAGGC
451  ACGCGCCTTG CGCCCGGAAA ACGCGGCAAA TACAACTCG GCGGCGCGCG
501  CATGCGGAAA ATGTTTGAGA TGGACATCGT CCCCGTCGCC CTCAACAGCG
551  GCGAATTTTG GCCGAAAAAC TCCTTTCTGA AATATCCGGG GGAAATCACC
601  GTCGTCATCT GTCCGACCAT CCGCACGCA AGCGGCAGCG AAGCCGAATT
651  GATGGAAAAA TGCGAACATC TCATCGAAAC GCAACAACCG CTTATTTCCG
701  GCGCAGGCCG GTTGGCCGCC AAAATGCCGT CTGAAACCGC ATGA

```

This corresponds to the amino acid sequence <SEQ ID 1652; ORF 560>:

m560.pep

```

1  MLIIRNLIYW LILCSTLIFL FPFMLLASPF RDGAHKMARV WVGILNWSLK
51  HIVGLKYRII GAENIPDRPA VICAKHQSGW ETLALQDIFP PQVYVAKREL
101  FKIPFFGWGL KLVKTIGIDR NNRREANEQL IKQGLVRKNE GYWITIFPEG
151  TRLAPGKRK YKLGGARMAK MFEMDIVPVA LNSGEFWPKN SFLKYPGEIT
201  VVICPTIPHA SGSEAELEMEK CEHLIETQQP LISGAGPFAA KMPSETA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 560 shows 97.2% identity over a 246 aa overlap with a predicted ORF (ORF 560.ng) from *N. gonorrhoeae*:

m560/g560

```

          10      20      30      40      50      60
m560.pep  MLIIRNLIYW LILCSTLIFL FPFMLLASPF RDGAHKMARV WVGILNWSLK HIVGLKYRII
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g560      MLIIRNLIYW LILCSSLIFL FPFMLLASPF RDGAHKMARV WVGILNWSLK HIVGLKYRII
          10      20      30      40      50      60

          70      80      90      100     110     120
m560.pep  GAENIPDRPA VICAKHQSGW ETLALQDIFP PQVYVAKREL FKIPFFGWGL KLVKTIGIDR
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g560      GAEHIPDRPS VICAKHQSGW ETLALQEIFP PQVYVAKREL FKIPFFGWGL KLVKTIGIDR

```

843

	70	80	90	100	110	120
	130	140	150	160	170	180
m560.pep	NNRREANEQLIKQGLVRKNEGYWITIFPEGTRLAPGKRGKYKLGARMAMKFEMDIVPVA					
	:					
g560	NNRREANEQLIKQGLVRKNEGYWITIFPEGTRLAPGKRGKYKLGARMAMKFEMDIVPVA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m560.pep	LNSGEFWPKNSFLKYPGEITVVICPTIPHASGSEAELEMEKCEHLIETQQPLISGAGPFAA					
	:					
g560	LNSGEFWPKNSFLKYPGEITVVICPTIPHASGSEAELEMEKCEHLIETQQPLISGAGPFAA					
	190	200	210	220	230	240
m560.pep	KMPSETAX					
	:					
g560	EMPSETX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1653>:

```

a560.seq
1  ATGCTCATCA TCCGCAACCT GATTACTGCG CTGATACTCT GTTCCACCCCT
51  GATTTTCCTC TTTCCCTTTA TGCTGCTCGC CTCGCCTTTC CGAGACGGGG
101 CGCACAAAGAT GCGCGGGGTC TGGGTCAAAA TCCTCAACCT CTCGCTCAAA
151 CACATCGTCG GGCTCAAATA CCGCATCATC GGCGCGGAAA ACATCCCCGA
201 CCGCCCCGCC GTCATCTGCG CCAAACACCA AAGCGGCTGG GAAACGCTCG
251 CCCTTCAGGA CATTTTTCGG CCGCAGGTTT ACGTTGCCAA ACGCGAGTTG
301 TTCAAATCC CCTTTTTCGG CTGGGGCTTG AAACCTGGTCA AAACCATAGG
351 CATAGACCGC AACAACCGCC GCGAAGCCAA CGAGCAGCTC ATAAACACAGG
401 GGTGGCGCG CAAAAACGAA GGCTATTGGA TTACCATTTT CCCCAGAGGC
451 ACACGCCCTG CGCCCGGAAA ACGCGGCAA TACAACTCG GCGGCGCGCG
501 CATGGCGAAA ATGTTTGAGA TGGACATCGT CCCCCTCGCC CTCACACAGCG
551 GCGAATTTTG GCCGAAAAAC TCCTTTCTGA AATATCCGGG GGAAATCACC
601 GTCGTCATCT GTCCGACCAT CCGGCACGCA AGCGGCAGCG AAGCCGAATT
651 GATGGGAAAA TCGAACACC TCATCGAAAC GCAGCAGCCG CTCATTTCCG
701 GCGCAGGCC GTTGCCGCC AAAATGCCGT CTGAAACCGC ATGA
  
```

This corresponds to the amino acid sequence <SEQ ID 1654; ORF 560.a>:

```

a560.pep
1  MLIIRNLIYW LILCSTLIFL FPFMLLASPF RDGAHKMARV WVKILNLSLK
51  HIVGLKYRII GAENIPDRPA VICAQHSGW ETLALQDIFP PQVYVAKREL
101 FKIPFFGWGL KLVKTIGIDR NNRREANEQL IKQGLARKNE GYWITIFPEG
151 TRLAPGKRGK YKLGARMAMK MFEMDIVPVA LNSGEFWPKN SFLKYPGEIT
201 VVICPTIPHA SGSEAELEMGK CEHLIETQQP LISGAGPFAA KMPSETA*
  
```

m560/a560 98.4% identity in 247 aa overlap

	10	20	30	40	50	60
m560.pep	MLIIRNLIYWLILCSTLIFLFPFMLLASPF RDGAHKMARVWVGILNWSLKHIVGLKYRII					
a560	MLIIRNLIYWLILCSTLIFLFPFMLLASPF RDGAHKMARVWVKILNLSLKHIVGLKYRII					
	10	20	30	40	50	60
	70	80	90	100	110	120
m560.pep	GAENIPDRPAVICAKHQSGWETLALQDIFPPQVYVAKRELFKIPFFGWGLKLVKTIGIDR					
a560	GAENIPDRPAVICAKHQSGWETLALQDIFPPQVYVAKRELFKIPFFGWGLKLVKTIGIDR					
	70	80	90	100	110	120
	130	140	150	160	170	180
m560.pep	NNRREANEQLIKQGLVRKNEGYWITIFPEGTRLAPGKRGKYKLGARMAMKFEMDIVPVA					
	:					
a560	NNRREANEQLIKQGLVRKNEGYWITIFPEGTRLAPGKRGKYKLGARMAMKFEMDIVPVA					

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	130	140	150	160	170	180
	190	200	210	220	230	240
m560 . pep	LNSGEFWPKNSFLKYPGEITVVICPTIPHASGSEAE	LMKCEHLIETQQPLISGAGPFAA				
a560	LNSGEFWPKNSFLKYPGEITVVICPTIPHASGSEAE	LMGKCEHLIETQQPLISGAGPFAA				
m560 . pep	KMPSETAX					
a560	KMPSETAX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1655>:

```

m561 . seq.
1  ATGATACTGC CAGCCCGTTT TTCAGACGGC ATCAGCCTTT CCCTGCGCCT
51  GAAACTCCTG ACCGGACTGT GGGTCGGGTT GCGCGCATTG TCTGTCGTTT
101 TGACACTGCT GCTCTCTTTG CGTCTGGAAG ACGCGGCCTC CGTCATCGAA
151 GAGGCGGGCA ACTTGAGAAT GCAGGCATAC CGTCTGGCAT ACATGGCGGG
201 TGAAGGCTCG CCCCGTGC GC AAATTGACAA TCAGGTGCC GAATTGAAA
251 AAAGTTTAAA ACGCATTGCC CAAAGCGATG CCATCCATCC GCTGATTCCT
301 TCGACACCCC CTCTTGCTTA TGATTGATA CAATCCATGC TGATTATAGA
351 TTGGCAGGCA CACATCCTCC CCCCGCTCCA GTCCATCCGG CGACCGACTC
401 AGGTCGATCT CTACCGCTTT GCCGAAACA TCGAACTGTT TTTGCAGGCA
451 TTGGAAAATG CCAACGAAAA AAACACATGG TGGCTCAGGC GTTTTCAATG
501 GGCAATTATG TTGATGACGC TGGTGTCTGC TGTACTGATG CTGTTTGGC
551 ACCAGATTTG GGTATCCGG CCGCTGCAGG CGTTAAGGGA AGGTGCGGAA
601 CGCATCGGAC GGAGGTGTTT CGATATCCG GTTCCCGAAG GCGGTACGCC
651 GGAAATCAAA CAGGTCGGGC GTTGTTCCTT TCAAATGGGC GGCAGGTTGA
701 AAATTTTATA TGATGATTTG GAAGGACAAG TCGCCGAGCA GACACGCAGT
751 CTCGAAAAAC AAAATCAAAA CCTGACCTG CTGTACCAA CTACACGGGA
801 CCTGCACCAA TCCTACATAC CGCAACAGGC TGCAGAACAT TTTCTAAACC
851 GTATCCTGCC CGCCGTAGGA GCAGATCCG GCAGAGTTTG TTTGGACGGC
901 GGATCCGATG TTTATGTTTC CATTTCATCAT GCGGATTGCG GCACAGCAGC
951 TTCGGATTTG GGAAGTACC ATGAGGAAAT CTTCCCATG GAGTACCAGA
1001 ACGAAACATT GGGCAGGCTG TTGCTCAGCT TTCCAACCG CATTCTCTT
1051 GATGAAGACG ACCGCATCCT GCTTCAAACA CTAGGCAGGC AATTGGGCGT
1101 ATCGCTTGCC GCGCAAAAC AGGAGGAAGA AAAACGCCTG CTTCAGTAT
1151 TCGAGGAACG CAACCTGATT GCGCAAGGAT TACATGACAG CATCGACAA
1201 GCATTAACGT TCCTAAACCT ACAGGTACAG ATGCTGGAAG CCGCCTTTGC
1251 CGAAACAAA CCGGAGGAAG CCGCAGAAA CATCAGCTTT ATCAAACAG
1301 GCGTGCAGGA ATGTTATGAA GATGTCGCG AACTGCTGCT CAACTTCCGT
1351 ACCAAATCA GCAATAAGA ATTTCCCGAA GCCGTTGCCG ACCTATTCGC
1401 CCGCTTTACG CAACAAACCG GGATAACGGT CGAAACCGCC TGGGAAACG
1451 GTTCGTTTCT GCGCCTCAG GAAGCGCAGC TCCAAATGAT TTTATCCTG
1501 CAGGAAAGCC TGTCCAACAT CCGCAAACAC GCCCGCGCCA CCCATGTAAA
1551 ATTCACCCTT TCCGAACACG GCGGACGCTT TACCATGACC ATCCAAGACA
1601 ACGGACAAGG TTTTCACACG GAGAAAATAG GAGAACCAC GGCAGCCAT
1651 GTCGGACTGC ACATCATGCA GGAGCGTGCC AAACGCATCC ATGCCGTTT
1701 AGAAATCCGT TCCCAAGCTC AACAGGGAAC CACCGTCTCA TTGACGGTTG
1751 CATCTGAAGA AAGCTTGAAA TGA

```

This corresponds to the amino acid sequence <SEQ ID 1656; ORF 561>:

```

m561 . pep
1  MILPARFSOG ISLSRLKLL TGLWVGLAAL SVVLTLLLSL RLENAASVIE
51  EAGNLRMQAY RLAYMAGEGS PRAQIDNQVA EFEKSLKRIA QSDAIHPLIP
101 SDTPLAYDLI QSMLIIDWQA HILPPLQSYR RPTQVDLYRF AGNIEFLQA
151 LENANEKNTW WLRFFOWAIM IMTLVSSVLM LFWHQIWRV FLQALREGAE
201 RIGRRCFDIP VPEGTPPEFK QVGRCFNQM GRLKILYDDL EGQVAEQTRS
251 LEKQNQNLT LYQTTRDLHQ SYIPQAAEH FLNRILPAVG ADSGRVCLDG
301 GSDVYVSIHH ADCGTAASDL GKYHEEIFPI EYQNETLRL LLSFPNGISL
351 DEDDRILLQT LGRQLGVSLA GAKQEEERL LAVLQERNLI AQLHDSIAQ
401 ALTFLNLQVQ MLETAFENK REEAENISF IKTGVQECYE DVRELLLNFR
451 TKISNKEFPE AVADLFARF QQTGITVETA WENGSLPQPQ EAQLQMIFIL

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501 QESLSNIRKH ARATHVKFTL SEHGRFTMT IQDNGQGFDT EKIGEPTGSH
 551 VGLHIMQERA KRIHAVLEIR SQAQGGTTVS LTVASEESLK *

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m561/g561 89.7% identity in 223 aa overlap

	10	20	30	40	50	60
m561.pep	MILPARFSDGISLSRLKLLTGLWVGLAALS	VVLTL	LSRL	ENAA	SVIEE	EAGNLRMQAY
g561	MILPTRFSDGIPLSLRLKLLTGLWVGLAALS	VVLTL	LSRL	ENAA	SVIEE	EAGNLRMQAY
	10	20	30	40	50	60
m561.pep	RLAYMAGEGSPRAQIDNQVAE	FEKSLKRIAQSDAIH	PLIPSDT	PLAYDL	IQSMLI	IDWQA
g561	RLAYMAGEGSPRAQIDNQIAE	FEKSLKRISQSDAIH	PLIPSDN	PLAYDL	IQSMLI	IDWQA
	70	80	90	100	110	120
m561.pep	HILPPLQSYRRPTQVDLYR	FAGNIELFLQALENANE	KNTWWLRR	FCWAIM	LM	TLVSSVLM
g561	NILPPLQAYRRPTQIELYR	FAGNIELFLQALENAGE	KNTWWLRR	FCWVIM	LM	TLVSSVLM
	130	140	150	160	170	180
m561.pep	LFWHQIWVIRPLQALREGA	ERIGRRCFDIP	VEGGTPE	FKQVGR	CFNQMG	GR
g561	LFWHQIWVIRPLQALREGA	ERIGRRCFDIP	VEGGTPE	FKQVGR	CFNQMG	GR
	190	200	210	220	230	240
m561.pep	EGQVAEQTRSLEKQNQNL	TLTYQTTRDLH	QSYIPQQA	AHFLNR	ILPAVG	ADSGRVCLDG
	250	260	270	280	290	300

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1657>:

a561.seq

1	ATGATACTGC	CAGCCCGTTT	TTCAGACGGC	ATCAGCCTTT	CCCTGCGCCT
51	GAAACTCCTG	ACCGGACTGT	GGGTCGGGTT	GGCGGCATTG	TCTGTCGTTT
101	TGACACTGCT	GCTCTCTTTG	CGTCTGGAAA	ACGCGGCCTC	CGTCATCGAA
151	GAGGCGGGCA	ACTTGAGAA	GCAGGCATAC	CGTCTGGCAT	ACATGGCGGG
201	TGAAGGCTCG	CCCCGTGCGC	AAATTGACAA	TCAGGTTGCC	GAATTTGAAA
251	AAAGTTTAAA	ACGCATTGCC	CAAAGCGATG	CCATCCATCC	GCTGATTCCT
301	TCGGACACCC	CTCTTGCTTA	TGATTTGATA	CAATCCATGC	TGATTATAGA
351	TTGGCAGGCA	CACATCCTCC	CCCCGCTCCA	GTCCTACCGG	CGACCGACTC
401	AGGTGCATCT	CTACCGCTTT	GCCGGAACA	TCGAAGTGT	TTTGCAAGCA
451	TTGGAAAATG	CCAACGAAAA	AAACACATGG	TGGCTCAGGC	GTTTTCATG
501	GGCAATTATG	TTGATGACGC	TGGTGTCTGC	TGTACTGATG	CTGTTTGGC
551	ACCAGATTG	GGTATCCGG	CCGCTGCAGG	CGTTAAGGGA	AGGTGCGGAA
601	CGCATCGGAC	GGAGGTGTTT	CGATATTCCG	GTTCCCGAAG	GCGGTACGCC
651	GGAAATCAAA	CAGGTCGGGC	GTGTTTCAA	TCAAATGGGC	GGCAGGTTGA
701	AAATTTTATA	TGATGATTG	GAAGGACAA	TGCGCGAGCA	GACACGCAGT
751	CTCGAAAAAC	AAAATCAAAA	CCTGACCCTG	CTGTACCAAA	CTACACGGGA
801	TCTGCACCAA	TCCTACATAC	CGCAACAGGC	TGCAGAACAT	TTTCTAAACC
851	GTATCTTGCC	CGCCGTAGGA	GCAGATTCCG	GCAGAGTTTG	TTTGGACGGC
901	GGATCCGATG	TTTATGTTTC	CATTATCAT	GCGGATTGCG	GCACAGCAGC
951	TTCGGATTG	GGGAAGTACC	ATGAGGAAAT	CTTCCCCATT	GAGTACCAGA
1001	ACGAAACATT	GGGCAGGCTG	TTGCTCAGCT	TTCCAAACGG	CATTTCCTCT
1051	GATGAAGACG	ACCGCATCCT	GCTTCAAACA	CTAGGCAGGC	AATTGGGCGT
1101	ATCGCTTGCC	GGCGCAAAAC	AGGAGGAAGA	AAAACGCTG	CTTGAGTAT
1151	TGCAGGAACG	CAACCTGATT	GCGCAAGGAT	TACATGACAG	CATCGCACAA
1201	GCATTAACTG	TCCTAAACCT	ACAGGTACAG	ATGCTGGAAA	CCGCTTTTGC
1251	CGAAAAACAA	CGGGAGGAAG	CCGCAGAAAA	CATCGGCTTC	ATCAAAACAG
1301	GCGTGCAGGA	ATGTTATGAA	GATGTCCGCG	AACTGCTGCT	CAACTCCGT
1351	ACCAAAATCA	GTAATAAAGA	ATTTCCCGAA	GCCGTTGCCG	ACCTATTCTC

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```

1401 GCGCTTTACG CAACAGACCG GCACGACTGT CGAAACCGCT TGGGAAAACG
1451 GCACGCACCT GCCTACACAG GACGAGCAGC TCCAAATGAT TTTCATCCTG
1501 CAAGAAAGCT TGTCCAACAT CCGAAAACAT GCCCAGGCCA CCCATATCAA
1551 ATTCAGACTG CTCAAACAGG ATGGAAGTTT TACAATGACC ATTCAGACA
1601 ACGGACAGGG TTTTGACACG GAAAACATTG GAGAACCATC GGGCAGCCAT
1651 GTCGACTGC ATATCATGCA GGAGCGTGCC AAACGCATCC ATGCCGTTT
1701 AGAAATCCGT TCCCAAGCTC AACAGGGAAC CACCGTCTCA TTGACGTTG
1751 CATCTGAAGA AAGCTTGAAA TGA

```

This corresponds to the amino acid sequence <SEQ ID 1658; ORF 561.a>:

```

a561.pep
1  MILPARFSDG ISLSRLKLL TGLWVGLAAL SVVLTLLSL RLENAASVIE
51  EAGNLRMQAY RLAYMAGEGS PRAQIDNQVA EFESLKRIA QSDAIHPLIP
101 SDTPLAYDLI QSMIIIDWQA HILPPLQSYR RPTQVDLYRF AGNIELFLQA
151 LENANEKNTW WLRRFQWAIM LMTLVSSVLM LFWHQIWVIR PLQALREGAE
201 RIGRRCFDIP VPEGGTPEFK QVGRCFNQM GRLKILYDDL EGQVAEQTRS
251 LEKQNQNLTLYQTTRDLHQ SYIPQAAEH FLNRILPAVG ADGSRVCLDG
301 GSDVYVSIHH ADCGTAASDL GKYHEEIFPI EYQNETLGR LLSFPNGISL
351 DEDDRILLQT LGRQLGVSLA GAKQEEKRL LAVLQERNLI AQGLHDSIAQ
401 ALTFNLQVQ MLETAFENK REEAENIGF IKTGVQECYE DVRELLNFR
451 TKISNKEFPE AVADLFSRFT QQTGTTVETA WENGTHLPTQ DEQLQMIFIL
501 QESLSNIRKH AHATHIKFRL LKQDGSFTMT IQDNGQCFDT ENIGEPSGSH
551 VGLHIMQERA KRIHAVLEIR SQAQGTTVS LTVASEESLK *

m561/a561 96.9% identity in 590 aa overlap

      10      20      30      40      50      60
m561.pep  MILPARFSDGISLSRLKLLTGLWVGLAALSVVLTLLSLRLENAASVIEEAGNLRMQAY
          |||
a561      MILPARFSDGISLSRLKLLTGLWVGLAALSVVLTLLSLRLENAASVIEEAGNLRMQAY
      10      20      30      40      50      60

      70      80      90      100     110     120
m561.pep  RLAYMAGEGSPRAQIDNQVAEFESLKRIAQSDAIHPLIPSDTPLAYDLIQSMIIIDWQA
          |||
a561      RLAYMAGEGSPRAQIDNQVAEFESLKRIAQSDAIHPLIPSDTPLAYDLIQSMIIIDWQA
      70      80      90      100     110     120

      130     140     150     160     170     180
m561.pep  HILPPLQSYRRPTQVDLYRFAGNIELFLQALENANEKNTWWLRRFQWAIMLMTLVSSVLM
          |||
a561      HILPPLQSYRRPTQVDLYRFAGNIELFLQALENANEKNTWWLRRFQWAIMLMTLVSSVLM
      130     140     150     160     170     180

      190     200     210     220     230     240
m561.pep  LFWHQIWVIRPLQALREGAERIGRRCFDIPVPEGGTPEFKQVGRCFNQMGRCLKILYDDL
          |||
a561      LFWHQIWVIRPLQALREGAERIGRRCFDIPVPEGGTPEFKQVGRCFNQMGRCLKILYDDL
      190     200     210     220     230     240

      250     260     270     280     290     300
m561.pep  EGQVAEQTRSLEKQNQNLTLLYQTTRDLHQSYIPQAAEHFLNRILPAVGADGSRVCLDG
          |||
a561      EGQVAEQTRSLEKQNQNLTLLYQTTRDLHQSYIPQAAEHFLNRILPAVGADGSRVCLDG
      250     260     270     280     290     300

      310     320     330     340     350     360
m561.pep  GSDVYVSIHHADCGTAASDLGKYHEEIFPIEYQNETLGRLLLSFPNGISLDEDDRILLQT
          |||
a561      GSDVYVSIHHADCGTAASDLGKYHEEIFPIEYQNETLGRLLLSFPNGISLDEDDRILLQT
      310     320     330     340     350     360

      370     380     390     400     410     420
m561.pep  LGRQLGVSLAGAKQEEKRLAVLQERNLIAQGLHDSIAQALTFLNLQVQMLETAFENK
          |||
a561      LGRQLGVSLAGAKQEEKRLAVLQERNLIAQGLHDSIAQALTFLNLQVQMLETAFENK

```

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	370	380	390	400	410	420
	430	440	450	460	470	480
m561.pep	REEAAENISFIKTGVQECYEDVRELLLNFRTKISNKEFPEAVADLFARETQQTGITVETA					
a561	REEAAENIGFIKTGVQECYEDVRELLLNFRTKISNKEFPEAVADLFSRFTQQTGTTVETA					
	430	440	450	460	470	480
	490	500	510	520	530	540
m561.pep	WENGSLFPQEAQLQMIFILQESLSNIRKCHARATHVKFTLSEHGGRFTMTIQDNGQGFD					
a561	WENGTHLPTQDEQLQMIFILQESLSNIRKHAHATHIKFRLLKQDGSFTMTIQDNGQGFD					
	490	500	510	520	530	540
	550	560	570	580	590	
m561.pep	EKIGEPTGSHVGLHIMQERAKRIHAVLEIRSQAQQT TVSLTVASEESLKK					
a561	ENIGEPSGSHVGLHIMQERAKRIHAVLEIRSQAQQT TVSLTVASEESLKK					
	550	560	570	580	590	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1659>:

g562.seq..

```

1  atggcaagcc cgtcgagtct gcctttcaat tcgggcaaga ccaaaccgac
51  ggcttttggc gcgccggttt tggtcggaat catgttttcc acgccgctgc
101  gggcgcgcg caggtctttg tggcgacgt cggtaacggt ttggtcgttg
151  gtcagtgcgt ggatgggtgt cattgcgctt ttgacgatgc cgacgctttc
201  gctcaacact ttggcaaccg gcgagaggca gttggtggtg caggaagcgt
251  tggaaacgac ggtcatgtcg gcggtcagga cgctgtcggt caccgcttac
301  acgacggttg catcgacatc gtcgccgccc ggtgcggaag agaggacttt
351  ttccgcgccc ctttcgaggt ggattttggc ttttctttg ctggtgaacg
401  cgccggtgca ttccatgacc aaatcgacac cgagttcttt ccacggcagt
451  tcggcagggg tcggggtcga gaagaagggg attttgtcgc cgttgacgat
501  gaggttgccc cgtcgtggg atacgtcggc ttcaaagcgt ccgtgtacgg
551  tgtcgaaatt ggtcagatgg gcgttggttt caaggctgcc gctggcggtg
601  acggcgacga tttggagttg gtcttga

```

This corresponds to the amino acid sequence <SEQ ID 1660; ORF 562.ng>:

g562.pep

```

1  MASPSSLPFN SGKTKPTAFA APVLVGIMFS TPLRARRRSL WRTSVTVWSL
51  VSAWMVVIAP LTMPTLSLNT LATGERQLVV QEALTTVMS AVRTLSFTPY
101  TTVASTSSPP GAEMRTFFAP LSRWILAFSL LVNAPVHSMT KSTPSSFHGS
151  SAGLRVEKKG ILSPLTMRLP PSWDTASAKR PCTVSNLVRW ALVSRPLPLAL
201  TATIWSWS*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1661>:

m562.seq

```

1  ATGGCAAGCC CGTCGAGCCT GCCTTTCAAT TCGGGCAGTA CCAAACCGAC
51  GGCTTTTGCC GCGCCGTTT TGGTCGGAAT CATGTTTTC ACGCCGCTGC
101  GGGCGCGCG CAGGTCTTTG TGGCGCACGT CGGTAACGGT TTGGTCGTTG
151  GTCAGCGCGT GGATGGTGGT CATCGCGCCT TTGACGATGC CGACGCTTTC
201  GCTCAACACT TTGGCAACCG GCGAGAGGCA GTTGGTGGTG CAGGAAGCGT
251  TGGAAACGAC GGTGATGTCG GCGGTCAGGA CGCTGTGCTT CACGCCGTAC
301  ACGACGGTTG CATCGACATC GTCGCCGCCC GGTGCGGAAA TGAGGACTTT
351  TTTCGCGCCG CTTTCGAGGT GGATTTTGGC TTTTCTTTG CTGGTGAACG
401  CGCCGGTGCA TTCCATGACC AAATCGACAC CGAGTTCTTT CCACGGCAGT
451  TCGGCAGGGT TCGGGTCTGA GAAGAAGGGG ATTTTGTGCG CGTTGACGAT
501  GAGGTTGCCG CCGTCGTGGG ATACGTCGGC TTCAAAGCGT CCGTGCACGG
551  TGTCGAATTT GGTGAGATGG GCGTTGTTT CAAGGCTGCC GCTGGCGTTG
601  ACGCGCACGA GTTGAGTTG GTCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1662; ORF 562>:

m562.pep

```

1  MASPSSLPFN SGKTKPTAFA APVLVGIMFS TPLRARRRSL WRTSVTVWSL
51  VSAWMVVIAP LTMPTLSLNT LATGERQLVV QEALTTVMS AVRTLSFTPY

```


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```

101 TTVASTSSPP GAEMRTFFAP LSRWILAFSL LVNAPVHSM TSTPSSFHGS
151 SAGLRVEKKG ILSPLTMLRP PSWDTASAKR PCTVSNLVRW ALVSRLPLAL
201 TATSWWS*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m562/g562 99.0% identity in 208 aa overlap

```

              10      20      30      40      50      60
m562.pep      MASPSSLPFNSGSKPTAFAAPVLVGIMFSTPLRARRRSLWRTSVTVWSLVSAMMVVIAP
              |||||
g562           MASPSSLPFNSGSKPTAFAAPVLVGIMFSTPLRARRRSLWRTSVTVWSLVSAMMVVIAP
              10      20      30      40      50      60

              70      80      90      100     110     120
m562.pep      LTMP TSLN TLATGERQLVVQEAL ETTVMSAVRTLSFTPTT VASTSSPPGAEMRTFFAP
              |||||
g562           LTMP TSLN TLATGERQLVVQEAL ETTVMSAVRTLSFTPTT VASTSSPPGAEMRTFFAP
              70      80      90      100     110     120

              130     140     150     160     170     180
m562.pep      LSRWILAFSLLVNAPVHSM TSTPSSFHGS SAGLRVEKKG ILSPLTMLRP PSWDTASAKR
              |||||
g562           LSRWILAFSLLVNAPVHSM TSTPSSFHGS SAGLRVEKKG ILSPLTMLRP PSWDTASAKR
              130     140     150     160     170     180

              190     200     209
m562.pep      PCTVSNLVRWALVSRLPLALTATSWWSX
              |||||
g562           PCTVSNLVRWALVSRLPLALTATSWWSX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1663>:

```

a562.seq
1  ATGGCAAGCC CGTCGAGTTT GTCTTTCAAT TCGGGCAGTA CCAAACCGAC
51  GGCTTTTGCC GCGCCAGTTT TGGTCGGAAT CATGTTTCC ACGCCGCTGC
101 GGGCGCGGCG CAGGTCTTTG TGGCGCACGT CGGTAACGGT TTGGTCGTTG
151 GTCAGCGCGT GGATGGTGGT CATCGCGCCT TTGACGATGC CGACGCTTTC
201 GCTCAACACT TTGGCAACCG GCGAGAGGCA GTTGGTGGTG CAGGAAGCGT
251 TGGAAACGAC GGTCAATGTCG CCGTCAGGA TGCTGTCGTT CACGCCGTAC
301 ACGACGGTTG CATCGACATC GTCGCCGCC GGTGCGGAAA TGAGGACTTT
351 TTTCGCGCCG CTTTCCASAT GAACTTTGGC TTTTCTTTG CTGGTGAACG
401 CGCCGGTGCA TTCCATGACC AAATCGACAC CGAGTTCTTT CCACGGCAGT
451 TCGGCAGGGT TCGGGGTCNA GAAGAANGGG ATTTTGTCGC CGTTGACGAT
501 GAGGTGCGCG CCGTCGTGGG ATACGTCGGC TTCAAAGCGT CCGTGACGCG
551 TGTCGAATTT GGTGAGGTGG GCGTTGGTTT CAAGGCTGCC GCTGGCGTTG
601 ACGGCGACGA TTTGGAGTTG GTCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1664; ORF 562.a>:

```

a562.pep
1  MASPSSLSFN SGSTKPTAFA APVLVGIMFS TPLRARRRSL WRTSVTVWSL
51  VSAWMVVIAP LTMP TSLN T LATGERQLVV QEAL ETTVMS AVRMLSFPT
101 TTVASTSSPP GAEMRTFFAP LSR*TLAFSL LVNAPVHSM TSTPSSFHGS
151 SAGLRVXXKG ILSPLTMLRP PSWDTASAKR PCTVSNLVRW ALVSRLPLAL
201 TATIWSWS*

```

m562/a562 96.6% identity in 208 aa overlap

```

              10      20      30      40      50      60
m562.pep      MASPSSLPFNSGSKPTAFAAPVLVGIMFSTPLRARRRSLWRTSVTVWSLVSAMMVVIAP
              |||||
a562           MASPSSLSFN SGSTKPTAFA APVLVGIMFS TPLRARRRSLWRTSVTVWSLVSAMMVVIAP
              10      20      30      40      50      60

```

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	70	80	90	100	110	120
m562.pep	LTMPTLSLNTLATGERQLVVQEALETTVMSAVRTLSTFTPYTTVASTSSPPGAEMRTFFAP					
a562	LTMPTLSLNTLATGERQLVVQEALETTVMSAVRMLSTFTPYTTVASTSSPPGAEMRTFFAP					
	70	80	90	100	110	120
m562.pep	LSRWILAFSLLVNAPVHSMTKSTPSSFHGSSAGLRVEKKGILSPLTMLRPPSWDTSASKR					
a562	LSRXTLAFSLLVNAPVHSMTKSTPSSFHGSSAGLRVXKXGILSPLTMLRPPSWDTSASKR					
	130	140	150	160	170	180
m562.pep	PCTVSNLVRWALVSRLPLALTATSWWSX					
a562	PCTVSNLVRWALVSRLPLALTATIWSX					
	190	200	209			

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1665>:

g563.seq

```

1  ATGAACAAAA CCCTCTATCG TGTGATTTTC AACCGCAAAC GCGGTGCTGT
51  GGTAGCTGTT GCCGAAACCA CCAAGCGCGA AGGTAAAAGC TGTGCCGATA
101 GTGGTTCGGG CAGCGTTTAT GTGAAATCCG TTTCTTTCAT TCCTACTCAT
151 TCCAAAGCCT TTTGTTTTTC TGCATTAGGC TTTTCTTTAT GTTTGGCTTT
201 GGGTACGGTC AATATTGCTT TTGCTGACGG CATTATTACT GATAAAGCTG
251 CTCCTAAAAC CCAACAAGCC ACGATTCTGC AAACAGGTAA CGGCATACCG
301 CAAGTCAATA TTCAAACCCc tACTTCGGCa ggGGTTTCTG TTAATCAATA
351 TGCCCAGTTT GATGTGGGTA ATcgCGGGC GATTTTAAAC AACAGTCGCA
401 GCAACACCCA AACACAGCTA GGCGGTGGA TTCAAGGCAA TCCTTGGTGT
451 ACAAGGGGCG AAGCACGTGT GGTGTAAAC CAAATCAACA GCAGCCATCC
501 TTCACAACTG AATGGCTATA TTGAAGTGGG TGGACGACGT GCAGAACTCG
551 TTATTGCCAA TCCGGCAGGG ATTGCAGTCA ATGGTGGTGG TTTTATCAAT
601 GCTTCCCGTG CCACTTTGAC GACAGGCCAA CCGCAATATC AAGCAGGAGA
651 CTTTAGCGGC TTTAAGATAA GGCAAGGCAA TGCTGTAATC GCCGGACACG
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This corresponds to the amino acid sequence <SEQ ID 1666; ORF 563.ng>:

g563.pep..

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The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1667>:

m563.seq.

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5751  TTATGCCGGA  GAAGACGGCT  ATCAAATCAA  GGTCCGAAAC  CATACAGACC
5801  TCAAAGCGG  CATCATCACC  AGTACCCAAA  GCGCAGAAGA  CAAGGGTAAA
5851  AACCGCTTTC  AGACGGCCAC  CCTACCCCAT  AGCGACATCA  AAAACCCAG
5901  CCAATACAAA  GGCGAAAGTT  TTGGATTGGG  CGCAAGTGCG  TCCATAAGCG
5951  GCAAAACACT  GGGACAGGGC  GCACAAAATA  AACCTCAAAA  CAAACACCTG
6001  ACAAGCGTAG  CCGATAAAAA  CAGCGCAAGT  TCATCAGTGG  GTTATGGCAG
6051  CGACAGCGAC  AGTCAAAGCA  GCATCACAAA  AAGCGGCATC  AACACCCGCA

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6101 ACATTCAAAT CACCGACGAA GCCGCACAAA TCCGGCTGAC AGGCAAAACA
6151 GCGGCACAAA CCAAAGCCGA TATTGATACA AACGTAACCA CAGACACCGC
6201 CGAACGACAT TCGGGCAGCT TGAAGAACAC CTTCAACAAA GAAGCGGTGC
6251 AAAGTGAAC TGGATTACAA AGAACCGTCA GCCAAGATTT TAGTAAAAAT
6301 GTTCAACAAG CCAATACCGA GATTAACCAA CATTTAGACA AACTCAAAGC
6351 AGACAAAGAA GCAGCCGAAA CAGCAGCAGC CGAGGCATTA GCCAATGGCG
6401 ATATGGAAAC TGCCAAACGC AAAGCCCATG AAGCTCAAGA TGCGGCAGCA
6451 AAAGCAGATA ATTGGCAACA AGGCAAAGTC ATTCTCAACA TGTTAGCCTC
6501 AGGTTTAGCT GCGCCGACCC AAAGCGGAGC GGGCATCGCT GCGGCTACCG
6551 CATCGCCAGC CGTATCGTAT GCGATTGGAC AGCACTTTAA AGATTTAGCC
6601 GGTCAAAACG CGAATGGTAA ACTAACCGCC AGTCAAGAAA CCGCACACGT
6651 TCTTGCCAC GCGGTATTAG GAGCAGCGGT TGCCGCAGTA GGAGACAACA
6701 ATGCTCTAGC AGGAGCATTG AGTGCGGGCG GGTGGAAGC GGCTGCGCCT
6751 TACATCAGCA AATGGTTATA CGGCAAAGAA AAAGGAAGCG ACTTAACGGC
6801 GGAAGAGAAA GAGACTGTAA CAGCGATTAC AAATGTATTG GGTACGGCTA
6851 CGGGTGC GCGC AGTCGCAAC AGCGCAACAG ATGCAGCGCA AGGCAGCCTG
6901 AATGCGCAA GTGCGGTGGA GAATAATGAT ACTGTAGAGC AAGTGAAATT
6951 TGCTCTTAGG CACCCTAGAA TTGCTATTGC AATTGGATCT GTACATAAAG
7001 ATCCTGGCTC TACATTAGAG CCTAATATTT CAACAATTGC TTCAACTTTT
7051 CAATTAATTT TATTTCTTAA TAGTGAATTT GGTGGTGAAG GTGGAGTTGG
7101 CAATGCATT AGGCACGTTT TATGGCAAGC AACCATCACA CGAGAATTTG
7151 GCAAAGATAT TGCTGTTAAA GTAGGAAATA GTCATGAAAG TGGGGAAAAA
7201 ATTAATTATT CTATAAGACG TAATCTTTCA TTAGATAAAG CAGATGAAAT
7251 GATTGATCAA CTAAATAACG AAATAGGAAG AGAAATAGCA TTAAATACCA
7301 ATAGGTTAAA CACAAAAGAG TTAGTTGGAT TAATCTGGA AACTTATAAA
7351 AATAATGGT TTTATCAAGC AGAAAGAAAC AGTAATGGAA ATTATGATGT
7401 TGTAAAGAAA AGATTATCTG AAAAAGATTA CCAGAATACA AGCAATATAT
7451 TGATTCACCT AGATAATACT GGTGCCGGAT TTAATTTCA GCAGAGGAGA
7501 AAACAAATCA GAGCACAAT TTCAGCCAGA CAATGGAGAA GATAA

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This corresponds to the amino acid sequence <SEQ ID 1668; ORF 563>:

m563.pep..

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1 MNKTLRYRIF NRKRGAVVAV AETTKREGKS CADSDSGSAH VKSVFPGTTH
51 APVCRSNIFS FSLGFSLCL AVGTANIAFA DGIADKAAP KTQQTILQT
101 GNGIPQVNIQ TPTSAGVSVN QYAQFDVGNR GAILNNSRSN TQTQLGGWIQ
151 GNPWLARGEA RVVVNQINSS HSSQMNGYIE VGGRRAEVVI ANPAGIAVNG
201 GGFINASRAT LTTGQPQYQA GDLSGFKIRQ GNVVIAGHGL DARDTDFTRI
251 LSYHKSIDAP VWGQDVRVVA QONDVVATGN AHSPILNNA ANTSNNTANN
301 GTHIPLFAID TGKLGMYAN KITLISTAEQ AGIRNQGLF ASSGNVAIDA
351 NGRLVNSGTM AAANAKDTDN TAEHKVNIRS QGVENSATV SQQTQIHSQ
401 SIQNTGTLLS SGEILIHNSG SLKNETSGTI EAARLADTD TLNNQGLKLSQ
451 TGSQKLHIDA QGKMDNRGRM GLQDTAPTAS NGSSNQTGNS YNASFHSSTT
501 TPTTATGTGT ATVSNITTA PTFADGTIRT HGALDNSGSI IANGQTDVSA
551 QQGLNNAGQI DIHQLNAKGS AFDNHNGTII SDAVHIQAGS LNNQNGNITT
601 RQOLEIETDQ LDNAHGKLLS AEIADLAVSG SLNNQNGEIA TNQQLIHDG
651 QQSTAVIDNT NGTIQSGRDV AIQAKSLSN GTLAADNKLD IALQDDFYVE
701 RNIVAGNELS LSTRGSLKNS HTLQAGKRIR IKANNLDNAA QGNIQSGGTT
751 DIGTQHNLTN RGLIDGQQTQ IQAGQMNNIG TGRIYGDNIA IAATRLDNQD
801 ENGTTGAIAA RENLNLGIGQ LNNRENSLIY SGNDMAVGGG LDTNGQATGK
851 AQRINHAGAT IEAAGKMLRG VEKLHNTNEH LKTQLVETGR EHIVDYEAFG
901 RHELLREBGTQ HELGWSVYND ESDHLRTPDG AAHENWHKYD YEKVTQKTQV
951 TQTAPAKIIS GNDLTIDGKE VFNTDSQIIA GGNLIVQTEK DGLHNEQTFG
1001 EKKVFSENGK LHSYWREKHK GRDSTGHSEQ NYTLPEBITR NISLGSFAYE
1051 SHRKALSHHA PSQGTLPQS NGISLPYTSN SFTPLPSSSL YIINPVNKGY
1101 LVETDPRFAN YRQWLGSYDM LDSLKLDPNN LHKRLGDGYE EORLINEQIA
1151 ELTGHRRLDG YONDEEQFKA LMDNGATAAR SMNLSVGIAL SAEQVAQLTS
1201 DIVWLQKEV KLPDGGTQTV LVPQVYVRVK NGDIDKGKAL LSGSNTQINV
1251 SGSLKNSGTI AGRNALIINT DTLDNIGGRI HAQSAVTAT QDINNIGGML
1301 SAEQTLNNA GNNINSQSTT ASSQNTQSS TYLDRMAGIY ITGKEKGVLA
1351 AQAGKDINII AQQISNQSEQ QQTRLQAGRD INLDTVQTSK HQATHFDADN
1401 HVIRGSTNEV GSSIQTGQDV TLLSGNNLNA KAAEVSSANG TLAVSAKNDI
1451 NISAGINTTH VDDASKHTGR SGGGNKLVIT DKAQSHHETA QSSTFEGKQV
1501 VLQAGNDANI LGSNVISDNG TQIQAGNHVR IGTQTQSQS ETYHQTQKSG

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855

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1551 LMSAGIGFTI GSKTNTQENQ SQSNEHTGST VGS�KGDTTI VAGKHYEQIG
1601 STVSSPEGNN TIYAQSIDIQ AAHNKLNSNT TQTYEQKGLT VAFSSPVTDL
1651 AQQAIIVAAQS SKQVQSKND RVNAMAANA GWQAYQTGKS AQNLANGTTN
1701 AKQVSIISITY GEOQNRCTTQ VQANQAQASQ IQAGGKTTLI ATGAAEQSNI
1751 NIAGSDVAGK AGTILIADND ITIQSAEQSN TERGQNKASG WNAGAAVSFG
1801 QGGWSLGVTA GGNVKGGYGN GDSITHRHS IGDKGSQTLI QSGGDTTIKG
1851 AQVRGKGVQV NAKNLSIQSV QDRETYQSKQ QNASAQVTVG YGFSAGGDYS
1901 QSKIRADHVS VTEQSGIYAG EDGYQIKVGN HTDLKGIIIT STQSAEDKKG
1951 NRPQTATLTH SDIKNHSQYK GESFGLGASA SISGKTGQAG AQNKPNKHL
2001 TSVADKNSAS SSVGYGSDSD SQSSITKSGI NTRNIQITDE AAQIRLTGKT
2051 AAQTKADIDT NVTTDTAERH SGSLKNTFNK EAVQSELDLQ RTVSQDFSKN
2101 VQQANTEINQ HLDKLKADKE AAETAAAEAL ANGDMETAKR KAHEAQDAAA
2151 KADNWQQKV ILNMLASGLA APTQSGAGIA AATASPAVSY AIGQHFKDLA
2201 GQANANGKLT SQETAHVLAH AVLGAAVAAG GDNNALAGAL SAGGSEAAAP
2251 YISKWLYGKE KGSDLTAEK ETVTAITNVL GTATGAAVGN SATDAAQGS
2301 NAQSAVENND TVEQVKFALR HPRIAIAGS VHKDPGSTLE PNISTIASTF
2351 QLNLFNPSEF GGEGGVGNF RHVLWQATIT REFGKDIAVK VGNSHESGEK
2401 INYSIRNLS LDKADEMIDQ LNNEIGREIA LNTNRLNKE LVGLILETYK
2451 NNGFYQAERN SNGNYDVVRK RLSEKDYQNT SNILIHLDNT GAGFKIQRR
2501 KQIRAQISAR QWRR*

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Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 563 shows 79.1% identity over a 2316 aa overlap with a predicted ORF (ORF 563.ng) from *N. gonorrhoeae*:

m563/g563

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              10      20      30      40      50
g563.pep      MNKTLYRVIFNRKRGAVVAVAETTKREGKSCADSGSGSVYVKSVSFIPTH-----SKAFC
              |||||
m563.pep      MNKTLYRVIFNRKRGAVVAVAETTKREGKSCADSDSGSAHVKSVPFGTTHAPVCRSNIFS
              10      20      30      40      50      60

              60      70      80      90      100     110
g563.pep      FSALGFSLCLALGTVNIAFADGIIITDKAAPKTQQTILQTNNGIIPQVNIQTPTSAGVSVN
              |||||
m563.pep      FSLGFSCLCLAVGTANIAFADGIIADKAAPKTQQTILQTNNGIIPQVNIQTPTSAGVSVN
              70      80      90      100     110     120

              120     130     140     150     160     170
g563.pep      QYAQFDVGNRGAILNNSRSNTQTQLGGWIQGNPWLTRGEARVVVNQINSSHPSQLNGYIE
              |||||
m563.pep      QYAQFDVGNRGAILNNSRSNTQTQLGGWIQGNPWLARGEARVVVNQINSSHSSQMNGYIE
              130     140     150     160     170     180

              180     190     200     210     220     230
g563.pep      VGGRRAEVVIANPAGIAVNGGGFINASRATLTGQPQYQAGDFSGFKIROGNVIAHGHL
              |||||
m563.pep      VGGRRAEVVIANPAGIAVNGGGFINASRATLTGQPQYQAGDLSGFKIROGNVVIAGHGL
              190     200     210     220     230     240

              240
g563.pep      DARDTDFTRIL-----
              |||||
m563.pep      DARDTDFTRILSYHSKIDAPVWGQDVRVVAGQNDVVATGNAHSPILNAAANTSNNTANN
              250     260     270     280     290     300

              250     260     270     280     290
g563.pep      -----LYANKITLISTAEQAGIRNQQLFASSGNVAIDANGRLVNSGTM
              :|||
m563.pep      GTHIPLFAIDTGKLGMYANKITLISTAEQAGIRNQQLFASSGNVAIDANGRLVNSGTM
              310     320     330     340     350     360

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	300	310	320	330	340
g563 . pep	AAANVQDMNNTAEHKVNIRSQAFENSGTAVSQQGTQIHSQSIQNTGKLLSAGT-----				
m563 . pep	AAANAKDNTAEHKVNIRSQGVENSGTAVSQQGTQIHSQSIQNTGTLSSGEILIHNSG				
	370	380	390	400	410
	420				
g563 . pep	-----				
m563 . pep	SLKNETSGTIEAARLAIDTDTLNNQKLSQTGSQKLHIDAQGMNDRGRMGLQDTAPTAS				
	430	440	450	460	470
	480				
g563 . pep	-----				
m563 . pep	NGSSNQTGNSYNASFHSSTTTPTTATGTGTATVSISNITAPTFADGTIRTHGALDNSGSI				
	490	500	510	520	530
	540				
g563 . pep	-----				
m563 . pep	IANGQTDVSAQQGLNNAQQIDIHQLNAKGSFAFDNHNGTIISDAVHIQAGSLNNQNGNITT				
	550	560	570	580	590
	600				
g563 . pep	-----				
m563 . pep	RQQLEIETDQLDNAHGKLLSAEIALDLAVSGSLNNQNGEIATNQQLIIHDGQQSTAVIDNT				
	610	620	630	640	650
	660				
g563 . pep	-----				
m563 . pep	NGTIQSGRDVAIQAKSLNNGTLAADNKLDIALQDDFYVERNI VAGNELSLSTRGSLKNS				
	670	680	690	700	710
	720				
g563 . pep	-----				
m563 . pep	HTLQAGKRIRIKANNLDNAVQGNIQSGGTTDIGTQHNLNTRGLIDGQQTQIQAGQMNNIG				
	730	740	750	760	770
	780				
g563 . pep	-----				
m563 . pep	TGRIYGDNIAIAATRLDNQDENGTAAGAAIARENLNLGIEQLNNRENSLIYSGNDMAVGGA				
	790	800	810	820	830
	840				
g563 . pep	-----				
m563 . pep	LDTNDQATGKAQRIHNAGATIEAAGKMRLGVEKLHNTNEHLKTQLVETGRERIVDYEAFG				
	850	860	870	880	890
	900				
g563 . pep	-----				
m563 . pep	RHELLREGTQHELGSVYNDES DHLRTPDGAHENVHKKYDYEKVTQKTQVQTAPAKIIS				
	910	920	930	940	950
	960				
g563 . pep	-----				
m563 . pep	RHELLREGTQHELGSVYNDES DHLRTPDGAHENVHKKYDYEKVTQKTQVQTAPAKIIS				
	970	980	990	1000	1010
	1020				

858

m563 . pep	LMSAGIGFTIGSKTNTQENQSQSNEHTGSTVGS LKGD TTI VAGKH YE QIGSTVSSPEGNN
	1560 1570 1580 1590 1600 1610
g563 . pep	1350 1360 1370 1380 1390 1400
	LISTQSM DIGAAQNQLNSKTTQT YE QKGLTVGIQFARYRFGTTSDCRSTQSSKQVGSKN
m563 . pep	TIYAQSIDIQA AHNKLSNTTQT YE QKGLTVAFSSPVTDLAQAQ - IAVAQSSKQVGSKN
	1620 1630 1640 1650 1660
g563 . pep	1410 1420 1430 1440 1450 1460
	DRVNAMA AANAGWQAYQTGKGAQNLANGTTNAKQVSI SITYGEQQNRQTQVQANQAQAS
m563 . pep	DRVNAMA AANAGWQAYQTGKSAQNLANGTTNAKQVSI SITYGEQQNRQTQVQANQAQAS
	1670 1680 1690 1700 1710 1720
g563 . pep	1470 1480 1490 1500 1510 1520
	QIQAGGKTTLYCRRCEQSNINITGSGVSGRAGTGLIADKQIHLQSAEQSNTERSQNKSA
m563 . pep	QIQAGGKTTLIATGA AEQSNINIAGSDVAGKAGTIL IADNDITLQSAEQSNTERGQNKSA
	1730 1740 1750 1760 1770 1780
g563 . pep	1530 1540 1550 1560 1570 1580
	GWNAGAAVSFGQGGWSLGVAAAGGNVKG YGYGDSVTHRHSHIGDKGSQTLIQSGGDTI IK
m563 . pep	GWNAGAAVSFGQGGWSLGVTAGGNVKG YGNGDSITHRHSHIGDKGSQTLIQSGGDTTIK
	1790 1800 1810 1820 1830 1840
g563 . pep	1590 1600 1610 1620 1630 1640
	GAQVRGKGVQVNAKNLSIQSVQDRETYQSKQONAGA QVTVGYGFSASGDYSQSKIRADHA
m563 . pep	GAQVRGKGVQVNAKNLSIQSVQDRETYQSKQONASA QVTVGYGFSAGGDYSQSKIRADHV
	1850 1860 1870 1880 1890 1900
g563 . pep	1650 1660 1670 1680 1690 1700
	SVTEQSGIYAGEDGYQIKVGNHTGLKGGIITSSQSAKDKGKNRFSTGTLAGSDIQNYSQY
m563 . pep	SVTEQSGIYAGEDGYQIKVGNHTDLKGGIITSTQSAEDKGKKNRFQTATLTHSDIKNHSQY
	1910 1920 1930 1940 1950 1960
g563 . pep	1710 1720 1730 1740 1750 1760
	EGKSFGLGASVAVSGKTLGQGAQKNKPQDKHLTSIADKN GASSSVGYGSDSDSQSSITKSG
m563 . pep	KGESFGLGASASISGKTLGQGAQKNKPQDKHLTSVADKNSASSSVGYGSDSDSQSSITKSG
	1970 1980 1990 2000 2010 2020
g563 . pep	1770 1780 1790 1800 1810 1820
	INTPKNIQITDEAAQIRLTGKIAAQTKADIDTNVTTDTAERHSGSLKNI FDKDRVQSELD
m563 . pep	INT-RNIQITDEAAQIRLTGKTAAQTKADIDTNVTTDTAERHSGSLKNTFNKEAVQSELD
	2030 2040 2050 2060 2070 2080
g563 . pep	1830 1840 1850 1860 1870 1880
	LQRTVSQDFSKNVQQTNT EINHLDK LKADKEAAETA AAEALANGDMETAKRKAHEAQDA
m563 . pep	LQRTVSQDFSKNVQQA NTEINHLDK LKADKEAAETA AAEALANGDMETAKRKAHEAQDA
	2090 2100 2110 2120 2130 2140
g563 . pep	1890 1900 1910 1920 1930 1940
	AAKADNWQOGKVILNMLASGLA EPTQSGAGIAAATASPDVSYAIGQHFKDLAQNWANGKL
m563 . pep	AAKADNWQOGKVILNMLASGLA EPTQSGAGIAAATASPAVSYAIGQHFKDLAQNWANGKL
	2150 2160 2170 2180 2190 2200

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	1950	1960	1970	1980	1990	2000
g563 . pep	TASQETAHVLAHAVLGA AVAAAXGN NAPAGALGAGGSEAAAF I I GKWLYGKG DGGSLNAE					
	: : : : : : :					
m563 . pep	TASQETAHVLAHAVLGA AVAAVGDNNALAGALSAGGSEAAAFYISKWLYGKEKGSDELTA E					
	2210	2220	2230	2240	2250	2260

	2010	2020	2030	2040	2049	
g563 . pep	EKETVSAITRMLGTAAGAAEGNSSADAVWGCFTQASDFASSFSYPINMX					
	: : : : : : :					
m563 . pep	EKETVTAITNVLTATGA AVGNSATDAAQGSLSNAQSAVENNLTVEQVKFALRHPRI AIAI					
	2270	2280	2290	2300	2310	2320

m563 . pep	GSVHKDPGSTLEPNISTIASTFQLNLFNPSEFGGEGGVGNAFRHVLWQATITREFGKDIA					
	2330	2340	2350	2360	2370	2380

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1669>:

```

m564 . seq
1  ATGAACCGCA CCCTGTACAA AGTTGTATTT AACAAACATC GAAACTGCAT
51  GATAGCCGTT GCTGAAAATG CCAAACGCGA GGGCAAAAAC ACAGCCGACA
101 CCCAAGCTGT AGGTATTTTG CCAAATGATA TTGCGGGCTT TCGCGGTTT
151 ATCCATTCTA TCTCTGTAT CTCTCTCTCC CTTTCATTAC TGCTCGGTTC
201 TGCCCTTATC CTGACTTCTT CTCTCTGTAC TGCCCAAGGT ATCGTTGCCG
251 ACAAAATCCG ACCTGCACAG CAACAGCCTA CCATCCTGCA AACAGGTAAC
301 GGCATACCGC AAGTCAATAT TCAAACCCCT ACTTCGGCAG GGGTTTCTGT
351 TAATCAATAC GCCCAGTTTG ATGTGGGTAA TCGCGGGGCG ATTTTAAACA
401 ACAGTCGCAG CAACACCCAA ACACAGCTAG GCGGTTGGAT TCAAGGCAAT
451 CCTTGGTTGG CAAGGGGCGA AGCAGCTGTG GTTGTAACC AAATCAACAG
501 CAGCCATTCT TCACAACTGA ATGGCTATAT TGAAGTGGG GACGACGTG
551 CAGAAATCGT TATTGCCAAT CCGGCAGGGA TTGCAGTCAA TGGTGGTGGT
601 TTTATCAATG CTTCCCGTGC CACTTTGACG ACAGCCCAAC CGCAATATCA
651 AGCAGGAGAC CTTAGCGGCT TTAAGATAAG GCAAGGCAAT GTTGTAATCG
701 CCGGACACGG TTTGGATGCA CGTGATACCG ATTACACAG TATTCTCAGT
751 TATCATTCCA AAATTGATGC ACCCGTATGG GGACAAGATG TTCGTGTCGT
801 CGCGGGACAA AACGATGTGG CCGCAACAGG TGATGCACAT TCGCCTATTC
851 TCAATAATGC TGCTGCCAAT ACGTCAAACA ATACAGCCAA CAACGGCACA
901 CATATCCCTT TATTGGCAT TGATACAGGC AAATTAGGAG GTATGTATGC
951 CAACAAAATC ACCTTGATCA GTACGGTCGA GCAAGCAGGC ATTCGTAATC
1001 AAGGGCAATG GTTGCCTCA GCCGGCAATG TGGCAGTGAA TGCTGAGGGT
1051 AAATGGTCA ACACGGGCAT GATTGCAGCG ACGGGAGAAA ATCATGCGGT
1101 TTCACTTCAT GCCCGCAATG TTCATAATAG CGGTACGGTT GCCTCACAGG
1151 ATGATGCCAA TATTACAGC CAGACGCTGG ACAATTCAGG TACGGTCTTA
1201 TCCTCAGGTC GATTGACTGT TCGTAATTTA GGCCGTCTGA AAAACCAAAA
1251 CAACGGTACG ATCCAGGCTG CCCGCTAGA TATGTCAACA GGTGGTTTGG
1301 ATAACACAGG TAATATTACT CAAACAGGTT CACAAGCATT GGATTTGGTA
1351 TCTGCCGGCA AATTGATATA CAGTGGCAAG ATTGGTGTA GTGACGTTCC
1401 ACAGACCGGT TTGAATCCCA ATCCATCAGT CATACCACAG ATTCCGAGTA
1451 CTGCAACAGG TTCAGGCAGC AGCACTGTCT CGGTATCTAA GCCTGGTTCA
1501 AACAAATCCG TTTCACCTAC AGCACCTGCA AAAAACTACG CCGTAGGACG
1551 CATTCAAACA ACAGGAGCAT TTGACAATGC AGGATCAATT AATGCGGGTG
1601 GGCAAATTGA CATTGCCGCC CAAAACGGTT TGGGAAATTC GGGTAGTCTG
1651 AATGCGGCTA AACTACGAGT ATCAGGCGAT TCATTTAACA ATACGGTAAA
1701 AGGCAAATC CAGGCACAGC ATCTGGCTGT TAACACTCAA ACTGCTAAAA
1751 ACAGCGGTCA CTTATTAACT CAAACCGGCA AGATTGATA CCGTGAAC TG
1801 CATAATGCCG GAGAAATTGC CGCCAACAAT CTGACACTCA TTCATTGGG
1851 CCGCTTGAGC AATGATAAAA AAGGCAATAT TCGAGCTGCA CATTTACAGC
1901 TTGATACCGC CGGTTTACAT AATGCAGGTA ACATTCTTGC CGATAGTGGA
1951 ACCGTTACCA CCAAGAATA TCTTCGCAAT ACAGGAAAAG TTTCTGTTGC
2001 ACGACTGAAT ACCGAAGGTC AGACTCTAGA TAATACGCGC GGACGTATAG
2051 AGGCTGAAAC GGTTAACATC CAAAGTCAGC AACTGACTAA CCAAAGCGGC
2101 CATATTACTG CTACCGAACA ACTGACTATC AATAGTCGAA ATGTAGACAA
2151 CCAAAACGGC AAACCTCTAT CTGCAAAACA AGCACAATTA GCTGTTTCAG
2201 ACGGCCTATA CAACCAACAT GGTGAATTG CCACCAACCG GCAGTTGTCT

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2251 ATTCACGATA AAAATCAAAA CACTTTGGCG TTAACAATG CGGATGGCAC
 2301 GATTCAATCT GCCGTAATG TATCGCTACA AGCCAAATCA CTCGCCAACA
 2351 ATGGCACATT AACAGCCGGT AACAACTGG ATATTGCTTT GACGGACGAT
 2401 TTCGTGCTAG AGCGCGACCT CACTGCAGGC AAACAATTAA ATCTAAGCAT
 2451 AAAAGGCCGT CTGAAAAATA CCCATACCCT ACAAGCAGGC CATACGCTCA
 2501 AACTCAATGC CGGCAATATA GATAACCAAG TTACAGGCAA AATTATTGGT
 2551 GGAGAACAAA CGGACATCAC ATCCGAACAG CATGTTGACA ACAGGGGCTT
 2601 GATCAACAGC GACGGTTTGA CCCACATCGG TGCAGGTCAA ACCCTGACCA
 2651 ACACCGGGAC AGGCAAAATC TATGGCAACC ATATTGCCCT GGACGCGCAA
 2701 ATACTGCTTA ACCGGGAAGA AACGACGGAA GGCAGTACCA AAGCGGGGGC
 2751 AATAGCTGCA AGGAAACGTT TGGATATTGG AGCGAAAGAG ATTCTAATCC
 2801 AAGAAGGTGC CCTACTATCC AGCGAAGTGA TTTTGGCGT AgGTAATCGA
 2851 CTGGATGAAC AACATCATGC GGCAGGCATG GCCGATACCT TTGTTAATGG
 2901 CAGTGCCGGT TTGGAAGTAC AAGGTGATGC ATTGATGTCC GTTCGGAATA
 2951 TGCAGAATAT CAATAATCAC TTTAAACAG AGACATACTT AGCCAAAGCG
 3001 GAAAAGCAAG TCCGCGACTA CACCGTACTG GGGCAAAATA CCTACTATCA
 3051 GGCGGGAAAA GACGGTTTAT TCGACAACTC GCAAGGACAA AAAGACCAAA
 3101 CTACTGCTAC GTTCCATTTA AAAAATGGTT CTCGTATTGA GGCCAACCAA
 3151 TGGCATGTCC GAGACTACCA CATCGAGACT TATAAAGAAC GCATCATCGA
 3201 AAACCGGCCG GCACACATTA CTGTGGGCGG TGATTGACT GCCTCAGGTC
 3251 AAAATTGGCT GAACAAAGAC AGCCGGATTG TAGTAGGCGG GCGTATTATC
 3301 ACTGATGATT TAAACCAGAA AGAAATTACC AATCAAAGTA CAACAGGCAA
 3351 AGGTGCGACA GATGCTGTCT GCACACAGTG GGATTCACTT ACAAAAAAAG
 3401 GATGGTACAG CGGTAGAAAA AGACAACGCC GTACTGAAAG AAACCATACT
 3451 CCTTACCATG ATACCCAATC ATTTACCAC GACTTCGACA CGCTGTATC
 3501 CGTCATCCAA CAGAATGCCG CCTCCCTTC CTTTCAACCC GCCGCATCTG
 3551 CAATCAAATC GATTGACGGA GTATCCACGG CAGCCGCAA TGGTCAGCGC
 3601 ATCCATACCG GTAATGTGGT CTCGTTAAAT AACGCTACTG TTAATCTGCC
 3651 TAACAGCAGC CTCTATACCA CCCATCCTGA CAATAAAGG TGGTTGGTTG
 3701 AAACCGATCC TCAATTTGCA GACTACCGCC GCTGGTTGGG CAGCGACTAC
 3751 ATGTTGCAAC AACTGCAATT GGACACCAAT CATCTACACA AACGGCTTGG
 3801 CGACGGCTAC TACGAACAAA AACTTGTAA TGAACAAATC CATCAGTTAA
 3851 CAGCCTACCG CCGACTCGAC GGTACAGGA GTGATGAAGA ACAATTCAAA
 3901 GCTCTGATGG ACAACGGCCT TACTGCTGCC AAAACATTCC GTCTCACCCC
 3951 AGGTATCGCC TTGAGTGCAG AGCAAGTTGC CCGCTTAATC TCAGATATCG
 4001 TTTGGATGGA AAATCAAACC GTCAACCTGT CTGACGGTTC GACTCAAACC
 4051 GTACTGGTTC CTAAAGTCTA TGCCCTGGCG CGCAAAGGTG ATCTCAATAC
 4101 CTCGGGTGGC CTGATTAGTG CCGAACAAGT CTTACTTAAA CTGCAAAACG
 4151 GCAACCTGAC TAACAGCGGT ACCATTGCGG GCGCAGAGGC CGTACTCATC
 4201 CAGGCACGGA ATATTAACAG CAACGGTAAC ATTCAAGCCG ACCAAATCGG
 4251 CTTAAAGCT GAAAAAGTA TCAATATCGA CGGCGGGCAG GTACAAGCAG
 4301 GCGACTGCT GACTGCCCAA GCGCAAAATA TCAACCTTAA CGGTACAACC
 4351 CAACTTCCG GTAATGAACG TAACGGCAAT ACCGCCATCG ATCGTATGGC
 4401 CGGCATTAAC GTGTCGGGAA GCCATACCTGA ACAAGTAGAT AACAGAACTT
 4451 CAGACGGCAT CCTATCCCTG CATGCCAGCA ACGATATCAA CCTCAATGCG
 4501 GCCACCGTCT CTAACCAAGT TAAAGACGGC ACTACCCAAA TTACCGCCGG
 4551 CAATAATCTC AACCTCGGCA CCATCCGTAC CGAACATCGC GAAGCCTATG
 4601 GTACATTAGA TGACGAGAAC CATCGCCATG TCCGCCAAG TACCGAAGTC
 4651 GGCAGCAGTA TCCGACGCA AAACGGCGCA CTGCTTAGAG CCGGTAACGA
 4701 CTTAAAAATC CGCCAAGCG AACTGGAGGC CGAAGAAGGC AAAACCGTCC
 4751 TTGCCGAGG ACGTGATGTC ACTATCAGCG AAGGACGCCA AATAACCGAA
 4801 CTGGATACCT CGGTAAGCGG AAAAAGCAAA GGCATCCTTT CCAGTACCAA
 4851 AACACACGAC CGCTACCGCT TCAGTCATGA TGAAGCAGTC GGCAGCAACA
 4901 TCGGCGGCGG CAAATGATT GTTGCAGCGG GGCAGGATAT CAATGTACGC
 4951 GGCAGCAACC TTATTTCTGA TAAGGGCATT GTTTTAAAG CAGGACACGA
 5001 CATCGATATT TCTACTGCCC ATAATCGCTA TACCGGCAAT GAATACCAG
 5051 AGAGCAAAAA ATCAGGCGTC ATGGGTACTG GCGGATTGGG CTTTACTATC
 5101 GGTAAACGGA AACTACCGA TGACACTGAT CGTACCAATA TTGTCCATAC
 5151 AGTCAGCATT ATAGGCAGCC TGAATGGAGA CACCGTTACA GTTGCAAGAA
 5201 ACCGCTACCG ACAACCGGC AGTACCGTCT CCAGCCCCGA GGGGCGCAAT
 5251 ACCGTCACAG CCAAAAGCAT AGATGTAGAG TTCGCAACA ACCGGTATGC
 5301 CACTGACTAC GCCCATACCC AGGAACAAAA AGGCCTTACC GTCCGCTCA
 5351 ATGTCCCGGT GTCCAAAGCT GCACAAACT TCATACAAGC AGCCCAAAAT
 5401 GTGGGCAAAA GTAAAAATA ACGCGTTAAT GCCATGGCTG CAGCCAATGC
 5451 TGCATGGCAG AGTTATCAAG CAACCCAACA AATGCAACAA TTTGCTCCAA
 5501 GCAGCAGTGC GGGACAAGGT CAAAACAACA ATCAAAGCCC CAGTATCAGT

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5551 GTGTCCATTA CCTACGGCGA ACAGAAAAGT CGTAACGAGC AAAAAAGACA
5601 TTACACCGAA GCGGCAGCAA GTCAAATTAT CGGCAAAGGG CAAACCACAC
5651 TTGCGGCAAC AGGAAGTGGG GAGCAGTCCA ATATCAATAT TACAGGTTCC
5701 GATGTCATCG GCCATGCAGG TACTGCCCTC ATTGCCGACA ACCATATCAG
5751 ACTCCAATCT GCCAAACAGG ACGGCAGCGA GCAAAGCAAA AACAAAAGCA
5801 GTGGTTGGAA TGCAGGCGTA GCCGTCAAAA TAGGCAACGG CATCAGGTTT
5851 GGAATTACCG CCGGAGGAAA TATCGGTAAA GGTAAAGAGC AAGGGGGAAG
5901 TACTACCCAC CGCCACACCC ATGTCGGCAG CACAACCGGC AAAACTACCA
5951 TCCGAAGCGG CGGGGATACC ACCCTCAAAG GTGTGCAGCT CATCGGCAAA
6001 GGCATACAGG CAGATACGCG CAACCTGCAT ATAGAAAGTG TTCAAGATAC
6051 TGAAACCTAT CAGAGCAAAC AGCAAAACGG CAATGTCCAA GTTACTGTCTG
6101 GTTACGGATT CAGTGCAAGC GGCAGTTACC GCCAAAGCAA AGTCAAAGCA
6151 GACCATGCCT CCGTAACCGG GCAAAGCGGT ATTTATGCCG GAGAAGACGG
6201 CTATCAAATC AAAGTCAGAG ACAACACAGA CCTCAAGGGC GGTATCATCA
6251 CGTCTAGCCA AAGCGCAGAA GATAAGGGCA AAAACCTTTT TCAGACGGCC
6301 ACCCTTACTG CCAGCGACAT TCAAAACCAAC AGCCGCTACG AAGGCAGAAG
6351 CTTCCGCATA GCGGCGAGTT TCGACCTGAA CGCGGCTGG GACGGCACGG
6401 TTACCGACAA ACAAGGCAGG CCTACCGACA GGATAAGCCC GGCAGCCGGC
6451 TACGGCAGCG ACGGAGACAG CAAAACAGC ACCACCCGCA GCGGCGTCAA
6501 CACCCACAAC ATACACATCA CCGACGAAGC GGGACAACCT GCCCGAACAG
6551 GCAGGACTGC AAAAGAAACC GAAGCGCGTA TCTACACCG CATCGACACC
6601 GAAACTGCGG ATCAACACTC AGGCCATCTG AAAACAGCT TCGACAAAGA
6651 CGCGGTGCGC AAAGAGATCA ACCTGCAAAG GGAAGTAACG AAGGAGTTCG
6701 GCAGAAACGC CGCCCAAGCC GTAGCGGCGG TTGCCGACAA ACTCGGCAAT
6751 ACCCAAAGTT ACGAACGGTA TCAGGAAGCC CGAACCTGC TGGAGGCCGA
6801 AAGCGCAAAAC ACGGACAGCG AAGCCGAAAA AGCCGCTTC CGCGCATCCC
6851 TCGGCCAAGT AAACGCCTAT CTTGCCGAAA ACCAAAGCCG CTACGACACC
6901 TGGAAAGAAG GCGGCATAGG CAGGAGCATA CTGCACGGGG CGGCAGGCGG
6951 ACTGACGACC GGCAGCCTCG GCGGCATACT GGCCGGCGGC GGCACCTCCC
7001 TTGCCGCACC GTATTGGAC AAAGCGGCGG AAAACCTCG TCCGGCGGGC
7051 AAAGCGGCGG TCAACGCACT GGGCGGTGCG GCCATCGGCT ATGCAACTGG
7101 TGGTAGTGGT GGTGCTGTGG TGGGTGCGAA TGTAAGATTGG AACAAATAGGC
7151 AGCTGCATCC GAAAGAAATG GCGTTGGCCG ACAAATATGC CGAAGCCCTC
7201 AAGCGCGAAG TTGAAAAACG CGAAGGCAGA AAATCAGCA GCCAAGAAGC
7251 GGCAATGAGA ATCCGCAGGC AGATACTGCG TTGGGTGGAC AAAGGTTCCC
7301 AAGACGGCTA TACCGACCAA AGCGTCATAT CCCTTATCGG AATGAAAGGC
7351 GAAGACAAAG CCTTGGGTTA TACTTGGGAC TACCGCGACT ACGGCGCAAG
7401 AAATCCGCAA ACCTACAACG ATCCGAAGCT GTTTGAGGAA TACCGCCGAC
7451 AGGACAAACC CGAATACCGC AACCTGACCT GGCTGCACAG CGGGACGAAA
7501 GACACCAAAA TCAGGCAGGG AGAGCGGAAA AACGAAGAGT TTGCACTGAA
7551 CGTTGCCGAA GGAATGACGA GCCTTGTCAA CCCCAATCCG AGGATAAAAG
7601 TCCCGATTCT TGCAGGCATC CGCAACCTGA AAAACATCAA GCCGACAGTT
7651 ACCGCGACGG ATCCCTTAT TGGCGGTGCG GGAATATACC GTATCCCTGC
7701 AAACGGCAAT GTTCCGAAG GGGACAGGAT TCCGGATACG GCATTGGCTA
7751 GCAAGGGAAT CAAACATAAA GATCGTAAAG ATCAACTGGA GAAAAAATAA

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This corresponds to the amino acid sequence <SEQ ID 1670; ORF 564>:

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m564.pep
1  MNRTLYKVVF NKHRNCMIIV AENAKREGKN TADTQAVGIL PNDIAGFAGF
51  IHSISVISFS LSLLLGSALI LTSSSATAQG IVADKSAPAQ QPTILQTGN
101 GIPQVNIQTP TSAGVSVNQY AQFDVGNRGA ILNNSRSNTQ TQLGGWIQGN
151 PWLARGEARV VVNQINSSHS SQLNGYIEVG GRRAEVVIAN PAGIAVNGGG
201 FINASRATLT TAQPQYQAGD LSGFKIRQGN VVIAGHGLDA RDTDYTRILS
251 YHSKIDAPVW GQDVRVVAGQ NDVAATGDAH SPILNNAAN TSNNTANNGT
301 HIPLFAIDTG KLGGMYANKI TLISTVEQAG IRNQGWFAF AGNVAVNAEG
351 KLVNTGMIAA TGENHAVSLH ARNVHNSGTV ASQDDANIHS QTLNDSGTVL
401 SSGRLTVRNL GRLKNQNNGT IQAARLDMST GGLDNTGNIT QTGSQALDLV
451 SAGKFDNSGK IGVSDVPQTG LNPNSVIPQ IPSTATGSGS STVSVSKPGS
501 NNPVSPTAPA KNYAVGRIQT TGAFDNAGSI NAGGQIDIAA QNGLGNSGSL
551 NAAKLRVSCD SFNNTVKKGL QAHDLAVENTQ TAKNSGHLT QTGKIDNREL
601 HNAGEIAANN LTLIHSGRLS NDKKGNIRAA HLQLDTAGLH NAGNILDGSG
651 TVTTKNNLRN TGKVSVARLN TEGQTLNTR GRIEAEVNI QSQQLTNQSG
701 HITATEQLTI NSRNVDNQNG KLLSANQAQL AVSDGLYNQH GEIATNRQLS
751 IHDKNQNTLA LNNADGTIQS AGNVSLQAKS LANNGTLTAG NKLDIALTDD
801 FVVERDLTAG KQLNLSIKGR LKNTHTLQAG HTLKLNAGNI DNQVTGKIIG
851 GEQTDITSEQ HVDNRGLINS DGLTHIGAGQ TLTNTGTGKI YGNHIALDAQ

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901 ILLNREETTE GSTKAGAI AA RKRLDIGAKE IHNQEGALLS SEGIFAVGNR
951 LDEQHHAAAGM ADTFVNGSAG LEVQGDALMS VRNMQNNHNN FKTETYLAKA
1001 EKQVRDYTVL GQNTYYQAGK DGLFDNSQGG KDQTTATFHL KNGSRIEANC
1051 WHVRDYHIET YKERIENRP AHITVGGDLT ASGQNWLNKD SRIVVGGRII
1101 TDDLNQKEIT NQSTTGKGR T DAVGTQWDSV TTKGWYSGRK RQRRTERNHT
1151 PYHDTQLFTH DFDTPVSVIQ QNAASPSFQP AASAIKLIDG VSTAANGQR
1201 IHTGNVSLN NATVTLPNSS LYTTHPDNKG WLVDTPQFA DYRRWLGSDY
1251 MLQQLQLDTN HLHKLRLGDGY YEQLVNEQI HQLTGYRRLD GYRSDEEQFK
1301 ALMDNGLTAA KTFGLTPGIA LSAEQVARLT SDIVWMENQT VTLSDGSTQT
1351 VLVPKVYALA RKGDLNTSGG LISAEQVLLK LQNGNLNLSG TIAGRQAVLI
1401 QARNINSNGN IQADQIGLKA EKSINIDGGQ VQAGRLTAQ AQNINLNGTT
1451 QTSNGERNGN TAI DRMAGIN VVGSHTEQVD NRTSDGILSL HASNDINLNA
1501 ATVSNOVKDG TTQITAGNNL NLGTIRTEHR EAYGTLEDEN HRHVRQSTEV
1551 GSSIRTQNGA LLRAGNDLKI RQGELEAEEG KTVLAAGRDV TISEGRQITE
1601 LDTSVSGKSK GILSSTKTHD RYRFSHDEAV GSNIGGGKMI VAAGQDINVR
1651 GSNLISDKGI VLKAGHDIDI STAHNRYTGN EYHESKKSGV MGTGGLGFTI
1701 GNRKTTDDTD RTNIVHTGSI IGS LN GDTVT VAGNRYRQTG STVSSPEGRN
1751 TVTAKSIDVE FANNRYATDY AHTQEQKGLT VALNVPVQA AQNFIAAQN
1801 VKSKNKRNV AMAAANA AWQ SYQATQQMQQ FAPSSSAGQG QNNNQSPSIS
1851 VSITYGEQKS RNEQKRHYTE AAASQIIGKG QTTLAATGSG EQSNINITGS
1901 DVIGHAGTAL IADNHIRLQS AKQDQSEQSK NKSSGWNAGV AVKIGNGIRF
1951 GITAGGNIGK GKEQGGSTTH RHTHVGSTTG KTTIRSGGDT TLKGVQLIGK
2001 GIQADTRNLH IESVQDTETY QSKQQNGNVQ VTVGYGFSAS GSYRQSKVKA
2051 CHASVTQSG IYAGEDGYQI KVRDNTDLKG GIITSSQSAE DKGKNLFQTA
2101 TLTASDIQNH SRYEGRSFGI GGSFDLNGGW DGTVTDKQGR PTDRISPAAG
2151 YGSDGDSKNS TTRSGVNTN IHITDEACQL ARTCRTAKET EARIYTGIDT
2201 ETADQHSGLH KNSFDKDAVA KEINLQREVT KEFGRNAAQA VAAVADKLGN
2251 TQSYERYQEA RTLLEAELQN TDSEAEKAAF RASLGQVNAY LAENQSRYDT
2301 WKEGGIGRSI LHGAAGGLT GSLGGILAGG GTSLAAPYLD KAAENLGPAG
2351 KAAVNALGGA AIGYATGGSG GAVVGANVDW NNRQLHPKEM ALADKYAEAL
2401 KREVEKREGR KISSQEAAMR IRRQILRWVD KGSQDGYTDQ SVISLIGMKG
2451 EDKALGYTWD YRDYGARNPQ TYNDPKLFEE YRRQDKPEYR NLTWLHSGTK
2501 DTKIROGERK NEEFALNVAE GLTSLVNPNP RIKVPILAGI RNLKNIKPTV
2551 TGSDPLLAGA GNIRIPANGN VAKGDRIPDT ALASKGIKHK DRKDQLEKK*

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Computer analysis of this amino acid sequence gave the following results:

Homology with fha

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m564/fha
ID FHAB BORPE STANDARD; PRT; 3591 AA.
AC P12255;
DT 01-OCT-1989 (REL. 12, CREATED)
DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE FILAMENTOUS HEMAGGLUTININ. . . .

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SCORES      Init1: 190 Initn: 524 Opt: 594
Smith-Waterman score: 866; 21.7% identity in 2427 aa overlap

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              10      20      30      40      50      60
m564 .pep  MNRTLYKVVENKHRNCMIAVAENAKREGKNTADTQAVGILPNDIAGFAGFIHSISVISFS
             || :||:|:|:|: |: :|:|: | || :| : :| : |:: :|
fhab_borpe MNTNLYRLVFSHVRGMLVPVSEHCTV-G-NTFCGRTRG---QARSGARATSLSVAPNALA
              10      20      30      40      50

              70      80      90      100     110     119
m564 .pep  LSLLLG-SALILTSSSATAQGIIVADKSAPAQOQPTILOTGNGIPOVNIQTPTSAGVSVNQ
             :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
fhab_borpe WALMLACTGLPLVTH---AQGLV-----P-QGQTQVLQGGNKVPVNIADPNSSGGVSHNK
              60      70      80      90      100

              120     130     140     150     160     170     179
m564 .pep  YAQFDVGNRGAILNNSRSNTQTQLGGWIQGNPWLARGEARVVVNQINSSHSQNLNGYIEV
             :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
fhab_borpe FQQFNVANPGVVFNNGLTDGVSRRIGGALTKNPNLTR-QASAILAEVTDTSPSRLAGTLEV
              110     120     130     140     150     160

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      180      190      200      210      220      230      239
m564 .pep  GGRRAEVVIANPAGIAVNGGGFINASRATLTTAQPQYQAGDLSGFKIRQGNVVIAGHGLD
      | : | : : | | | | | : : | | | | : : | : | : : | | : | : |
fhab_borpe YGKGADLIIANPNGISVNLSTLNASNLTLTTGRPSVNGGRI-GLDVQQGTVTIERGGVN
      170      180      190      200      210      220

      240      250      260      270      280      290
m564 .pep  ARDTDYTRILSYHSKIDAPV---WGQ---DVRVVAGQNDVAATGDAHSPILNNAANTSN
      | : : : | : : : | : : | : | : | | : : | : : | : : | : : |
fhab_borpe ATGLGYFDVVARLVKLQGA VSSKQKPLADI AVVAGANRYDHATRRATPI----AAGARG
      230      240      250      260      270      280

      300      310      320      330      340      350
m564 .pep  NTANNGTHIPLFAIDTGKLGMYANKITLISTVEQAGIRNQGWFFASAGNVAVNAEGKLV
      : | : : : | : | : : | : | : : | : | : : | : | : : | : | : : |
fhab_borpe AAAGA-----YAIDGTAAGAMYGKHITLVSSDSGLGVRQLGS-LSSPSAITVSSQGEIA
      290      300      310      320      330

      360      370      380      390      400      410
m564 .pep  NTGMIAATGENHAVSLHARNVHNSGTVASQDDANIHSQTLDNSTVLSSGRLTVRNIGRL
      : | : : : | : | : : | : | : : | : | : : | : | : : | : | : : |
fhab_borpe ---LGDATVQRGPLSLKAGVVSAGKLASGGGAV---NVAGGGAVKIA---SASSVGNL
      340      350      360      370      380

      420      430      440      450      460      470
m564 .pep  KNQNGTIQARLD MSTGGLDNTGNITQTGSQALDLVSAGKFDNSGKIGVSDVPQTGLNP
      | : | : | : | : : : | : : | : | : | : : : | : : : : | : : : : |
fhab_borpe AVQGGGKVQATLLNAG-----GTLVSGRQAVQLGAASSRQALSVNAGGALKADKLSA
      390      400      410      420      430

      480      490      500      510      520      530
m564 .pep  NPSV-IPQIPSTATGSGSSTVS VSKPGSNNPVSP TAPAKNYAVGRIQTTGAFD-NAGSIN
      : | : : : | : | : : | : | : : | : | : : | : | : : | : | : : |
fhab_borpe TRRVVDGKQAVALGSASSNALSVRAGGA-----LKAGKLSATGRLDVDGKQAVTLGSA
      440      450      460      470      480      490

      540      550      560      570      579
m564 .pep  AGGQIDIAAQNLGNSGSLNAAKL RVSG-----DSFNNT-----VKGKLOAHDLA VNT
      : | : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
fhab_borpe SDGALSVSAGGNLRANELVSSAQLEVRGQREVALDDASSARGMTVVAAGALAAARNLQSKG
      500      510      520      530      540      550

      580      590      600      610      620      630
m564 .pep  QTAKNSGHLITQTGKIDNRELH--NAGEIAANNLTLIHSGRLSNDKKG NIRAHLQ LDTA
      : : : : : : : : : | : : : : | : : : : | : : : : | : : : : |
fhab_borpe AIGVQGGAEVSVANANSDAELRVGRGQVDLHDLAARGADISGEGRVNIGRARS DSDVK
      560      570      580      590      600      610

      640      650      660      670      680      690
m564 .pep  GLHNAGNILADSGTVTTKNNLRNTGKVSVARLNTGQTLDNTRGRIEAE TVNIQSQQLTN
      : | : | : : : : : : | : : : : | : : : : | : : : : | : : : : |
fhab_borpe -VSAHGALSIDSMTALGAIGVQAGGSVSAKDMRSRGAVTVSGGG-----AVNLGDVQ---
      620      630      640      650      660

      700      710      720      730      740      750
m564 .pep  QSGHITATEQLTINSRNVNDNQKLLSANQAQLAVSDGLYNQHGEIATNRQLSIHDKNQ
      : : : : | : : : | : : : : | : : : : | : : : : | : : : : |
fhab_borpe SDGQVRATSAGAMTVRDV-----AAAADLALQAGDALQAGFLKSAGAMTVNGRDAV
      670      680      690      700      710
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m564	.pep	760	770	780	790	800	810
		TLALNNADGTIQSAGNVSLQAKSLANNGTLTAGNKLDIALTEDFVVERDLTAGKQL-NLS					
fhab_borpe		RL-----DGA-HAGGQLRVSSDGAALGSLAAKGELTVSAARAATVA-EL---KSLDNIS					
		720	730	740	750	760	
m564	.pep	820	830	840	850	860	870
		IKGRLLK-NHTLTQAGHTLKLNA-GNIDNQVTGKIIGGEQTDITSEQHVDNRGLINS DGLT					
fhab_borpe		VTGGERVSVQSVNSASRVAISAHGALD---VGKV--SAKSGIGLE----GWGAVGADSL-					
		770	780	790	800	810	
m564	.pep	880	890	900	910	920	930
		HIGAGQTLTNTGTGKIYGNHIALDAQILLNREETEGSTKAGAI AARKRLDI-GAKEIHN					
fhab_borpe		--GSDGAISVSGRDAVRVDQARSLADISLG----AEGGATLGAVEAAGSIDVRGGSTV--					
		820	830	840	850	860	
m564	.pep	940	950	960	970	980	990
		QEGALLSSEGIFAVGNRLDEQHHAAGMADTFVNGSAGLEVQGDALMSVRNMQNINNHFKT					
fhab_borpe		AANSLHANRDVRVSGK--DAVRVTAATSGGGLHVSSGRQLDLGAVQA-RGALALDGGAGV					
		870	880	890	900	910	920
m564	.pep	1000	1010	1020	1030	1040	1050
		ETYLAKAEK--QVRDYTVLGQNTYYQAGKDGLFDNSQGGKQDTTATFHLKNGSRIEANQ-					
fhab_borpe		ALQSAKASGTLHVQGGELDLGLTAAVGAVDV----NGTGDVRVAKLVSDAGADLQAGRS					
		930	940	950	960	970	
m564	.pep	1060	1070	1080	1090	1100	
		--WHVRDYHIETYKERIENRPAHITVGGDLTASGQNWLNKDSRIVVGGRIITDDLNQKE					
fhab_borpe		MTLGIVDTTGDQLQARAQQKLELGSVKSDGGLQAAAGGALSAAA EVAGALELS---GQGV					
		980	990	1000	1010	1020	1030
m564	.pep	1110	1120	1130	1140	1150	1160
		ITNQSTTGKGRD DAVGTQWDSVTKKGWY--SGRKRQRRTERNHTPYHDTQLFTHDFDTPV					
fhab_borpe		TVDRASASRARIDSTGSVGIGALKAGAVEAASPRRARRALR-----QDFFTPG					
		1040	1050	1060	1070	1080	
m564	.pep	1170	1180	1190	1200	1210	1220
		SVI---QONAASPSFQPAASAIKLIDGVSTA AVNGQRIHTGNVVS LNNATVTLPNSSLYT					
fhab_borpe		SVVVRAGQNVTVGRGDPHQGVLAQGD IIMDA--KGGTLLLRNDALTENGTVTISADSAVL					
		1090	1100	1110	1120	1130	1140
m564	.pep	1230	1240	1250	1260	1270	1280
		THPDNKGWL VETD-PQFADYRRWLGS DYMLQQLQD TNHLHKRLGDGYEQKLVNEQIHQ					
fhab_borpe		EHSTIESKISQSVLAAGDKGKPAVS VKVAKKLFL--NGTLRAVNDN--NETMSGRIQIDV					
		1150	1160	1170	1180	1190	
m564	.pep	1290	1300	1310	1320	1330	1340
		LTGYRRLDGYRSDEEQFKALMDNGLTAAKT FGLTPG-IALSAEQVARLTSDIVWMENQTV					
fhab_borpe		VDGRPQI----TDAVTGEARKDES VVSDAALVADGGPIVVEAGELVSHAGGIGNGRNK--					
		1200	1210	1220	1230	1240	1250

[illegible]

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		1960	1970	1980	1990	2000	2010
m564	.pep	GITAGGNIGKKEQGGSTTHRHTHVGSTTGKTTIRSGGDTTLKGVQLIGKGIQADTRNLH					
fhab_borpe		GKDLYLNAGARKDE-----HRHL-----LNEGVIQAGGHGHIGG-----DVDNRSV-					
		1870	1880	1890	1900		

		2020	2030	2040	2050	2060
m564	.pep	IESVQDTETYSKQKQNGNVQTVGYGFSASGSYRQSKVKA-----DHASVTGQSGIYAGE				
fhab_borpe		VRTVSAMEYFKTFLPVSLTALDNRAGLSPATWNFQSTYELLDYLLDQNRYYIWLGLYPTY				
		1910	1920	1930	1940	1950

		2070	2080	2090	2100	2110	2120
m564	.pep	DGYQIKVRDNTDLKGGIITSSQSAEDKGKNLFQTATLTASDIQNHSS--RYEGRSFGIGGS					
fhab_borpe		TEWSVNTLKNLDL-GYQAKPAPTAPMPKA-----FELDLRGHTLESAGGRKI-FGEY					
		1970	1980	1990	2000	2010	

		2130	2140	2150	2160	2170
m564	.pep	FDLNGGWDGT-----VTDKQGRPTDRISPAAGYGSDDGSKNSTTRSGVNTNHIHITDEAG				
fhab_borpe		KKLQGEYKAKMAVQAVEAYGEATRRVHDQLG-----QRYGKALGGMDAETKEVDGIIQ				
		2020	2030	2040	2050	2060

		2180	2190	2200	2210	2220	2230
m564	.pep	QLARTGR TAKETEARIYTGIDTETADQHSGLKNSFDKDAVAKEINLQREVTFEGRNAA					
fhab_borpe		EFAADLRTVYAKQADQAT-IDAET-DKVAQRYKSQID--AVRLQAIQPGRVT--LAKALS					
		2080	2090	2100	2110	2120	

		2240	2250	2260	2270	2280	2290
m564	.pep	QAVAAVADKLGNTQSYERYQEARTLLE-AELQNTDSEAEKAAFRASLGQVNAVY-----					
fhab_borpe		AALGADWRALGHSQLMQRWKDFKAGKRGAEIAFYPKQTVLAAGAGLTLNGAIHNGENA					
		2130	2140	2150	2160	2170	2180

		2300	2310	2320	2330	2340	2350
m564	.pep	AENQSRDYTWKEGGIGRSILHGAAGGLTTGSLGGILAGGGTSLAAPYLDKAAENLGPAGK					
fhab_borpe		AQNRGRPEGLKIGAHSATSVSGSFDALRDVGLEKRLDIDDALAAVLVNPFIHTRIGAAQT					
		2190	2200	2210	2220	2230	2240

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1671>:

```

g565.seq
1   atggacagca cattgtctaa aacgtgttgc gtttcgtgca tattgttgag
51  cgtaaccacc accattttcg cccgtcccag accggcggct tccaataactt
101 ccctgcgttt cgcacgccc aacgacaccg gctcgcctgc acttctggct
151 acctgcacgc gtgcgatgct caagtcgagc gcgaaatacg gaatatacttc
201 ttggggcgaa gacgcgtccg accgtctgcc cgcccctgcc gaagccgaca
251 atcagcacat gatcagactt gctcgcgct tccaccaaca tgctgtgcag
301 atcgagcgac ttcattgtccc agcttga

```

This corresponds to the amino acid sequence <SEQ ID 1672; ORF 565.ng>:

```

g565.pep
1   MDSTLSKTCC VSCILLSVTT TIFARPRPAA SNTSLRFASP NDTGSPALLA
51  TCTRAMSKSS AKYGISSLGE DASDRLPAPA EADNQHMIRL AHRFHQHAVQ
101 IERLHVPA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1673>:

```

m565.seq
1   ATGGACAGCA CATTGTCTAA AACGTGTTGC GTTTCGTGCA TATTGTTGAG
51  CGTAACCACC ACCATTTTTCG CCCGTCCCAG ACCGGCGGCT TCCAATACTT
101 CCCTGCGTTT CGCATCGCCG AACGACACCG GTTCGCCCCG ACTTCTGGCA
151 ACCTGCACCC GCGCAATGTC CAAGTCGAGC GCGAAATACG GAATATCCTC
201 TTGGGCAAGG ACGCGTCCGA CCGTCTGCCC GCCCTGCCCC AAGCCGACAA

```

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```

251 TCAGCACATG GTCGGACTTG CTCATGGTTT CTACCAGCAT ACTGTGCAGA
301 TCGAGCGACT TCATGTCCCA GCTTGACTTG ACCAAACGCC CGACCAGCGC
351 ATCGCTGCCG CCCAAGAGGA AGGGCGCGAT AATCATCGAC AGCAGAACCG
401 CCGCCGTCGC CGCCTGTTCC CATTCTGGCG AAACCATATC AAGCTGCCCG
451 GCAATGGCCA GCATCACGAA GCCGAACTCG CCGCCCTGCG CGAGATACAA
501 AGCCGTTTTG AGGCTGTCGC CGACCGAATG TTTCATTTTG AAGGCAATGG
551 CAAACACAAC CAGTGCCTTC AACACCAGCA GCATTGCCAA CAGCATCAAT
601 ACCTGCCGCC AGCCGCCGAT CAATGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1674; ORF 565>:

```

m565.pep
  1 MDSTLSKTCC VSCILLSVTT TIFARPRPAA SNTSLRFASP NDTGSPALLA
  51 TCTRAMSKSS AKYGISSWAR TRPTVCPPLP KPTISTWSDL LMVSTILCR
 101 SSDFMSQLDL TKRPTSASLP PKRKGAIID SRTAAVAACS HSGETISSCP
 151 AMASITKPNS PPCARYKAVL RLSPTTEFIL KAMANTTSF NTSSIAN SIN
 201 TCRQPPINA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m565/g565 100.0% identity in 67 aa overlap

```

                10      20      30      40      50      60
m565.pep      MDSTLSKTCCVSCILLSVTTTIFARPRPAA SNTSLRFASPNDTGSPALLATCTRAMSKSS
                |||
g565          MDSTLSKTCCVSCILLSVTTTIFARPRPAA SNTSLRFASPNDTGSPALLATCTRAMSKSS
                10      20      30      40      50      60

                70      80      90     100     110     120
m565.pep      AKYGISSWARTRPTVCPPLPKPTISTWSDL LMVSTILCRSSDFMSQLDLTKRPTSASLP
                |||
g565          AKYGISSLGEDASDRLPAPAEADNQHMIRLAHRFHQHAVQIERLHVPA

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1675>:

```

a565.seq
  1 ATGGACAGCA CATGTCTTAA AACGTGTTGC GTTTCGTGCA TATTGTGAG
  51 CGTAACCACC ACCATTTTCG CCCGTCCCAG ACCGGCGGCT TCCAATACTT
 101 CCCTGCGTTT CGCATCGCCG AACGACACCG GTTCGCCCGC ACTTCTGGCA
 151 ACCTGCACCC GCGCAATGTC CAAGTCGAGC GCGAAATACG GAATATCCTC
 201 TTGGGCAAGG ACGCGTCCGA CCGTCTGCCC GCCCCTGCCG AAGCCGACAA
 251 TCAGCACATG GTCGGACTTG CTCATGGTTT CTACCAGCAT ACTGTGCAGA
 301 TCGAGCGACT TCATGTCCCA GCTTGACTTG ACCAAACGCC CGACCAGTGC
 351 ATCGCTGCCG CCCAAGAGGA AGGGCGCGAT AATCATCGAC AGCAGAACCG
 401 CCGCCGTCGC CGCCTGTTCC CATTCTAGCG AAACCATATC AAGCTGCCCG
 451 GCAATGGCCA GCATCACGAA GCCGAACTCG CCGCCCTGCG CGAGATACAA
 501 AGCCGTTTTG AGGCTGTCGC CGACCGAATG TTTCATTTTG AAGGCAATGG
 551 CAAACACAAC CAGTGCCTTC AACACCAGCA GCATTGCCAA CAGCATCAAT
 601 ACCTGCCGCC AGCCGCCGAT TAATGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1676; ORF 565.a>:

```

a565.pep
  1 MDSTLSKTCC VSCILLSVTT TIFARPRPAA SNTSLRFASP NDTGSPALLA
  51 TCTRAMSKSS AKYGISSWAR TRPTVCPPLP KPTISTWSDL LMVSTILCR
 101 SSDFMSQLDL TKRPTSASLP PKRKGAIID SRTAAVAACS HSSETISSCP
 151 AMASITKPNS PPCARYKAVL RLSPTTEFIL KAMANTTSF NTSSIAN SIN
 201 TCRQPPINA*

```

m565/a565 99.5% identity in 209 aa overlap

```

                10      20      30      40      50      60
m565.pep      MDSTLSKTCCVSCILLSVTTTIFARPRPAA SNTSLRFASPNDTGSPALLATCTRAMSKSS
                |||

```

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```

a565      MDSTLSKTCVSCILLSVTTTIFARPRPAASNTSLRFASPNDTGSPALLATCTRAMSKSS
           10      20      30      40      50      60
           70      80      90      100     110     120
m565.pep  AKYGISSWARTRPTVCPLPKPTISTWSDLLMVSTSLCRSSDFMSQLDLTKRPTSASLP
           |||
a565      AKYGISSWARTRPTVCPLPKPTISTWSDLLMVSTSLCRSSDFMSQLDLTKRPTSASLP
           70      80      90      100     110     120
           130     140     150     160     170     180
m565.pep  PKRKGAIIDSRTAAVAACSHSGETISSCPAMASITKNSPPCARYKAVLRLSPTECFIL
           |||
a565      PKRKGAIIDSRTAAVAACSHSSETISSCPAMASITKNSPPCARYKAVLRLSPTECFIL
           130     140     150     160     170     180
           190     200     210
m565.pep  KAMANTTSAFNTSSIANSTCRQPPINAX
           |||
a565      KAMANTTSAFNTSSIANSTCRQPPINAX
           190     200     210

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1677>:

```

g566.seq..
1  atgccgtctg aacaatatct tttcagacgg cattttgtat ggggggtaac
51 ggttggttcag cccgagtagc tcctgcatat cgtacaaacc cgttttgccg
101 tttacccaaa ctgcggcgcg gacggcaccg gcggcaaagg tcatgaggct
151 gccggctttg tgggtgattt ccacgcgttc gccgtcgggt gcgaagaggg
201 cgggtgtggtc gccgactatg tcgcctgcgc ggacggtggc aaagccgatg
251 gtggaaggat cgcgcgacc agtgtggcct tcgcggccgt aaacggcgca
301 ttgtttgagg tcgcggccga gcgcggccgc gatgacttcg cccattcgta
351 a

```

This corresponds to the amino acid sequence <SEQ ID 1678; ORF 566.ng>:

```

g566.pep..
1  MPSEQYLFRR HFVWGLTVVQ PEYVLHIVQT RFAVYPNCGA DGTGGKGHAA
51 AGFVGDFHAF AVGGEEGGVV ADYVACADGG KADGGRIART SVAFAAVNGA
101 LFEVAAERAG DDFAHSA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1679>:

```

m566.seq..
1  ATGCCGTCGT AACAAATATCT TTTCAGACGG CATTTTGTAT GGGGGTTAAC
51 GGTGTGTTTCA CCGAGTAGC TCCTGCATAT CGTACAAACC CGTTTGTCCG
101 TTGACCCAAA CTGCGGCGCG GACGGCACCG GCGGCAAAGG TCATGCGGCT
151 GCTGGCCTTG TGGGTGATT CCACGCCTC GCCGTCGGTG GCGAAGAGGG
201 CGGTGTGGTC GCCGACGATG TCGCTGCGC GGACGGTGGC AAAGCCGATG
251 GTCGACGGAT CGCGCGGACC GGTGTGGCCT TCGCGGCCGT AAACGGCGCA
301 TTGTTTGAGG TCTCTGCCGA GCGCGCCGGC GATGACTTCG CCCATGCGTA
351 A

```

This corresponds to the amino acid sequence <SEQ ID 1680; ORF 566>:

```

m566.pep..
1  MPSEQYLFRR HFVWGLTVVQ PEYVLHIVQT REAVDPNCGA DGTGGKGHAA
51 AGLVGDFHAL AVGGEEGGVV ADDVACADGG KADGRRART GVAFAAVNGA
101 LFEVSAERAG DDFAHSA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m566/g566 93.1% identity in 116 aa overlap

```

           10      20      30      40      50      60
m566.pep  MPSEQYLFRRHFVWGLTVVQPEYVLHIVQTRFAVDPNCGADGTGGKGHAAAGLVGDFHAL
           |||

```

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```

g566      MPSEQYLFRRHFWGLTVVQPEYVLHIVQTRFAVYPNCGADGTGGKGHAAAGFVGDFHAF
           10      20      30      40      50      60

           70      80      90      100     110
m566.pep  AVGGEEGGVVADDVACADGGKADGRRRIARTGVFAAVNGALFEVSAERAGDDFAHAX
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g566      AVGGEEGGVVADYVACADGGKADGGRIARTSVFAAVNGALFEVAAERAGDDFAHSX
           70      80      90      100     110

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1681>:

```

a566.seq
1  ATGCCGCTCTG  AACAAATATCT  TTTCAGACGG  CATTTTGTAT  GGGGGTTAAC
51 GGTGTGTTACG  CCCGAGTACG  TCCTGCATAT  CGTACAAACC  CGTTTTACCG
101 TTTACCCAAA  CTGCGGCGCG  GACGGCGCCG  GCGGCAAAGG  TCATGCGGCT
151 GCTTGCCTTG  TGGGTGATT  CCACGCGCTC  GCCGTCGGTG  GCGAAGAGGG
201 CGGTGTGGTC  GCCGACGATG  TCGCCCGCGC  GGACGGTGGC  AAAGCCGATG
251 GTGGACGGAT  CGCGCGGGCC  GGTGTGGCCT  TCGCGGCCGT  AAACGGCGCA
301 TTGTTGAGG  TCTCTGCCGA  GCGCGCCGGC  GATGACTTCG  CCCATGCGTA
351 A

```

This corresponds to the amino acid sequence <SEQ ID 1682; ORF 566.a>:

```

a566.pep
1  MPSEQYLFRRHFWGLTVVQPEYVLHIVQTRFAVYPNCGA  DGAGGKGHAA
51  ACLVGDFFHAL  AVGGEEGGVV  ADDVARADGG  KADGGRIARA  GVAFAAVNGA
101 LFEVSAERAG  DDFAHAX*

m566/a566  94.0% identity in 116 aa overlap

           10      20      30      40      50      60
m566.pep  MPSEQYLFRRHFWGLTVVQPEYVLHIVQTRFAVDPNCGADGTGGKGHAAAGLVGDFHAL
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a566      MPSEQYLFRRHFWGLTVVQPEYVLHIVQTRFAVYPNCGADGAGGKGHAAACLVGDFHAL
           10      20      30      40      50      60

           70      80      90      100     110
m566.pep  AVGGEEGGVVADDVACADGGKADGRRRIARTGVFAAVNGALFEVSAERAGDDFAHAX
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a566      AVGGEEGGVVADDVARADGGKADGGRIARAGVFAAVNGALFEVSAERAGDDFAHAX
           70      80      90      100     110

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1683>:

```

g567.seq..
1  atcgacgac  gggcagcggc  atcgacaagg  cgggtttgca  gtccggcggt
51  tatcaggtct  tattgggcga  tgcggacgtg  cagtcggcgg  cggtagcgag
101 caaagagggc  ggatacggcg  tgttggtgca  gaacgcgcgc  gcttgccggc
151 gcggaaatcg  agctgggtga  ggaaatcgcc  cgggaagtgc  gtttgaaaaa
201 cgcgtcaag  gcagtggcgg  aagattacga  cttatcctg  atcgactgtc
251 cgcttcgct  gacgtgttg  acgcttaacg  gcttggtggc  ggcgggcggc
301 gtgattgtgc  cgatgtgtg  cgaatattac  gcgctggaag  ggatttcgga
351 ttgattgtgc  accgtgcgca  aaatccgtca  ggcggtcaat  cccgatttgg
401 acatcacggg  catcgtgcgt  acgatgtacg  acagccgcag  caggctgggt
451 gccgaagtca  gcgaacagtt  gcgcagccat  ttcggggatt  tgctttttga
501 aaccgccatc  ccgcgcaata  tccgccttgc  ggaagcgccg  agccacggta
551 tgcgggtgat  ggcttacgac  gcgcaggcaa  aggggtgcaa  ggcgtatctc
601 gccttgccgg  acgaacgggc  ggcgaggggt  tcggggaaat  ag

```

This corresponds to the amino acid sequence <SEQ ID 1684; ORF 567.ng>:

```

g567.pep
1  MRRRAAATR  RVCSPAFIRS  YWAMRTCSRR  RYAAKRADTA  CWVRTRALAG
51  AEIELVQEIA  REVRLKNALK  AVAEDYDFIL  IDCPPSLTLL  TLNGLVAAGG
101 VIVPMLCEYY  ALEGISDLIA  TVRKIRQAVN  PDLDITGIVR  TMYDSRRLV
151 AEVSEQLRSH  FGDLLFETAI  PRNIRLAEAP  SHGMPVMAYD  AOAKGAKAYL
201 ALADELAARV  SGK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1685>:

```
m567.seq..
1  ATGAGTGC GA ACATCCTTGC CATCGCCAAT CAGAAGGGCG GTGTGGGCAA
51  AACGACGACG ACGGTAAATT TGGCGGCTTC GCTGGCATCG CGCGGCAAAC
101 GCGTGCTGGT GGTGATTTTG GATCCGCAGG GCAATGCGAC GACGGGCAGC
151 GGCATCGACA AGGCGGTTT GCAGTCCGGC GTTTATCAGG TCTTATTGGG
201 CGATGCGGAC GTGCAGTCGG CGGCGGTACG CAGCAAAGAG GCGGATACG
251 CTGTGTTGGG TCGGAACCGC GCGCTGGCCG GCGCGGAAAT CGAACTGGTG
301 CAGGAAATCG CCCGGGAAGT GCGTTGAAA AACGCGCTCA AGGCAGTGGA
351 AGAAGATTAC GACTTTATCC TGATCGACTG CCCGCCTTCG CTGACGCTGT
401 TGACGCTTAA CGGGCTGGTG GCGGCGGGCG GCGTGATTGT GCCGATGTTG
451 TGCGAATATT ACGCGCTGGA AGGGATTTCG GATTTGATTG CGACCGTGCG
501 CAGAAATCCG CAGGCGGTCA ATCCCGATTG GGACATCAGC GGCATCGTGC
551 GCACGATGTA CGACAGCCGC AGCAGGCTGG TTGCCGAAGT CAGCGAACAG
601 TTGCGCAGCC ATTTTCGGGA TTTGCTTTT GAAACCGTCA TCCGCGCAA
651 TATCCGCCTT GCGGAAGCGC CGAGCCACGG TATGCCGGTG ATGGCTTACG
701 ACGCGCAGG AAAGGTACC AAGCGTATC TTGCCTTGGC GGACGAGCTG
751 GCGGCGAGG TGTCGGGGA ATAG
```

This corresponds to the amino acid sequence <SEQ ID 1686; ORF 567>:

```
m567.pep..
1  MSANILAIAN QXGGVGKTTT TVNLAASLAS RGKRIVVVDL DPQGNATTGS
51  GIDKAGLQSG VYQVLLGDAD VQSAAVRSKE GGYAVIGANR ALAGAEIELV
101 QEIAREVRLK NALKA VEEDY DFILDCPPS LTLLTLNGLV AAGGVIVPML
151 CEYYALEGIS DLIATVRKIR QAVNPDLDT GIVRTMYDSR SRLVAEVSEQ
201 LRSFGDLLF ETVIPRNIRL AEAPSHGMPV MAYDAQAKGT KAYLALADEL
251 AARVSGK*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

```
m567/g567 98.2% identity in 168 aa overlap

m567.pep      60      70      80      90      100      110      119
GVYQVLLGDADVQSAAVRSKEGGYAVLGNRALAGAEIELVQEIAREVRLKNALKAVEED
g567          AFIRSYWAMRTCSRRRYAAKRDTACWVRTRALAGAEIELVQEIAREVRLKNALKAVEED
                20      30      40      50      60      70

m567.pep      120      130      140      150      160      170      179
YDFILIDCPPSLTLLTLNGLVAAGGVIVPMLCEYYALEGISDLIATVRKIRQAVNPDLDT
g567          YDFILIDCPPSLTLLTLNGLVAAGGVIVPMLCEYYALEGISDLIATVRKIRQAVNPDLDT
                80      90      100      110      120      130

m567.pep      180      190      200      210      220      230      239
TGIVRTMYDSRSRLVAEVSEQLRSHFGDLLFETVIPRNIRLAEAPSHGMPVMAYDAQAKG
g567          TGIVRTMYDSRSRLVAEVSEQLRSHFGDLLFETAIPRNIRLAEAPSHGMPVMAYDAQAKG
                140      150      160      170      180      190

m567.pep      240      250
TKAYLALADELAARVSGKX
g567          :|||||||||||||
AKAYLALADELAARVSGKX
                200      210
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1687>:

```
a567.seq
1  ATGAGTGC GA ACATCCTTGC CATCGCCAAT CAGAAGGGCG GTGTGGGCAA
51  AACGACGACG ACGGTAAATT TGGCGGCTTC GCTGGCATCG CGCGGCAAAC
101 GCGTGCTGGT GGTGATTTTG GATCCGCAGG GCAATGCGAC GACGGGCAGC
151 GGCATCGACA AGGCGAGTTT GCAGTCCGGC GTTTATCAGG TCTTATTGGG
201 CGATGCGGAC GTGAAATCGG CGGCGGTACG CAGCAAAGAG GCGGATACG
```

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```

251 GCGTGTGGG TCGGAACCGC GCGCTGGCCG GCGCGGAAAT CGAGCTGGTG
301 CAGGAAATCG CCCGGGAAGT GCGTTTGAAA AACGCGCTCA AGGCAGTGGC
351 GGAAGATTAC GACTTTATCC TGATCGACTG CCCGCCTTCG CTGACGCTGT
401 TGACGCTTAA CCGCTTGGTG GCGGCAGGCG GCGTGATTGT GCCGATGTTG
451 TGCGAATATT ACGCGCTGGA AGGGATTTCG GATTTGATTG CGACCGTGCG
501 CAAAATCCGT CAGGCGGTCA ATCCCGATTG GGATATCACG GGCATCGTGC
551 GTACGATGTA CGACAGCCGC AGCAGGCTAG TTGCCGAAGT CAGCGAACAG
601 TTGCGCAGCC ATTTCGGGGA TTTGCTGTTT GAAACCGTCA TCCCGCGCAA
651 TATCCGCCTT GCGGAAGCGC CGAGCCACGG TATGCCGGTG ATGGCTTATG
701 ATGCGCAGGC AAGGGTGCC AAGCGTATC TTGCCTTGGC GGACGAGCTG
751 ATGCGGAGGG TETCGGGGAA ATAG

```

This corresponds to the amino acid sequence <SEQ ID 1688; ORF 567.a>:

```

a567.pep
  1 MSANILAIAN QKGGVGKTTT TVNLAASLAS RGKRVLVVDL DPQGNATTGS
  51 GIDKASLQSG VYQVLLGDAD VKSAAVRSKE GYGVLGANR ALAGAEIELV
 101 QEIAREVRLK NALKAVAEDY DFILIDCPPS LTLLTLNGLV AAGGVIVPML
 151 CEYYALEGIS DLIATVRKIR QAVNPDLDT GIVRTMYDSR SRLVAEVSEQ
 201 LRSHFGDLLF ETVIPRNIRL AEAPSHGMPV MAYDAQAKGA KAYLALADEL
 251 MARVSGK*

m567/a567 97.7% identity in 257 aa overlap

              10      20      30      40      50      60
m567.pep    MSANILAIANQKGGVGKTTTTVNLAASLASRGKRVLVVDLDPQGNATTGSGIDKASLQSG
              |||||
a567         MSANILAIANQKGGVGKTTTTVNLAASLASRGKRVLVVDLDPQGNATTGSGIDKASLQSG
              10      20      30      40      50      60

              70      80      90      100     110     120
m567.pep    VYQVLLGDADVQSAAVRSKEGGYAVLGNALAGAEIELVQEIAREVRLKNALKAVEEDY
              |||||
a567         VYQVLLGDADVQSAAVRSKEGGYAVLGNALAGAEIELVQEIAREVRLKNALKAVEEDY
              70      80      90      100     110     120

              130     140     150     160     170     180
m567.pep    DFILIDCPPSLTLLTLNGLVAAGGVIVPMLCEYYALEGISDLIATVRKIRQAVNPDLDT
              |||||
a567         DFILIDCPPSLTLLTLNGLVAAGGVIVPMLCEYYALEGISDLIATVRKIRQAVNPDLDT
              130     140     150     160     170     180

              190     200     210     220     230     240
m567.pep    GIVRTMYDSRSRLVAEVSEQLRSHFGDLLFETVIPRNIRLAEAPSHGMPVMAYDAQAKGT
              |||||
a567         GIVRTMYDSRSRLVAEVSEQLRSHFGDLLFETVIPRNIRLAEAPSHGMPVMAYDAQAKGA
              190     200     210     220     230     240

              250
m567.pep    KAYLALADELAARVSGKX
              |||||
a567         KAYLALADELMARVSGKX
              250

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1689>:

```

g568.seq
  1 atgctcaggg tcagaccggt attatttgcc gtcaaggctt ccgcctcttc
  51 gataccttgc agaattctgcc gattaaagcg ttcgcggctg cccaatattt
 101 tcagcgcat attgttttcg tgcaggcggc gtacctgttt ttgcaaagcc
 151 tgtaaaaaa gccccatcag gaacgaaact tcgtcttcgg ggcgacgcca
 201 gttttcgtt gaaaaggcaa acacggtcag atattgcacg cccagtttgg
 251 cgcaatgctt caccatattt tccaacgcgt ccaagccgct tttgtgtccc
 301 attatacgcg ggagaaacg ttttttcgcc caacggcctg tgccgtccat
 351 aattacggcg atgtgcctcg ggatggcggt gtgttccaaa atggtctgcg

```


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401 tgctgctctt catatctgcc ttctcgcggtt cggcggtcaa atgccgtctg
451 aacgcgcgcg cgtga

This corresponds to the amino acid sequence <SEQ ID 1690; ORF 568.ng>:

g568.pep
1 MLRVRPVLFA VKASASSIPC RICRLKRSRL PNIFRRILFS CRRRTCFCKA
51 CKNSPIRNET SSSGRRQFSV EKANTVRYCT PSLAQCFITF SNASKPRLCP
101 IIRGRKRFFA QRPLPSIITA MCLGMAVCSK MVCVLLFISA FRGSAFKCRL
151 NAAP*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1691>:

m568.seq
1 ATGCTCAGGG TCAGGCCGGT ATTGTTTGCC GTCAACGCTT CCGCCTCTTC
51 GATGCCTTGC AGAATCTGCC GGTGAAGCG TTCGCGGCTG CCCAATATCT
101 TCAGGCGCAT ATTGTTTTCG TGCAGGCGGC GTACCTSTT TTGCAAAGCC
151 TGTAAAAACA GCCCCATCAG GAACGAAACT TCGTCTTCGG GCGGCGCGCA
201 GTTTTCGGTT GAAAAGGCAA ACACGGTCAG ATATTGCACA CCCAGTTTGG
251 CGCAATGCTT CACCATATTT TCCAATGCGT CCAAACGCG TTTGTGTCC
301 ATTATGCGCG GGAGGAAACG TTTTTCGCC CAACGGCGGT TGCCGTCCAT
351 AATCAGGCG ATATGCTTGG GAATGGCGGT GTGTCCAAA ACGCCTGCG
401 TGCTGCTTTT CATGTCTGCC TTTTCGGTT CCGCATTCAA ATGCCGCTG
451 AACGCCGAAC CGTGCAGGTT AAATGCCAT CAAATCTTCT TCTTTGGCAG
501 TCAGGAGTTT GTCGGCTTCG GTAATGTATT TGTGGTCCAG TTTTGAACC
551 GCTTCTTCG CGCGACGTGC CTCGTCTTCG GAAATTTCTT TGTCTTTGAG
601 GAGTTTTTTG ATGTGGTCGT TGGCATCGCG GCGCACGTTG CGGATAGAGA
651 CGCGGCCTTC TTCCGCTTCG CCGGTACGA CTTAATCAG GTCTTTGCGG
701 CGTTCCTCG TCAGCATGGG CATCGGCACG CGGATCAGGT CGCGACAGC
751 TGCCGGGTTT AGTCCCAAGT TTGA

This corresponds to the amino acid sequence <SEQ ID 1692; ORF 568>:

m568.pep..
1 MLRVRPVLFA VNASASSMPC RICRLKRSRL PNIFRRILFS CRRRTCFCKA
51 CKNSPIRNET SSSGRRQFSV EKANTVRYCT PSLAQCFITF SNASKPRLCP
101 IMRGRKRFFA QRPLPSIITA ICLGMAVCSK TACVLLFMSA FRGSAFKCRL
151 NAEPCLRNCH QIFFFGSQEF VGFNGVFGVQ FLNRFFAATC LVFGNFFVFE
201 EFFDVVVGIA AHVADRDAAF FRFAAYDFNQ VFAAFLGQHG HRHADQVADS
251 CRVQSQV*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m568/g568 94.8% identity in 154 aa overlap

	10	20	30	40	50	60
m568.pep	MLRVRPVLFAVNASASSMPCRICRLKRSRLPNIFRRILFSCRRRTCFCKACKNSPIRNET					
g568	MLRVRPVLFAVKASASSIPCRICRLKRSRLPNIFRRILFSCRRRTCFCKACKNSPIRNET					
	10	20	30	40	50	60
	70	80	90	100	110	120
m568.pep	SSSGRRQFSVEKANTVRYCTPSLAQCFTIFSNASKPRLCPIMRGRKRFFAQRPLPSIITA					
g568	SSSGRRQFSVEKANTVRYCTPSLAQCFTIFSNASKPRLCPIIRGRKRFFAQRPLPSIITA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m568.pep	ICLGMVCSKTACVLLFMSAFRGSFAFKCRLNAEPCRLNCHQIFFFGSQEFVGFNGVFGVQ					
g568	MCLGMVCSKMVCVLLFISAFRGSFAFKCRLNAAPX					
	130	140	150			
	190	200	210	220	230	240
m568.pep	FLNRFFAATCLVFGNFFVEEFFDVVVGIAAHVADRDAAFRFAAYDFNQVFAAFLGQHG					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1693>:

```
a568.seq
1  ATGCTCAGGG TCAGGCCGGT ATTGTTTGCC GTCAAGGCTT CCGCCTCTTC
51  GATGCCCTTC AGGATTGAC GGTGAAGCG TTCGCGGCTG CCCAGTATTT
101 TCAGGCGCAT ATTGTTTCG TGCAGGCGGC GTACCTGTTT TTGCAAAGCC
151 TGTA AAAACA GCCCCATCAG GAACGAACT TCGTCTTCGG GCGGCGGCCA
201 GTTTTCGGTT GAAAAGGCAA ACACGGTCAG ATATTGCACA CCCAGTTTGG
251 CGCAATGCTT CACCATATTT TCCAATGCGT CCAAACCGCG TTTGTGTCCC
301 ATTATGCGCG GGAGGAAACG TTTTTCGCC CAACGGCCGT TGCCGTCCAT
351 AATCAGGCG ATATGCTTGG GAATGGCGGT GTGTCCAAA ACGGCCTGCG
401 TGCTGCTTTT CATGTCTGCC TTTTCGGGT CGGCATTCAA ATGCCGCTCTG
451 AACGCCGAAC CGTGCAAGTT AAATGCCAT CAAATCTTCT TCTTTGGCAG
501 TCAGGAGTTT GTCGGCTTCG GTAATGTATT TGTGGTCAG TTTTGAACC
551 GCTTCTTCGC CGCGACGTGC CTCGTCTTCG GAAATTTCTT TGTCTTTGAG
601 GAGTTTTTTG ATGTGGTCGT TGGCATCGCG GCGCACGTTG CGGATGGAGA
651 CGCGGCCTTC TTCCGCTTCG CCGCGTACGA CTTAATCAG GTCTTTGCCG
701 CGTTCCTCG TCAGCATGGG CATCGGCACG CGGATCAGGT CGCCGACAGC
751 TGCCGGGTTT AGTCCCAAGT TTGA
```

This corresponds to the amino acid sequence <SEQ ID 1694; ORF 568.a>:

```
a568.pep
1  MLRVRPVLFA VKASASSMPF RI*RLKRSRL PSIFRRILFS CRRRTCFCCKA
51  CKNSPIRNET SSSGRRQFSV EKANTVRYCT PSLAQCFITF SNASKPRLCP
101 IMRGRKRFFA QRPLPSIITA ICLGMAVCSK TACVLLFMSA FRGSAFKCRL
151 NAEPCRLNCH QIFFFGSQEF VGFGNVFVGQ FLNRFFAATC LVFGNFFVEE
201 EFFDVVVGIA AHVADGDAF FRFAAYDFNQ VFAAFLGQHG HRHADQVADS
251 CRVQSQV*
```

m568/a568 98.1% identity in 257 aa overlap

	10	20	30	40	50	60
m568.pep	MLRVRPVLFAVNASASSMPCRICRLKRSRLPNIFRRILFSCRRRTCFCCKACKNSPIRNET					
a568	MLRVRPVLFAVKASASSMPFRIKRLKRSRLPSIFRRILFSCRRRTCFCCKACKNSPIRNET					
	10	20	30	40	50	60
	70	80	90	100	110	120
m568.pep	SSSGRRQFSVEKANTVRYCTPSLAQCFTIFSNASKPRLCPIMRGRKRFFAQRPLPSIITA					
a568	SSSGRRQFSVEKANTVRYCTPSLAQCFTIFSNASKPRLCPIMRGRKRFFAQRPLPSIITA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m568.pep	ICLGMVCSKTACVLLFMSAFRGSFAFKCRLNAEPCRLNCHQIFFFGSQEFVGFGNVFVGQ					
a568	ICLGMVCSKTACVLLFMSAFRGSFAFKCRLNAEPCRLNCHQIFFFGSQEFVGFGNVFVGQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
m568.pep	FLNRFFAATCLVFGNFFVEEFDVVVGIAAHVADRDAAFFRFAAYDFNQVFAAFLGQHG					
a568	FLNRFFAATCLVFGNFFVEEFDVVVGIAAHVADGDAAFFRFAAYDFNQVFAAFLGQHG					
	190	200	210	220	230	240
	250					
m568.pep	HRHADQVADSCRVSQVX					
a568	HRHADQVADSCRVSQVX					
	250					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1695>:

```
g569.seq..
1  atgctgaaac aacgggtaat aaccgctatg tggctgctgc cgctgatgct
51  gggcatgctg ttttacgcgc cgcaatggct gtgggctgca ttttgcgggc
101 tgattgccct gaccgccttg tgggagtatg cccgtatggc cggtttgtgc
```

874

```

151 aaaaccgaaa ccaaccatta cctcgccgca accttggttt tggcgtagt
201 tgectatgcg ggcggctgga tgetgcctaa tttggtttg tatgttgttt
251 tggcattttg gctcgccgtt atgcctttgt ggttgagatt caaatggagg
301 ctcaacggcg gttggcaggt ttatgccgtc ggctgggttt tgctcatgcc
351 gttttggttc gcgctcgat ccctggcgcc cgcatccga tga

```

This corresponds to the amino acid sequence <SEQ ID 1696; ORF 569.ng>:

```

g569.pep
  1 MLKQRVITAM WLLPLMLGML FYAPQWLWAA FCGLIALTAL WEYARMAGLC
  51 KTETNHYLAA TLVFGVVAYA GGWMLPNLVW YVVLAFWLAV MPLWLRFKWR
 101 LGGWQVYAV GWLLMPFWF ALVSLAPASR *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1697>:

```

m569.seq..
  1 ATGCTGAAAC AACGGGTAAT AACCGCCATG TGGCTGCTGC CGCTGATGCT
  51 GGGCATGCTG TTTTACGCGC CGCAATGGTT GTGGGCTGCA TTTTGCGGAC
 101 TGATTGCCCT GATTGCCTTG TGGGAATATG CCCGTATGGG CGGTTTGTGC
 151 AAAATTAATA CCAACCATTA CCTCGCCGCA ACCTIGGTTT TCGGCGTGGT
 201 TGCCTATGCG GCGGGCTGGA TGCTGCCTAA TTTGGTTTGG TATGTTGTTT
 251 TGGCATTTTG GCTCGCCGTT ATGCCTTTAT GGTGAGATT CAAATGGAGG
 301 CTCACGCGCG GTTGGCAGGT TTATGCCGTC GGCTGGCTTC TGGTCATGCC
 351 GTTTTGGTTC GCGCTCGTAT CCTGCGGCC GCATCCCGAT GATGCCCTGC
 401 CGCTGCTCGC CGTGATGGGT TTGGTGTGGG TTGCCGATAT TTGCGCGTAT
 451 TTCAGCGGCA AGGCGTTCGG CAAACACAAA ATCGCGCCGG CAATCAGCCC
 501 CGGCAAAAGC TGGGAAGGTG CAATCGGCGG CGCGGTTTGC GTGGCAGTGT
 551 ACATGACCGC CGTACGAAGT GCCGGCTGGC TGGCATTCGA TACAGGCTGG
 601 TTCGATACCG TGTTAATCGG TTTGGTGTCT ACCGTTGTCA GCGTATGCGG
 651 CGACCTTTTG GAAAGCTGGC TCAAGCGCGC GGCAGGCATC AAACACAGCA
 701 GCAAGCTGCT GCCCGGACAC GCGGCGGTGT TCGACCGTAC CGACAGCCTG
 751 ATTGCCGTTA TCAGCGTCTA TGCAGCGATG ATGTCGGTTT TAAATTGA

```

This corresponds to the amino acid sequence <SEQ ID 1698; ORF 569>:

```

m569.pep..
  1 MLKQRVITAM WLLPLMLGML FYAPQWLWAA FCGLIALIAL WEYARMGGLC
  51 KIKTNHYLAA TLVFGVVAYA GGWMLPNLVW YVVLAFWLAV MPLWLRFKWR
 101 LGGWQVYAV GWLLVMPFWF ALVSLRPHPD DALPLAVMG LVVWADICAY
 151 FSGKAFGKHK IAPAIKPGKS WEGAIGGAVC VAVYMTAVRS AGWLAFDTGW
 201 FDTVLIGLVL TVSVCGDLL ESWLKRAAGI KDSSKLLPGH GGVFDRDTSI
 251 IAVISVYAAM MSVLN*

```

m569/g569 95.3% identity in 127 aa overlap

	10	20	30	40	50	60
m569.pep	MLKQRVITAMWLLPLMLGMLFYAPQWLWAAFCGLIALIALWEYARMGGLCKIKTNHYLAA					
g569	MLKQRVITAMWLLPLMLGMLFYAPQWLWAAFCGLIALTALWEYARMAGLCKTETNHYLAA					
	10	20	30	40	50	60
m569.pep	TLVFGVVAYAGGWMLPNLVWYVVLAFWLAVMPLWLRFKWRLGGWQVYAVGWLLVMPFWF					
g569	TLVFGVVAYAGGWMLPNLVWYVVLAFWLAVMPLWLRFKWRLGGWQVYAVGWLLVMPFWF					
	70	80	90	100	110	120
m569.pep	ALVSLRPHPD DALPLAVMGLVWVADICAYFSGKAFGKHKIAPAIKPGKSWEGAIGGAVC					
g569	ALVSLAPASRX					
	130	140	150	160	170	180

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1699>:

```

a569.seq
  1 ATGCTGAAAC AACGGGTGAT AACCGCCATG TGGCTGCTGC CGCTGATGCT
  51 GGGCATGCTG TTTTACGCGC CGCAATGGTT GTGGGCTGCA TTTTGCGGAC
 101 TGATTGCCCT GATTGCCTTG TGGGAATATG CCCGTATGGG CGGTTTGTGC

```

875

```

151 AAAATTAAAA CCAACCATTA CCTCGCCGCA ACCTTGGTTT TCGGCGTGGT
201 TGCCTATGCG GCGCGCTGGA TGCTGCCTAA TTTGGTTTGG TATGTTGTTT
251 TGGCATTTTG GCTCGCCGTT ATGCCCTTAT GGTGAGATT CAAATGGAGG
301 CTCAACGGCG GTTGGCAGGT TTATGCCGTC GGCTGGCTTC TGGTCATGCC
351 GTTTTGGTTC GCGCTCGTAT CCCTGCGCCC GCATCCCGAT GATGCCCTGC
401 CGCTGCTCGC CGTGATGGGT TTGGTGTGGG TTGCCGATAT TTGCGCGTAT
451 TTCAGCGGCA AGGCGTTCGG CAAACACAAA ATCGCACCGG CAATCAGCCC
501 CGGCAAAAGC TGGGAAGGTG CAATCGGCGG CGCGGTTTGC GTGGCCGTGT
551 ACATGACCGC CGTACGAAGT GCCGGCTGGC TGGCATTCTGA TACAGGCTGG
601 TTCGATACCG TGTTAATCGG TTTGGTGTG ACCGTTGTCA GCGTATGCGG
651 CGACCTTTTG GAAAGCTGGC TCAAGCGCGC GGCAGGCATC AAAGACAGCA
701 GCAACCTGCT GCCCGGACAC GCGGCGGTGT TCGACCGCAC CGACAGCCTG
751 ATTGCCGTTA TCAGCGICTA TGCAGCGATG ATGTCGGTTT TAAATTGA

```

This corresponds to the amino acid sequence <SEQ ID 1700; ORF 569.a>:

```

a569.pep
1  MLKQRVITAM WLLPLMLGML FYAPQWLWAA FCGLIALIAL WEYARMGGLC
51  KIKTNHYLAA TLVFGVVAYA GGWMLPNLVW YVVLAFWLAV MPLWLRFKWR
101 LNGGWQVYAV GWLLVMPFWF ALVSLRPHPD DALPLLAVMG LVWVADICAY
151 FSGKAFGKHK IAPAI SPGKS WEGAIGGAVC VAVYMTAVRS AGWLAFTDGTW
201 FDTVLIGLVL TVSVCGDLL ESWLKRAAGI KDSSNLLPGH GGVFDRDTS
251 IAVISVYAAM MSVLN*

```

m569/a569 99.6% identity in 265 aa overlap

	10	20	30	40	50	60
m569.pep	MLKQRVITAMWLLPLMLGMLFYAPQWLWAAFCGLIALIALWEYARMGGLCIKTNHYLAA					
a569	MLKQRVITAMWLLPLMLGMLFYAPQWLWAAFCGLIALIALWEYARMGGLCIKTNHYLAA					
	10	20	30	40	50	60
m569.pep	TLVFGVVAYAGGWMLPNLVWYVVLAFWLAVMPLWLRFKWRLNGGWQVYAVGWLLVMPFWF					
a569	TLVFGVVAYAGGWMLPNLVWYVVLAFWLAVMPLWLRFKWRLNGGWQVYAVGWLLVMPFWF					
	70	80	90	100	110	120
m569.pep	ALVSLRPHPD DALPLLAVMGLVWVADICAYFSGKAFGKHKIAPAI SPGKS WEGAIGGAVC					
a569	ALVSLRPHPD DALPLLAVMGLVWVADICAYFSGKAFGKHKIAPAI SPGKS WEGAIGGAVC					
	130	140	150	160	170	180
m569.pep	VAVYMTAVRSAGWLAFTDGTWFDTVLIGLVLTVSVCGDLLESWLKRAAGIKDSSKLLPGH					
a569	VAVYMTAVRSAGWLAFTDGTWFDTVLIGLVLTVSVCGDLLESWLKRAAGIKDSSNLLPGH					
	190	200	210	220	230	240
m569.pep	GGVFDRDTSLIAVISVYAAMMSVLNX					
a569	GGVFDRDTSLIAVISVYAAMMSVLNX					
	250	260				
m569.pep	GGVFDRDTSLIAVISVYAAMMSVLNX					
a569	GGVFDRDTSLIAVISVYAAMMSVLNX					
	250	260				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1701>:

g570.seq..

```

1  atgatccgtt tgaccgcgcg gtttgccgcc gccctgatcg gtttatgetg
51  caccacaggc gcgcacgcgc acaccttcca aaaaatcggc tttatcaaca
101 cggagcgcat ctacctcgaa tccaagcagg cgcgcaacat ccaaaaaacg
151 ctggacggcg aattttccgc cgcgcaggac gaattgcaaa aactgcaacg
201 cgaaggtctg gatattgaaa ggcagctcgc cggcgcaaaa cttaaggacg
251 caaaaaaggc gcaagccgaa gaaaaatggc gcgggctggc cgaagcgctc
301 cgcaaaaaac aggcgcagtt tgaagaagac tacaacctcc gccgcaacga
351 agagtttgcc tccctccagc aaaaacgcaa ccgcgctcatc gtcaaatcgc

```

876

401 ccaaacagga aggttacgat gtcattttgc aggacgtgat ttacgtcaac
 451 acccaatcag acgttaccga cagcgtcatt aaagaaatga acgcccgcgtg
 501 a

This corresponds to the amino acid sequence <SEQ ID 1702; ORF 570.ng>:

g570.pep..

1 MRLTRAFAA ALIGLCCTTG AHADTFQKIG FINTERIYLE SKQARNIQKT
 51 LDGEFSARQD ELQKLQREGL DLERQLAGGK LKDAKKAQAE EKWRGLVEAF
 101 RKKQAQFEED YNLRNNEEFA SLQQNANRVI VKIAKQEGYD VILQDVIYVN
 151 TQYDVTDSVI KEMNAR*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1703>:

m570.seq..

1 ATGACCCGTT TGACCCGCGC GTTGGCCGCG GCTCTGATCG GTTGTGCTG
 51 CACCGCAGGC GCGCAGCCCG ACACCTTCCA AAAAATCGGC TTTATCAACA
 101 CCGAGCGCAT CTACCTCGAA TCCAAGCAGG CGCGCAAGAT TCAAAAAACG
 151 CTGGACAGCG AATTTTCCGC TCGTCAGGAC GAATTGCAAA AACTGCAACG
 201 CGAAGGTCTG GATTTGGAAG GGCAGCTTGC CGAAGGCAAA CTCAGAAACG
 251 CAAAAAAGGC GCAAGCCGAA GAAAAATGGC GCGGGCTGGT CGCAGCGTTC
 301 CGCAAAAAAC AGGCGCAGTT TGAAGAAGAC TACAACCTCC GCCGCAACGA
 351 AGAGTTTGCC TCCCTCCAGC AAAACGCCAA CCGCGTCATC GTCAAAATCG
 401 CCAAACAGGA AGGTTACGAT GTCATTTTGC AGAACGTGAT TTACGTCAAC
 451 ACCCAATACG ACGTTACCGA CAGCGTCATT AAAGAAATGA ACGCCCGCTG
 501 A

This corresponds to the amino acid sequence <SEQ ID 1704; ORF 570>:

m570.pep

1 MRLTRAFAA ALIGLCCTAG AHADTFQKIG FINTERIYLE SKQARKIQKT
 51 LDSEFSARQD ELQKLQREGL DLERQLAEGK LRNAKKAQAE EKWRGLVAAF
 101 RKKQAQFEED YNLRNNEEFA SLQQNANRVI VKIAKQEGYD VILQNVIIYN
 151 TQYDVTDSVI KEMNAR*

m570/g570 94.6% identity in 166 aa overlap

	10	20	30	40	50	60
m570.pep	MRLTRAFAAALIGLCCTAGAHADTFQKIGFINTERIYLESKQARKIQKTLDSEFSARQD					
g570	MIRLTRAFAAALIGLCCTTAGAHADTFQKIGFINTERIYLESKQARNIQKTLDBFSARQD					
	10	20	30	40	50	60
	70 80 90 100 110 120					
m570.pep	ELQKLQREGLDLERQLAEGKLRNAKKAQAE EKWRGLVAAFRRKQAQFEEDYNLRNNEEFA					
g570	ELQKLQREGLDLERQLAGGKLRNAKKAQAE EKWRGLVEAFRRKQAQFEEDYNLRNNEEFA					
	70	80	90	100	110	120
	130 140 150 160					
m570.pep	SLQQNANRVIVKIAKQEGYDVILQNVIIYVNTQYDVTDSVIKEMNARX					
g570	SLQQNANRVIVKIAKQEGYDVILQDVIYVNTQYDVTDSVIKEMNARX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1705>:

a570.seq

1 ATGACCCGTT TGACCCGCGC GTTGGCCGCG GCTCTGATCG GTTGTGCTG
 51 CACCGCAGGC GCGCAGCCCG ACACCTTCCA AAAAATCGGC TTTATCAACA
 101 CCGAGCGCAT CTACCTCGAA TCCAAGCAGG CGCGCAAGAT TCAAAAAACG
 151 CTGGACAGCG AATTTTCCGC CCGCCAGGAC GAATTGCAAA AACTGCAACG
 201 CGAAGGTCTG GATTTGGAAG GGCAGCTTGC CGAAGGCAAA CTCAGAAACG
 251 CAAAAAAGGC GCAAGCCGAA GAAAAATGGT GCGGGCTGGT CGCAGCGTTC
 301 CGCAAAAAAC AGGCGCAGTT TGAAGAAGAC TACAACCTCC GCCGCAACGA
 351 AGAGTTTGCC TCCCTCCAGC AAAACGCCAA CCGCGTCATC GTCAAAATCG
 401 CCAAACAGGA AGGTTACGAT GTCATTTTGC AGGACGTGAT TTACGTCAAC
 451 ACCCAATACG ACGTTACCGA CAGCGTCATT AAAGAAATGA ACGCCCGCTG

877

501 A

This corresponds to the amino acid sequence <SEQ ID 1706; ORF 570.a>:

```

a570.pep
  1  MTRLTRAFAA ALIGLCCTAG AHADTFQKIC FINTERIYLE SKQARKIQKT
  51  LDSEFSARQD ELQKLQREGL DLERQLAEGK LKDAKKAQAE EKWCGLVAAF
 101  RKKQAQFEED YNLRNNEEFA SLQQNANRVI VKIAKQEGYD VILQDVIYVN
 151  TQYDVTDSVI KEMNAR*

m570/a570    97.6% identity in 166 aa overlap

              10      20      30      40      50      60
m570.pep     MTRLTRAFAAALIGLCCTAGAHADTFQKIGFINTERIYLESKQARKIQKTL DSEFSARQD
              |||||
a570          MTRLTRAFAAALIGLCCTAGAHADTFQKIGFINTERIYLESKQARKIQKTL DSEFSARQD
              10      20      30      40      50      60

              70      80      90     100     110     120
m570.pep     ELQKLQREGLDLERQLAEGKLRNNAKKAQAEKWRGLVAAFRKKQAQFEEDYNLRNNEEFA
              |||||
a570          ELQKLQREGLDLERQLAEGKLRNNAKKAQAEKWRGLVAAFRKKQAQFEEDYNLRNNEEFA
              70      80      90     100     110     120

              130     140     150     160
m570.pep     SLQQNANRVIVKIAKQEGYDVILQNVIIYVNTQYDVTDSVIKEMNARX
              |||||
a570          SLQQNANRVIVKIAKQEGYDVILQDVIYVNTQYDVTDSVIKEMNARX
              130     140     150     160

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1707>:

```

g571.seq (partial)
  1  atgcgcggtt tccgagtaaa ccgatttgtt gttaccgttt tcggcgccgg
  51  tataggttct gccgtcccac acgctgcctg cgtcggaaca caggctcagg
 101  cggacgggtg gtgcgtcttt cgcacggggc atcggaaga gcagctcggc
 151  ggagacgttg gcttttttgt tgcgcgta gctgatttt tcgcgtatt
 201  cgtcatacac ttccgggccc agcgtgcgc ttcttagcc gcgcaccgaa
 251  cccaggccgc cgcgtagaa gttttcaaag aaggggattt ctttggttct
 301  gccgtagccg cccgcaatgc cgacttcgc gccgagcatc agcgtgaagg
 351  ttttgc...

```

This corresponds to the amino acid sequence <SEQ ID 1708; ORF 571.ng>:

```

g571.pep (partial)
  1  MRVFRVNRV VTVFGGGIGS AVPHAACVGK QAQADGACVF RTGHRBEEQG
  51  GDVGGFFVA AVFFAVFVIH FRAERAAFWA AHRTQAAAVE VFKEGDPFGS
 101  AVAARNADFA AEHQREGFA...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1709>:

```

m571.seq
  1  ATGGGTATTG CCGGCGCCGT AAATGTTTG AACCTGCGG CCGTTCGCGG
  51  AACTGCTGTT GTCGTCGTAG GTTTTGCCGT CCCACACGCT GCCTGCGTCG
 101  GCAAACAGGC TCAGGCGGAC GGTGCGCGCG TCTTTCGCGC CGGGCATCGG
 151  GAAGAGCAGC TCGGCGGAGA CGTTGGCTTT TTTGTTGCGG CCGTAGCTGA
 201  TTTTTCGCC GTATTCGTCA TAGACTTTCG GACCGAGCGT GCCGCTTTCG
 251  TATCCGCGCA CCGAACCCAG GCCGCGCGCG TAGAAGTTT CAAAGAAGGG
 301  GATTTCCTTG GTTCTGCCGT AGCGCCCGC AATGCCGACT TCGCCGCCGA
 351  GCATCAGCGT GAAGGTTTTC CTCAGGGGGA AGAACCGGT TTGTTGTGG
 401  GTGGCGGAGT AGTATTGCAG TTTGCTGCCA GGCAGGGCGA TTTGCGCGTT
 451  CACGCCCGTC AGGTAGCCGC GCGTCGCCA TAA

```

This corresponds to the amino acid sequence <SEQ ID 1710; ORF 571>:

```

m571.pep
  1  MGIAGAVNVL NPAAGRGTAV VVVGFAVPHA ACVGKQAQAD GARVFRAGHR
  51  EEQLGGDVGF FVAADVDFFA VFVIDFRTER AAFVSAHRTQ AAAVEVFKEG
 101  DFPGSAVAAR NADFAAEHQE EGFAQGEEPG LVVGGGVVLQ FAARQGDFGV
 151  HARQVAARRP *

```

878

m571/g571 93.1% identity in 102 aa cverlap

```

      10      20      30      40      50      60
m571.pep  MGIAGAVNVNLPAAAGRGTA VVVVGFAVPHAACVKGQAQADGARVFRAGHREEQLGGDVGF
      :| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g571      MRVFRVNRFFVTVFVG GIGSAVPHAACVKGQAQADGACVFRTGHREEQLGGDVGF
      10      20      30      40      50

      70      80      90      100     110     120
m571.pep  FVAAVADFFFAVFVIDFRTERAAAFVSAHRTQAAAVEVFKEGDFFGSAVAARNADFAAEHQ
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g571      FVAAVADFFFAVFVIHFRAERAAFAAHRTQAAAVEVFKEGDFFGSAVAARNADFAAEHQ
      60      70      80      90      100     110

      130     140     150     160
m571.pep  EGFAQGEEPLVVG GGVVLQFAARQDGFVHARQVAARRPX
      ||||
g571      EGFA
      119

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1711>:

```

a571.seq
1  ATGGGTATTG CCGGCGCCGT AAATGTTTGT AACCTGCCG CCGGTCGCGG
51  AACTGCTGTT GTCGTCGTAG GTTTTGCCGT CCCACAGCT GCCTGCGTCG
101 GCAAACAGGC TCAGGCGGAC GGTGCGCGC TCTTTCGCGC CGGGCATCGG
151 GAAGAGCAGC TCGGCGGAGA CGTTGGCTTT TTTGTTGCCG CCGTAGCTGA
201 TTTTTCGCGC GTATTCGTCA TACACTTTCG GACCGAGCGT GCCGCTTTCG
251 TATCCGCGCA CCGAACCCAG GCCGCCCGC TAGAAGTTT CAAAGAAGGG
301 GATTTCTTTG GTTCTGCCGT AGCCGCCCGC AATGCCGACT TCGCCGCCGA
351 GCATCAGCGT GAAGGTTTGT CTTAAGGGGA AGAACCAGG TTGGTTGTGG
401 GTGGCGGAGT AGTATTGCAG TTTGCTGCCG GGCAGGCGA TTTCGGCGTT
451 CACGCCCGTC AGGTAGCCGC GCGTCGGCCA TAA

```

This corresponds to the amino acid sequence <SEQ ID 1712; ORF 571.a>:

```

a571.pep
1  MGIAGAVNVN NPAAGRGTA VVVVGFAVPHA ACVKGQAQAD GARVFRAGHR
51  EEQLGGDVGF FVAAVADFFA VFVIHFRTER AAFVSAHRTQ AAAVEVFKEG
101 DFFGSAVAAR NADFAAEHQ EGFA*GEEPG LVVGGGVVLQ FAAGQDGFV
151 HARQVAARRP *

```

m571/a571 98.1% identity in 160 aa overlap

```

      10      20      30      40      50      60
m571.pep  MGIAGAVNVNLPAAAGRGTA VVVVGFAVPHAACVKGQAQADGARVFRAGHREEQLGGDVGF
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a571      MGIAGAVNVNLPAAAGRGTA VVVVGFAVPHAACVKGQAQADGARVFRAGHREEQLGGDVGF
      10      20      30      40      50      60

      70      80      90      100     110     120
m571.pep  FVAAVADFFFAVFVIDFRTERAAAFVSAHRTQAAAVEVFKEGDFFGSAVAARNADFAAEHQ
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a571      FVAAVADFFFAVFVIHFRTERAAAFVSAHRTQAAAVEVFKEGDFFGSAVAARNADFAAEHQ
      70      80      90      100     110     120

      130     140     150     160
m571.pep  EGFAQGEEPLVVG GGVVLQFAARQDGFVHARQVAARRPX
      ||||
a571      EGFAQGEEPLVVG GGVVLQFAAGQDGFVHARQVAARRPX
      130     140     150     160

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1713>:

g572.seq.

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```
1 atgtgcgcca tgcgcggggc ggcggggctg ccttcgcgc tcgcagcggc
51 gcaaaaaggc aaaaccattt atctggcaaa caaagaaacg ctggtggttt
101 ccggcgctgt gtttatggaa accgcccgcg caaacggcgc ggcagtggtg
151 cccgtcgaca gcgaacacaa cgcatttttc caagtgttgc cgcgcgatta
201 cacagaccgt ctgaacgaac acggcatcga ttcgattatc ctgaccgctt
251 ccggcgggcc gtttttaaca accgatttaa gcacgttcga cagcattacg
301 cccgagcagg cgggtcaaca ccccaattgg cgtatggggc gcaaaatctc
351 cgtcgattca gccactatgg caaacaaggg cttggaactg attgaagcgc
401 attggtgtgt caactgtccg cccgacaaac tcgaagtcgt catccatccc
451 caatccgtga tacacagtat ggtgcgttac cgcgacggct ccgtgctggc
501 gcaactgggc aatcccgata tgcgaacgcc catcgccat tgtttggcct
551 tgcccagcgc catcgattcg ggtgtcggca aactcgattt cggcgcattg
601 tcgcgcgtga ccttccaaaa gcccgacttc ggcgcgttcc cctgcctgaa
651 gttcgccat gaaaccataa acgcaggcgg agccgcgccc tgcgtattga
701 acgcgcgcaa cgaaaccgcc gtgcgcgctt ttttggacgg acagattaag
751 tttaccgaca ttgcaaaac cgtcgccac tgccttgac aagacttttc
801 aaacggcatg ggcgatatag aagyaactgt ggcgaagat gcccgacac
851 gcgcacaagc gcgggcattt atcggcacac tgcgtga
```

This corresponds to the amino acid sequence <SEQ ID 1714; ORF 572.ng>:

m572.pep..

```
1 MCAIVGAAGL PSALAAQKG KTIYLANKET LVVSGALFME TARANGAAVL
51 PVDSEHNAIF QVLPRDYTDRLNEHGIDSII LTASGGPFLT TDLSTFDSIT
101 PAQAVKHPNW RMGRKISVDS ATMANKGLEL IEAHWLFNCP PDKLEVVIHP
151 QSVIHSVMRY RDGSVLAQLG NPD MRTPIAY CLGLPERIDS GVGKLDLFDAL
201 SALTFFQKPDF GRFPCLKFAY ETINAGGAAP CVLNAANETA VAAFLDGQIK
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1715>:

m572.seq..

```
1 ATGTGCGCCA TCGTCGGGGC GGTGGGGCTG CCTTCCGCGC TCGCAGCGGC
51 GCAAAAAGGC AAAACCATTT ATCTGGCAAA CAAAGAAACG CTGGTGTTT
101 CCGGCGCTGT GTTTATGGAA ACCGCCCCTG CAAACGGCGC GGCAGTGCTG
151 CCCGTCGACA GCGAACACAA CGCCGTTTTC CAAGTTTTCG CGCGCGATTA
201 CGCCCGCCGT CTGAACGAAC ACGGCATCGC TTCGATTATC CTGACCGCTT
251 CCGGCGGCCC GTTCTGACC GCCGATTAA ACACGTTTCA CCGCATTACG
301 CCCGCCCAAG CGGTCAAACA CCCCATTGG CGTATGGGAC GCAAAATCTC
351 CGTCGATTCC GCCACCATGA TGAACAAAGG TTTGGAGCTG ATTGAAGCGC
401 ATTGGCTGTT CAACTGTCCG CCCGACAAAC TCGAAGTCGT CATCCATCCG
451 CAATCCGTGA TACACAGCAT GGTGCGCTAC CGGACGGCT CCGTGCTGGC
501 GCAACTGGGC AATCCCGATA TCGAACGCC CATCGCTTAT TGTTTGGGTT
551 TGCCCGAGCG CATCGATTCT GGTGTGGCG ACCTGGATT CTGACGATTG
601 TCCGCGCTGA CCTTCCAAA GCCCGACTTT GACCGCTTCC CCTGCCTGAG
651 GCTCGCTTAT GAAGCCATGA ACGCAGGCGG AGCCGCGCCC TCGCTATIGA
701 ACGCCGCCAA CGAAGCCGCC GTCCGCGCCT TTTTGGACGG ACAGATTAAG
751 TTTACCGACA TTGCCAAAC CGTCGCCAC TGCTTGCAC AAGACTTTTC
801 AGACGCATA GCGATATAG GGGGGCTCTT GGCACAAGAT GCCCGACAC
851 GCGCACAAGC GCGAGCATTT ATCGGCACAC TCGCTGA
```

This corresponds to the amino acid sequence <SEQ ID 1716; ORF 572>:

m572.pep..

```
1 MCAIVGAVGL PSALAAQKG KTIYLANKET LVVSGALFME TARANGAAVL
51 PVDSEHNAIF QVLPRDYAGR LNEHGLASII LTASGGPFLT ADLNTFDRIT
101 PAQAVKHPNW RMGRKISVDS ATMMNKGLEL IEAHWLFNCP PDKLEVVIHP
151 QSVIHSVMRY RDGSVLAQLG NPD MRTPIAY CLGLPERIDS GVGDLDFDAL
201 SALTFFQKPDF DRFPCLRLAY EAMNAGGAAP CVLNAANETA VAAFLDGQIK
251 FTDIAKTVAH CLAQDFSDGI GDIGLLAQD ARTRAQARAF IGTLR*
```

m572/g572 92.9% identity in 295 aa overlap

```
10 20 30 40 50 60
m572.pep MCAIVGAVGLPSALAAQKGKTIYLANKETLVVSGALFMETARANGAAVL PVDSEHNAIF
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g572 MCAIVGAAGLPSALAAQKGKTIYLANKETLVVSGALFMETARANGAAVL PVDSEHNAIF
10 20 30 40 50 60

70 80 90 100 110 120
m572.pep QVLPRDYAGRLNEHGLASII LTASGGPFLTADLNTFDRITPAQAVKHPNWRMGRKISVDS
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g572 QVLPRDYTDRLNEHGIDSII LTASGGPFLTDLSTFDSITPEQAVKHPNWRMGRKISVDS
```


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	70	80	90	100	110	120
m572 . pep	130	140	150	160	170	180
	ATMMNKGLELEIAHWLFNCP	PPDKLEVVIHPQSVIHS	MVRYRDG	SVLAQLGNPDMRTPIAY		
g572	ATMANKGLELEIAHWLFNCP	PPDKLEVVIHPQSVIHS	MVRYRDG	SVLAQLGNPDMRTPIAY		
	130	140	150	160	170	180
m572 . pep	190	200	210	220	230	240
	CLGLPERIDSGVGDLD	FDALSALTFQKPDFRFP	CLRLAYEAMNAGGAAP	CVLNAANEAA		
g572	CLGLPERIDSGVGKLD	FGALSALTFQKPDFRFP	CLKFAYETINAGGAAP	CVLNAANETA		
	190	200	210	220	230	240
m572 . pep	250	260	270	280	290	
	VAAFLDGQIKFTDI	AKTVAHCLAQDFSDG	IGDIGLLAQDAR	TRAQARAFIGTLRX		
g572	VAAFLDGQIKFTDI	AKTVAHCLAQDFSDG	IEGLLAQDAR	TRAQARAFIGTLRX		
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1717>:

```
a572.seq
1   ATGTGCGCCA TCGTCGGGGC GGTGGGGCTG CCTTCCGCGC TCGCAGCGGC
51  GCAAAAAGGC AAAACCATTT ATCTGGCGAA CAAAGAGACG CTGGTGGTTT
101 CCGGCGCGTT GTTTATGGAA ACCGCCCGTG CAAACGGCGC GGCAGTGC TG
151 CCCGTCGACA GCGAACACAA CGCCGTTTTC CAAGTTTTCG CGCGCGATTA
201 CACAGGTCGC CTGAACGAAC ACGGCATCGC TTCGATTATC CTGACCGCTT
251 CCGGCGGCCC GTTTCGACC GCCGATTAA ACACGTTTGA CAGCATTACG
301 CCCGACCAAG CGGTCAAACA CCCCAATTGG CGTATGGGAC GCAAAATCTC
351 CGTCGATTCC GCCACCATGA TGAACAAAGG TTTGGAGCTG ATTGAAGCGC
401 ATTGCTGTT CAACTGTCCG CCGACAAAC TCGAAGTCGT CATCCATCCG
451 CAATCTGTGA TACACAGCAT GGTGCGCTAC CGCGACGGCT CCGTGTGGGC
501 GCAACTGGGC AATCCCGATA TCGAACGCC TATCGCTTAT TGTTTGGGTT
551 TGCCCGAGCG CATCGATTCC GGTGTCGGCG ACCTGGATT TCGACGCATTG
601 TCCGCGCTGA CCTTCCAAA GCGCGACTTT GACCGCTTCC CCGCCTGAA
651 GCTCGCCTAT GAAGCCATGA ACGCAGGCGG AGCCGCGCCC TCGGTATTGA
701 ACGCCGCCAA CGAAGCCGCC GTCGCCGCT TTTGGACGG ACAGATTAAG
751 TTTACCGACA TTGCCAAAC CGTCGCCCAT TGTCTTTCAC AAGACTTTC
801 AGACGGCATA GCGACATAG GGGGGCTCTT GCGCAAGAT GCCCGGACAC
851 GCGCACAAAG GCGGCATT TATCGGCACAC TCGCTGA
```

This corresponds to the amino acid sequence <SEQ ID 1718; ORF 572.a>:

```
a572.pep
1   MCAIVGAVGL PSALAAQKG KTIYLANKET LVS GALFME TARANGAAVL
51  PVDSEHNAVF QVLPDYTGRLNEHGIASII LTASGGPFLT ADLNTFDSIT
101 PDQAVKHPNW RMGRKISVDS ATMMNKGLELEIAHWLFNCP PDKLEVVIHP
151 QSVIHSMVRY RDG SVLAQLGNPDMRTPIAY CLGLPERIDS VGDLDLFDAL
201 SALTFQKPDF DRFPCLKLAY EAMNAGGAAP CVLNAANEAA VAAFLDGQIK
251 FTDI AKTVAH CLSQDFSDGI GDIGLLAQD ARTRAQARAF IGTLR*
```

m572/a572 98.3% identity in 295 aa overlap

	10	20	30	40	50	60
m572 . pep	MCAIVGAVGLPSALAAQKGKTIYLANKETLVVSGALFME	TARANGAAVL	PVDSEHNAVF			
a572	MCAIVGAVGLPSALAAQKGKTIYLANKETLVVSGALFME	TARANGAAVL	PVDSEHNAVF			
	10	20	30	40	50	60
m572 . pep	QVLPDYAGRLNEHGIASII	LTASGGPFLTADLNTFDRIT	FAQAVKHPNWRMGRKISVDS			
a572	QVLPDYTGRLNEHGIASII	LTASGGPFLTADLNTFDSIT	FDQAVKHPNWRMGRKISVDS			
	70	80	90	100	110	120

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	130	140	150	160	170	180
m572.pep	ATMMNKGLELIEAHWLFNCPDKLEVVIHPQSVIHSVMRYRDGSVLAQLGNPDMRTPIAY					
a572	ATMMNKGLELIEAHWLFNCPDKLEVVIHPQSVIHSVMRYRDGSVLAQLGNPDMRTPIAY					
	130	140	150	160	170	180
	190	200	210	220	230	240
m572.pep	CLGLPERIDSGVGDLDLFDALSALTFOKPDFDRFPCLRLAYEAMNAGGAAPCVLNAANEAA					
a572	CLGLPERIDSGVGDLDLFDALSALTFOKPDFDRFPCLRLAYEAMNAGGAAPCVLNAANEAA					
	190	200	210	220	230	240
	250	260	270	280	290	
m572.pep	VAAFLDGQIKFTDIAKTVAHCLAQDFSDGIGDIGLLAQDARTRAQARAFIGTLRX					
a572	VAAFLDGQIKFTDIAKTVAHCLSQDFSDGIGDIGLLAQDARTRAQARAFIGTLRX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1719>:

g573.seq..

```

1  atgccctggt tgtgccgect taatcgcaat atcggcagtt tccaaatcac
51  gaatctcacc gaccataatg atgtccgggt cctgacgcag gaaagacttc
101 aaagcagcgg caaaagtcag accctgctta tcattgacgt taacctgatt
151 gatgccccgc aggttaatct cggcagggtc ttccgcgctt gcaatattta
201 ccgactccgt attcaaaata ttcaaacagg tatagagcga caccgtctta
251 ccgaaccggc tcggaccggg taccagcacc atcccgtaag gacggggaat
301 cgcttccaac aacaattttt tctggaacgg ctcaaaaccg agctggtcga
351 tcttcaaaaga cgcggcatcg gaattcaaaa tccgcacac gaccttttcg
401 ccaaacacgg tcggcaatgt gctgacacgg aaatcgacag gcttgccgcc
451 cttttgaaag gtcagctgca tctaccgtc ctgcggtatc cgtttttcgg
501 aaatgtccaa acgcgacatt accttaatcc ggggaagcaag ctgccccctt
551 accgcaatgg gcggctgaac cacctcgcgg agctgccgtt ccacacggaa
601 acggatacgc gcattgtgtt cgtaaaactc gaaatggatg tcggatgccc
651 cgctacgcaa ggcacccgac aaagttttat ggataaacct cggaaacagg
701 cgtctctctg cctcctcgtc gtcgatatac aggggtgggc ttctctcttc
751 ctcttgcccc tccccaaagt cctgaagcag cgatgtcgaa cgcgaacca
801 cccaatcgag caaacccgac aactggtcat cctcgacaat gaccaactca
851 accgcaatcc ctgcccgcga aaccgttttc tgaatttgcg gcatctgggt
901 cggatcgcaa accgcaaaaa atactttgtc gcccccacgg aaaaccggca
951 cacagtggaa ctccaccatc tgctcctcgg tcaacacccc catcagcacc
1001 ctgtggcgcg gataatgacg caaatcaaga atcgataaac tgaacaccct
1051 cgcaatcaat gccgcaagcg acttgggcga aatgacaccg tctga

```

This corresponds to the amino acid sequence <SEQ ID 1720; ORF 573.ng>:

g573.pep..

```

1  MPCLCLRLNRN IGSFQITNLT DHNDVRVLTQ BRLQSSGKSQ TLLIIDVNL
51  DARQVNLGRV FRRCNLYRLR IQNIQTGIER HRLTRTRRTG YQHHPVRTVN
101 RFQQQFFLER LKTELVDVQR RGIGIQNPHH DLFAKQRQRC ADTEIDRLAA
151 LLKGQLHPTV LRYPPFFGNVQ TRHYLNPGSK LPPYRNGRLN HLAELPVHTE
201 TDTRIVFVKL EMDVGCPATQ GIRQSPMDKP RNRAVFCLLV VDIQGVAFLE
251 LLPLPKLLKQ RCRTRTHPIE QTRQLVILDN DQLNRNPGCR NRFLNLRHLG
301 RIGNRKKYFV APTENRHTVE LHHLLLRQHP HQHPVARIMT QIKNRITEHP
351 RNQCRKRLGR NDTV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1721>:

m573.seq..

```

1  ATGCCCTGTT TGTGCCGCCT TAATCGCAAT ATCGGCAGTT TCCAAATCAC
51  GAATCTCACC GACCATAATG ATGTCCGGGT CCTGACGCAG GAAAGACTTC
101 AAAGCAGCGG CAAAAGTCAG GCCTGCTTAT TCATTGACGT TAACCTGATT
151 GATGCCCGGC AGGTTAATCT CGGCAGGGTC TTCCGCCGTT GCAATATTTA
201 CCGACTCCGT ATTCAAAATA TTCAACAGG TATAGAGCGA CACCGTCTTA
251 CCGAACCCTG TCGGACCGGT TACCAGCACC ATCCCGTAGG GACGGTGAAT
301 CGCTACCAAC aCaw.TTTT TCTGAAACGG CTCAAACCG AGCTGGTCTGA
351 TGTTCAAAGA CGCGGCATCG GAATTCAAAA TCCGCATCAC GACCTTTTCG
401 CCAACACAGC TCGGCAATGT GCTGACACGG AAATCGACAG GCTTGCCGCC
451 CTTTTGAAAG GTCAGCTGCA TCCTGCCGTC CTGCGGTATC CGTTTTTCGG
501 AAATGTCCAA ACGCGACATT ACCTTAATCC GTGAAGCAAG CTGCCCCCTT

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551 ACCGCAATGG GCGGCTGAAC CACCTCGCGG AGCTGCCCGT CCACACGGAA
601 ACGGATACGG GCATTGTGTT CGTAAACTC GAAATCGATG TCCGATGCCC
651 CGCTGCGCAA GGCATCCGAC AAAGTCTTAT GGATAAACC CTGGAACAGG
701 CCGTCTTCTG CCTCCTCGTT GTCGATATAC AGGGTGTGGC TTTCCTCTTC
751 CTCTGCCCC TCCCAAGCT CCTGAAGCAG CGATGTGCGA CGCGAACCCA
801 CCCAATCGAG CAAACCCGCC AACTGGTCAT CCTCGACAAT GACCAACTCA
851 ACCTCAATCC CTGCGGCAGA AACGGTTTTC TGAATTGCG GCATCTGTGT
901 CGGATCGGAA ACCGCAAAAA ATACTTTGTC GCCCGACGG AAAACCGGCA
951 CACAGTGGAA CTCCACCATC TGCTCCTCCG TCAACACCCC CATCAGCACC
1001 CTGTGGCGCG GATAATGACG CAAATCAAGA ATCGAATAAC TGAACACCCCT
1051 CGCAATCAAT GCCGCAAGCG ACTTGGCGCA AATGACACCG TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1722; ORF 573>:

m573.pep..

```

1  MPCLCRLNRN IGSFQITNLT DHNDVRVLTQ ERLQSSGKSQ ALLIIDVNLI
51  DARQVNLGRV FRCNIYRLR IQNIQTGIER HRLTRTRRTG YQHHPVGTVN
101 RYQHXFFLKR LKTELVDVQR RGIGIQNPHH DLPKQRRQC ADTEIDRLAA
151 LLKGQLHPAV LRYPPFGNVQ TRHYLNP*SK LPPYRNGRLN HLAELPVHTE
201 TDTGIVFVKL EMDVRCPPAQ GIRQSLMDKP RNRAVFCLLV VDIQGVAFLE
251 LLPLPKLLKQ RCRTRTHPIE QTRQLVILDN DQLNLNPGCR NGFLNLRHLC
301 RIGNRKKYFV APTENRHTVE LHHLLLRQHP HQHPVARIMT QIKNRITEHP
351 RNQCRKRLGR NDTV*

```

m573/g573 95.9% identity in 364 aa overlap

m573.pep	10	20	30	40	50	60
	MPCLCRLNRNIGSFQITNLTDHNDVRVLTQERLQSSGKSQALLIIDVNLI DARQVNLGRV					
g573	MPCLCRLNRNIGSFQITNLTDHNDVRVLTQERLQSSGKSQTLIIIDVNLI DARQVNLGRV					
	10	20	30	40	50	60
m573.pep	70	80	90	100	110	120
	FRCNIYRLRIQNIQTGIERHRLTRTRRTGYQHHPVGTVMRYQHXFFLKR LKTELVDVQR					
g573	FRCNIYRLRIQNIQTGIERHRLTRTRRTGYQHHPVGTVMRFQQFFLER LKTELVDVQR					
	70	80	90	100	110	120
m573.pep	130	140	150	160	170	180
	RGIGIQNPHHDLFAKQRRQCADTEIDRLAALLKGQLHPAVLRYPPFGNVQTRHYLNPXSK					
g573	RGIGIQNPHHDLFAKQRRQCADTEIDRLAALLKGQLHPTVLRYPFGNVQTRHYLNPXSK					
	130	140	150	160	170	180
m573.pep	190	200	210	220	230	240
	LPPYRNGRLNHLAELPVHTETDTGIVFVKLEMDVRCPPAQGIRQSLMDKPRNRAVFCLLV					
g573	LPPYRNGRLNHLAELPVHTETDTRIVFVKLEMDVGCPTAQGIRQSFMDKPRNRAVFCLLV					
	190	200	210	220	230	240
m573.pep	250	260	270	280	290	300
	VDIQGVAFLLPLPKLLKQRCRTRTHPIEQTRQLVILDNDQLNLNPGCRNGFLNLRHLC					
g573	VDIQGVAFLLPLPKLLKQRCRTRTHPIEQTRQLVILDNDQLNRNPGCRNRFNLRHLC					
	250	260	270	280	290	300
m573.pep	310	320	330	340	350	360
	RIGNRKKYFVAPTENRHTVELHHLLLRQHPHQHPVARIMTQIKNRITEHPRNQCRKRLGR					
g573	RIGNRKKYFVAPTENRHTVELHHLLLRQHPHQHPVARIMTQIKNRITEHPRNQCRKRLGR					
	310	320	330	340	350	360
m573.pep	NDTVX					
g573	NDTVX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1723>:

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a573.seq

```

1 ATGCCCTGTT TGTGCCGCCT TAATCGCAAT ATCGGCAGTT TCCAAATCAC
51 GAATCTCACC GACCATAATG ATGTCCGGGT CCTGACGCAG GAAAGACTTC
101 AAAGCAGCGG CAAAAGTCAG ACCCTGCTTA TCATTGACGT TAACCTGATT
151 GATGCCCGGC AGGTTAATCT CGGCAGGGTC TTCCGCCGTT GCAATATTTA
201 CCGACTCCGT ATTCAAAATA TTCAAACAGG TATAGAGCGA CACCGTCTTA
251 CCCGAACCCG TCGGACCGGT TACCAGCACC ATCCCGTAGG GACGGTGAAT
301 CGCTTCCAAC AACAATTTTT TCTGAAACGG CTCAAACCG AGCTGGTCGA
351 TGTTCAAAGA CGCGGCATCG GAATTCAAAA TCCGCATCAC GACCTTTTCG
401 CCAAACAGCG TCGGCAATGT GCTGACACGG AAATCGACAG GCTTGCCGCC
451 CTTTTGAAAG GTCAGCTGCA TCCTGCCGTC CTGCGGTATC CGTTTTTCGG
501 AAATGTCCAA ACGCGACATT ACCTTAATCC GGAAGCAAG CTGCCCCCTT
551 ACCGAATGG GCGGTGAAC CACCTCGCG AGCTGCCCGT CCACACGGAA
601 ACGGATACGG GCATTGTGTT CGTAAAACTC GAAATGGATG TCCGATGCCC
651 CGCTGCGCAA GGCATCCGAC AAAGTCTTAT GGATAAACCT CGGAACAGGG
701 CCGTCTTCTG CCTCCTCGTT GTCGATATAC AGGGTGTGGC TTTCTCTTTC
751 CTCCTGCCCC TCCCAAGCT CCTGAAGCAG CGATGTCGAA CGCGAACCCA
801 CCAATCGAG CAAACCGCC AACTGGTCAT CCTCGACAAT GACCAACTCA
851 ACCTCAATCC CTGCGGCAGA AACGGTTTTT TGAATTTGCG GCATCTGTGT
901 CGGATCGGAA ACCGCAAAAA ATACTTTGTC GCCCGACGG AAAACCGGCA
951 CACAGTGGA CTCCACCATC TGCTCCTCCG TCAACACCCC CATCAGCACC
1001 CTGTGGCGCG GATAATGACG CAAATCAAGA ATCGAATAAC TGAACACCCCT
1051 CGCAATCAAT GCCGAAGCG ACTTGGGCGA AATGACACCG TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1724; ORF 573.a>:

a573.pep

```

1 MPCLCRLNRN IGSFQITNLT DHNDVRVLTQ ERLQSSGKSQ TLLIIDVNLI
51 DARQVNLGRV FRCNIYRLR IQNIQTGIER HRLTRTRRTG YQHHPVGTVN
101 RFQQQFFLKR LKTELVDVQR RGIGIQNPHH DLFAKQRRQC ADTEIDRLAA
151 LLKGQLHPAV LRYPPFGNVQ TRHYLNPGSK LPPYRNGRLN HLAELPVHTE
201 TDTGIVFVKL EMDVRCFAAQ GIROSLMDKP RNRAVFCLLV VDIQGVAFLE
251 LLPLPKLLKQ RCRTRTHPIE QTRQLVILDN DQLNLNPGCR NGFLNLRHLC
301 RIGNRKQYFV APTENRHTVE LHHLLLRQHP HQHPVARIMT QIKNRITEHP
351 RNQCRKRLGR NDTV*

```

m573/a573 98.6% identity in 364 aa overlap

	10	20	30	40	50	60
m573.pep	MPCLCRLNRNIGSFQITNLT DHNDVRVLTQ ERLQSSGKSQ ALLIIDVNLI DARQVNLGRV					
a573	MPCLCRLNRNIGSFQITNLT DHNDVRVLTQ ERLQSSGKSQ TLLIIDVNLI DARQVNLGRV					
	10	20	30	40	50	60
m573.pep	FRCNIYRLRIQNIQTGIERHRLTRTRRTGYQHHPVGTVNRYQHXXFLKRLKTELVDVQR					
a573	FRCNIYRLRIQNIQTGIERHRLTRTRRTGYQHHPVGTVNRFQQQFLKRLKTELVDVQR					
	70	80	90	100	110	120
m573.pep	FRCNIYRLRIQNIQTGIERHRLTRTRRTGYQHHPVGTVNRYQHXXFLKRLKTELVDVQR					
a573	FRCNIYRLRIQNIQTGIERHRLTRTRRTGYQHHPVGTVNRFQQQFLKRLKTELVDVQR					
	70	80	90	100	110	120
m573.pep	RGIGIQNPHHDLFAKQRRQCADTEIDRLAALLKGQLHPAVLRYPPFGNVQTRHYLNPGSK					
a573	RGIGIQNPHHDLFAKQRRQCADTEIDRLAALLKGQLHPAVLRYPPFGNVQTRHYLNPGSK					
	130	140	150	160	170	180
m573.pep	RGIGIQNPHHDLFAKQRRQCADTEIDRLAALLKGQLHPAVLRYPPFGNVQTRHYLNPGSK					
a573	RGIGIQNPHHDLFAKQRRQCADTEIDRLAALLKGQLHPAVLRYPPFGNVQTRHYLNPGSK					
	130	140	150	160	170	180
m573.pep	LPPYRNGRLNHLAELPVHTETDTGIVFVKLEMDVRCFAAQGIROSLMDKPRNRAVFCLLV					
a573	LPPYRNGRLNHLAELPVHTETDTGIVFVKLEMDVRCFAAQGIROSLMDKPRNRAVFCLLV					
	190	200	210	220	230	240
m573.pep	LPPYRNGRLNHLAELPVHTETDTGIVFVKLEMDVRCFAAQGIROSLMDKPRNRAVFCLLV					
a573	LPPYRNGRLNHLAELPVHTETDTGIVFVKLEMDVRCFAAQGIROSLMDKPRNRAVFCLLV					
	190	200	210	220	230	240
m573.pep	VDIQGVAFLELLPLPKLLKQRCRTRTHPIEQTRQLVILDNDQLNLNPGCRNGFLNLRHLC					
a573	VDIQGVAFLELLPLPKLLKQRCRTRTHPIEQTRQLVILDNDQLNLNPGCRNGFLNLRHLC					
	250	260	270	280	290	300
m573.pep	VDIQGVAFLELLPLPKLLKQRCRTRTHPIEQTRQLVILDNDQLNLNPGCRNGFLNLRHLC					
a573	VDIQGVAFLELLPLPKLLKQRCRTRTHPIEQTRQLVILDNDQLNLNPGCRNGFLNLRHLC					
	250	260	270	280	290	300

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	310	320	330	340	350	360
m573.pep	RIGNRKKYFVAPTENRHTVELHLLLRQHPHQHPVARIMTQIKNRITEHPRNQCRKRLGR					
a573	RIGNRKKYFVAPTENRHTVELHLLLRQHPHQHPVARIMTQIKNRITEHPRNQCRKRLGR					
	310	320	330	340	350	360

m573.pep	NDTVX
a573	NDTVX

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1725>:

g574.seq

```

1 atgctgccga atctgccaaa cagccttaag aaagccgata tggacaacga
51 attgtggatt atcctgctgc cgattatcct tttgcccgtc ttcttcacga
101 tgggtcggtt tgcgcgccgc gtggatatga aaaccgtatt gaagcaggca
151 aaaagcatcc cttegggatt ttataaaagc ctggacgctt tggtcgacccg
201 caacagcggg cgcgcggcaa gggagttggc ggaagtcgtc gacggccggc
251 cgcaatcgta tgatttgaa cttaccctcg gcaaaactta ccgtcagcgc
301 ggcgaaaacg acaaagccat caacatacac cggacaatgc tcgattctcc
351 cgatacggtc ggcgaaaagc gcgcgcgcgt cctgtttgaa ttggcgcaaa
401 actaccasag cgcgggtttg gtcgatcggt ccgaacagat ttttttgggg
451 ctgcaagacg gtgaaatggc gcgtgaagcc agacagcacc tgctcaatat
501 ctaccagcag gacagggatt gggaaaaagc ggttgaaacc gcccaacttc
551 ttagtccaga cgaacagaca tatcagtttg agattgcaca gttttattgc
601 gaacttgccc aagccgcgct gttcaagtcc aatttcgatg ccgcgcggtt
651 caatgtcgcc aaggcaactc aagccaacaa aaaatgcacc cgcgccaaaca
701 tgattttggg cgacattgaa caccgacaag gcaatttccc tgcgcgcgtc
751 gaagcctatg ccgccatcga gcagcaaaac catgcatact tgagcatggt
801 cggcgagaag ctttacgaag cctatgccgc gcagggaaaaa cctgaagaag
851 gcttgaacgc tctgacagga tatacgaga cgtttcccca acttgacctg
901 atcaatgtcg tgtacgagaa atccctgctg ctttaaggcg agaaaagaagc
951 cgcgcaaaac gccgtcgagc ttgtccgcgc caagcccgac cttaacggcg
1001 tgtaccgcct gctcggtttg aaactcagcg atttggatcc ggcttggaag
1051 gccgatgccg acatgatgcg ttccggtatc ggaaggcagc tccagcgtag
1101 cgtgatgtac cgttgccgca actgccactt caaatcccaa gtctttttct
1151 ggcactgtcc cgcctgcaac aaatggcaga cgtttacgcc gaataaaatc
1201 gaagttaa
```

This corresponds to the amino acid sequence <SEQ ID 1726; ORF 574.ng>:

g574.pep..

```

1 MNLPLNSLIK KADMDNELWI ILLPIILLPV FFTMGWFAAR VDMKTVLKQA
51 KSIPSGFYKS LDALVDRNSG RAARELAENV DGRPQSYDLN LTLGKLYRQR
101 GENDKAINIH RTMLDSPDTV GEKRARVLFE LAQNYQSAGL VDRAEQIFLG
151 LQDGSMAREA RQHLLNIYQQ DRDWEKAVET AQLLSHDEQT YQFETAFQYC
201 BLAQAAALPKS NFDAARFNVG KALBANKKCT RANMILGDIE HRQGNFPAAV
251 BAYAAIEQQN HAYLSMVGEK LYEAYAAQCK PEBGLNRLTG YMQTFPELDL
301 INVVEKSLIL LKBEKEAAQT AVELVRRKPD LNGVYRLGLL KLSDLDPWAK
351 ADADMRSVI GRQLQRSVMY RCRNCHFQSQ VFFWHCPACN KWQTFTPNKI
401 EV*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1727>:

m574.seq..

```

1 ATGCGCCCGA ATCTACCAA CAGCCTTAAG AAAGCCGATA TGGACAACGA
51 ATTGTGGATT ATCCTGCTGC CGATTATCCT TTTGCCCGTC TTCTTCGCGA
101 TGGGCTGGTT TGCCGCCCGC GTGGATATGA AAACCGTATT GAAGCAGGCA
151 AAAAGCATCC CTTCCGGATT TTATAAAAGC TTGGACGCTT TGGTCGACCG
201 CAACAGCGGG CGCGCGGCAA GGGAGTTGGC GGAAGTCGTC GACGGCCGGC
251 CGCAATCGTA TGATTGAA CTTACCCCTG GCAAACTTTA CCGCCAGCGT
301 GGCAGAAAAG ACAAAGCCAT CAACATACAC CGGACAATGC TCGATTCTCC
351 CGATACGGTC GGCAGAAAAG CCGCGCGCGT CCTGTTTGAA TTGGCGCAAA
401 ACTACCAAGG TGCGGGGTTG GTCGATCGTG CCGAACAGAT TTTTTCGGGG
451 CTGCAAGACC GTAAAATGGC GCGTGAAGCC AGACAGCACC TGCTCAATAT
501 CTACCAACAG GACAGGGATT GGGAAAAAGC GGTGAAAACC GCCCGGCTGC
551 TCAGCCATGA CGATCAGACC TATCASTTTG AAATCGCCCA GTTTTATATG
601 GAACCTMGCC AAGCCGCGCT GTTCAAGTCC AATTTCGATG TCGCGCGTTT
```

885

```
651 CAATGTCGGC AAGGCACTCG AAGCCAACAA AAAATGCACC CGCGCCAACA
701 TGATTTTGGG CGACATCGAA CACCGACAAG GCAATTTCCC TGCCGCCGTC
751 GAAGCCTATG CCGCCATCGA GCAGCAAAAC CATGCATACT TGAGCATGGT
801 CGCGGAGAAG CTTTACGAAG CCTATGCCGC GCAGGGAAAA CCTGAAGAAG
851 GCTTGAACCG TCTGACAGGA TATATGCAGA CGTTTCCCGA ACTTGACCTG
901 ATCAATGTCTG TGTACGAGAA ATCCCTGCTG CTTAAGTGGC AGAAAGAAGC
951 CGCGCAAAAC GCCGTCGAGC TTGTCCGCGC CAAGCCCAC CTTAACGGCG
1001 TGTACCGCCT GCTCGGTTTG AAACCTCAGCG ATATGAATCC GGCTTGGAAA
1051 GCCGATGCCG ACATGATGCG TTCGGTTATC GGACGGCAGC TACAGCGCAG
1101 CGTGATGTAC CGTTGCCGCA ACTGCCACTT CAAATCCCAA GTCCTTTTCT
1151 GGCAC TGCC CCGCTGCAAC AAATGGCAGA CGTTTACCCC GAATAAAATC
1201 GAAGTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1728; ORF 574>:

m574.pep..

```
1 MRPNLPNSLK KADMDNELWI ILLPIILLPV FFAMGWFAAR VDMKTVLKQA
51 KSTPSGFYKS LDALVDRNSG RAARELAEVV DGRPQSYDLN LTLGKLYRQR
101 GENDKAINIH RTMLDSPDTV GEKRARVLFE LAQNYQSAGL VDRAEQIFLG
151 LQDGKMAREA RQHLLNIYQQ DRDWEKAVET ARLLSHDDQT YQFEIAQFYC
201 BLAQAAFLKS NFDVARFNVG KALEANKKCT RANMILGDIE HRQGNFPAAV
251 BAYAAIEQQN HAYLSMVGEK LYEAYAAQCK PEEGLNRLTG YMQTFPELDL
301 INVVEKSLLL KCEKEAAQT AVELVRRKPD LNGVYRLGL KLSDMNPAWK
351 ADADMRSVI GRQLQRSVMY RCRNCHFKSQ VFFWHCPACN KWQTFTPNKI
401 EV*
```

m573/g573 97.8% identity in 402 aa overlap

	10	20	30	40	50	60
m574.pep	MRPNLPNSLKADMDNELWIILLPIILLPVFFAMGWFAARVDMKTVLKQAKSIPSGFYKS					
g574	MLPNLPNSLKKADMDNELWIILLPIILLPVFTMGWFAARVDMKTVLKQAKSIPSGFYKS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m574.pep	LDALVDRNSGRAARELAEVVDGRPQSYDLNLTGLKLYRQRGENDKAINIHRTMLDSPDTV					
g574	LDALVDRNSGRAARELAEVVDGRPQSYDLNLTGLKLYRQRGENDKAINIHRTMLDSPDTV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m574.pep	GEKRARVLPFLAQNYQSAGLVDRAEQIFLGLQDGKMAREARQHLLNIYQQDRDWEKAVET					
g574	GEKRARVLPFLAQNYQSAGLVDRAEQIFLGLQDGKMAREARQHLLNIYQQDRDWEKAVET					
	130	140	150	160	170	180
	190	200	210	220	230	240
m574.pep	ARLLSHDDQTYQFEIAQFYCELAQAALFKSNFDVARFNVGKALEANKKCTRANMILGDIE					
g574	AQLSHDEQTYQFEIAQFYCELAQAALFKSNFDAARFNVGKALEANKKCTRANMILGDIE					
	190	200	210	220	230	240
	250	260	270	280	290	300
m574.pep	HRQGNFPAAVEAYAAIEQQNHAYLSMVGEKLYEAYAAQCKPEEGLNRLTGYMQTFPELDL					
g574	HRQGNFPAAVEAYAAIEQQNHAYLSMVGEKLYEAYAAQCKPEEGLNRLTGYMQTFPELDL					
	250	260	270	280	290	300
	310	320	330	340	350	360
m574.pep	INVVEKSLLLKCEKEAAQTAVELVRRKPD LNGVYRLGLKLSDMNPAWKADADMRSVI					
g574	INVVEKSLLLKCEKEAAQTAVELVRRKPD LNGVYRLGLKLSDLPAWKADADMRSVI					
	310	320	330	340	350	360
	370	380	390	400		
m574.pep	GRQLQRSVMYRCRNCHFKSQVFFWHCPACN KWQTFTPNKIEVX					
g574	GRQLQRSVMYRCRNCHFKSQVFFWHCPACN KWQTFTPNKIEVX					
	370	380	390	400		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1729>:

```
a574.seq
1   ATGCGCCCGA ATCTGCCAAA CAGCCTTGAG AAAGCCGATA TGGACAATGA
51  ATTGTGGATT ATCCTGCTGC CGATTATCCT TTTGCCCGTT TTCTTCGCGA
101 TGGGCTGGTT TGCCGCCCGC GTGGATATGA AGACTGTATT AAAGCAGGCA
151 AAAAGCATAAC CGTCGGGATT TTATAAAAGT CTGGATGCCT TGGTTGACCG
201 CAACAGCCGGC CGCGCGGCAA GGGAGTTGGC GGAAGTCGTC GACGGCCGGC
251 CGCAATCGTA TGATTTGAAC CTCACCCTCG GCAAACCTTA CCGCCAGCGT
301 GGCAGAAAACG ACAAAGCCAT CAATATGCAC CAAACATTGC TTGACTCTCC
351 CGATACAACC GGAGCCAAGC GCGCGCGCGT CCTGTTTGAA TTGGCGCAAA
401 ACTACCAAAG TGCGGGGTTG GTCGATCGTG CCGAACAGAT TTTTTTGGGG
451 CTGCAAGACG GTGAAATGGC GCGTGAAGCC AGACAGCACC TGCTCAATAT
501 CTACCAACAG GACAGGGATT GGGAAAAAGC GGTTGAAACC GCCCGGCTGC
551 TCAGCCATGA CGATCAGACC TATCAGTTTG AAATCGCCCA GTTTTATTGC
601 GAACCTGCCC AAGCCGCGCT GTTCAAGTCC AATTTCGATG CCGCGCGTTT
651 CAATGTCGGC AAGGCACTCG AAGCCAACAA AAAATGCACC CGCGCCAACA
701 TGATTTTGGG CGACATCGAA CACCGACAAG GCAATTTCCC TGCCGCGGTC
751 GAAGCCTATG CCGCCATCGA GCAGCAAAAC CATGCATACT TGAGTATGGT
801 CGGCGAGAAG CTTTACGAAG CCTATGCCGC GCAGGGAAAA CCTGAAGAAG
851 GCTTGAACCG TCTGACAGGA TATATGCAGA CGTTTCCCGA ACTTGACCTG
901 ATCAATGTCG TGACGAGAA ATCCCTGCTG CTTAAGTGGC AGAAAGAAGC
951 CGCGCAAACC GCCGTCGAGC TTGTCCGCCG CAAGCCCGAC CTCAACGGCG
1001 TGTACCGCCT GCTTGGTTTG AAATCAGCGC ATTTGGATCC GGCTTGGA
1051 GCCGATGCCG ATATGATGCG TTCGGTTATC GGACGGCAGC TACAGCGCAG
1101 CGTGATGTAC CGGTGCCGAA ACTGCCACTT CAAATCACAA GTCTTTTCT
1151 GGCATTGTCC TGCCTGCAAC AAATGGCAGA CGTTTACGCC AAACAAAATC
1201 GAAGTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1730; ORF 574.a>:

```
a574.pep
1   MRPNLPNSLE KADMDNELWI ILLPIILLPV FFAMGWFAAR VDMKTVLKQA
51  KSIPSGFYKS LDALVDRNSG RAARELAEVV DGRPQSYDLN LTGLKLYRQR
101 GENDKAINMH QTLDSPDTT SAKRARVLFE LAQNYQSAGL VDRAEQIFLG
151 LDQGEMAREA RQHLNLIYQQ DRDWEKAVET ARLLSHDDQT YQFEIAQFYC
201 ELAQAAALFKS NFDAARFNVG KALEANKKCT RANMILGDIE HRQGNFPAAV
251 EAYAAIEQQN HAYLSMVGEK LYEAYAAQSK PEEGLNRLTG YMQTFPELDL
301 INVVYEKSL LKCEKEAAQT AVELVRRKPD LNGVYRLGL KLSDLDPAWK
351 ADADMRSVI GRQLQRSVMY RCRNCHFKSQ VFFWHCPACN KWQTFTPNKI
401 EV*
```

m574/a574 97.5% identity in 402 aa overlap

	10	20	30	40	50	60
m574.pep	MRPNLPNSL	KADMDNELWI	ILLPIILLPV	FFAMGWFAAR	VDMKTVLKQA	KSIPSGFYKS
a574	MRPNLPNSLE	KADMDNELWI	ILLPIILLPV	FFAMGWFAAR	VDMKTVLKQA	KSIPSGFYKS
	70	80	90	100	110	120
m574.pep	LDALVDRNSG	RAARELAEVV	DGRPQSYDLN	LTGLKLYRQR	GENDKAINIH	RMTLDSPD
a574	LDALVDRNSG	RAARELAEVV	DGRPQSYDLN	LTGLKLYRQR	GENDKAINMH	QTLDSPDTT
	130	140	150	160	170	180
m574.pep	GEKRARVLFE	LAQNYQSAGL	VDRAEQIFLG	LDQGEMARE	ARQHLNLIY	QQDRDWEKAVET
a574	GAKRARVLFE	LAQNYQSAGL	VDRAEQIFLG	LDQGEMARE	ARQHLNLIY	QQDRDWEKAVET
	190	200	210	220	230	240
m574.pep	ARLLSHDDQT	YQFEIAQFYC	ELAQAAALFKS	NFVARFNVG	KALEANKKCT	RANMILGDIE
a574	ARLLSHDDQT	YQFEIAQFYC	ELAQAAALFKS	NFVARFNVG	KALEANKKCT	RANMILGDIE

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	190	200	210	220	230	240
	250	260	270	280	290	300
m574.pep	HRQGNFPAAVEAYAAIEQQNHAYLSMVGEKLYEAYAAQKGPEEGLNRLTGVMQTFPELDL					
a574	HRQGNFPAAVEAYAAIEQQNHAYLSMVGEKLYEAYAAQKGPEEGLNRLTGVMQTFPELDL					
	250	260	270	280	290	300
	310	320	330	340	350	360
m574.pep	INVVYEKSLLLKCEKAAQTAVELVRRKPDINGVYRLLGLKLSDMNPAWKADADMMRSVI					
a574	INVVYEKSLLLKCEKAAQTAVELVRRKPDINGVYRLLGLKLSDLPAWKADADMMRSVI					
	310	320	330	340	350	360
	370	380	390	400		
m574.pep	GRQLQRSVMYRCRNCHFKSQVFFWHCPACNKWQTFTPNKIEVX					
a574	GRQLQRSVMYRCRNCHFKSQVFFWHCPACNKWQTFTPNKIEVX					
	370	380	390	400		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1731>:

```

g575.seq (partial)
1 ..atgccgtgcc tccgccggca agcagcaagg tgtaaccaacc gccgaacaga
51 ccgtcaaaca gtccgcttcc ggtttcttct tcggcagaaa cctgttcgac
101 aggttcggca acgggttcgg cggcaacttc actggctgtt tccgcaacag
151 gttcggaaac ggtgttaccg gtttcgtcgg tcggcgtgtc gatggcagaa
201 gcggcggttt cttggggggg cggattcgcc agcgggttcc gatgcggcag
251 tatttgcagc ggttacaggt cgggtttggc gttctgtcgc cgaagccgga
301 gtttcggaca ctgcgggttt ggggttcggg cgaacggccg gtttttcgcg
351 ttttgcttcg ggcgcggcaa cttttgcttc aggtttttca accggttttt
401 cgacagggtt ctctatcggt ttctccacag ttgcctgttt ggacgggtta
451 gacggcatgg atgcagtttc ggcctttggg ttgcgcgttt gcggtttggg
501 ttggtccgct ttgatttttt tgggtgctgc cgctttgatc ctgttcagat
551 tcggaatgtg a*

```

This corresponds to the amino acid sequence <SEQ ID 1732; ORF 575.ng>:

```

g575.pep (partial)
1 ..MPCLRRQAAR CTNRRTDROT VRFRELLRQK PVRQVRQVR RQLHNLFPQO
51 VRKRCYRFRR SACRWQKRRL LGGADSAVVS DAAVFAAGTG PGWRSVAEAG
101 VSDTAGLGSG RTAGFSAFAS GAATFASGFS TGFSTGFSIG FSTVACLDS
151 DGMDAVSALG FAVCGLGCSA LIPLGAAALI LRFPGM*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1733>:

```

m575.seq..
1 ATGGTTTCGG GCGAGGAAGC CTTACGGAAG CCTGCCAGTC CGGAGGGTGA
51 GGCAGGTTT GCGGAAGCTG TTTCTTCTGT GCCGATATGG TTGTTTGAGG
101 GCAGGTTGTC GGAGAAATCG GTATCGACGG TTCCCGGTTT GTTTTCGGCA
151 GTTTGGGCGA CAGATTCCGG TTCGGGCGTG TCGATGACGA TTTCGACAGG
201 GTTGTTACGG TTGAAGTCT CCGGCTCGTA CACGCTGTCT GTGATTTCGA
251 TGGCGTTCCA ATCGGCATCC GCGCGTTTTT GGGTTTCTTC ATCCTGCGTA
301 AGTGCGCCGG ATAAAATGCC GTTTTGCGCG GCTGCCAGGC TGTGAAATC
351 CAAGTCGATG CGGTTGGAAG GCGTATCGGT TTCGACATCG AACGTTTGTT
401 TTGCGGATAA CTCTTCTTCA GATTCCCAT CTAAGGCAAG TGTGCTGTTT
451 ACATCGTTTT TCGGAGCGGG TTCGGGCGTT GCGGAGTTT CGACTTCGSC
501 AAAGGTGATT TCTATGCCGT CGTCTGCCGC GTCGTCAAGG TCAGGCTCTT
551 CCTCAGGAC GGATTCTTCG GTACGGCGCG CGGTTTGA TTGGGCAAGG
601 CGCAAAAGCA GCAGCAGGGC GATTAATGCC GCGCCTCCGC CGGCAAGCAG
651 CAAGGTGTAC GAACCGCGA ACAGACCGTC AAACAGTCCG CTTTCGGTTT
701 CTTCTTCGCG AGAAACCTGT TCGACAGGTT CGGAAACGGC GTTACCGGTT
751 TCGTCGGTCG GCGTGTGAT GGCAGAACGG GCGGCTTCTT GGGGGCGGSA
801 TTCGGCAGCG GTTTCGATG CGGCAGTATT TGCAGCGGGT ACAGGTTTCG
851 GTCGAACGGC CGGTTTTTCC GCTTTTGCTT CGGCGCGGCG AACTTTTGCT
901 TCAGGTTTTT CAACCGGTTT CTCTACGTT GCCTGTTTGG ACGGTTTCGSA
951 CGGCATGAT GCGGTTTCGG CTTTGGGTTT CGCGGTTTGC GGTTCGGGTT
1001 GTTCCGCTTT GATCCTGTTT AGATTGCGAA TGTGA

```


888

This corresponds to the amino acid sequence <SEQ ID 1734; ORF 575>:

```
m575.pep
  1  MVSGEAEFRK PASPEGEAGF AEA VSSVPIW LFEGR LSEKS VSTVSGLFSA
 51  VWATDSGSGV SMTISTGLYG LKVS GSYTLS VDSMAFQSAS ARFWVSSSCV
101  SAPDKMPFCA AARLSKSKSM RLEGVSVSTS NVC FADNSSS DSPSKASVSF
151  TSFFGAGSGV AGVSTSAKVI SMPSSAASSR SGSSSGTDSS VRRARLDWAR
201  RKSSSRAINA APPPASSKVY EPPNR?SNSP LSVSSSAETC STGSETALPV
251  SSVGVSMABA AASWGADSAV VSDAAVFAAG TSGRTAGFS AFASGAATFA
301  SGFSTGFSTV ACLDGS DGM D AVSALGFAVC GLGCSALILF RFGM*
```

m575/g575 70.2% identity in 114 aa overlap

```

      240      250      260      270      280
m575.pep  SSABTCSTGSETALPVSSVGVSMAEAAASWGADSAVSDAAVFAAGT-----
              |||||
g575      LHWLFPQQRKRCYRPRRSACRWQKRLLGGADSAVSDAAVFAAGTGPWNRVSAEAGVS
              50      60      70      80      90      100

      290      300      309      310      320
m575.pep  -----SORTAGFSAPASGAATFASGFSTGFST-----VACLDGSDGMDAVSALGFA
              |||||
g575      DTAGLGSGRTAGFSAPASGAATFASGFSTGFSTGFSIGFSTVACLDGSDGMDAVSALGFA
              110     120     130     140     150     160

      330      340
m575.pep  VCGLGCSALI-----LFRFGMX
              |||||
g575      VCGLGCSALIFLGAAALILFRFGMX
              170     180

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1735>:

```
a575.seq
  1  ATGTTTTCGG GCGAGGAAGC CTT CAGGAAG CCTGCCAGTC CGGAGGGTGA
 51  GGCAGGTTTT GCGGAAGCTG TTTCTTCTGT GCCGATATGG TTGTTTGAGG
101  GCAGGTTGTC GGAGAAATCG GTATCGACGG TTTCCGGTTT GTTTTCGGCA
151  GTTTGGGCGA CAGATTCCGG TTCGGGCGTG TCGATGACGA TTTCGACAGG
201  GTTGTACGGG TTGAAGGTCT CGGGCTCGTA CACGCTGTCT GTGGATTCTGA
251  TGGCGTTCCA ATCGGCATCC GCGCGTTTTT GGGTTTCTTC ATCCTGCGTA
301  AGTGCGCCGG ATAAATGCC GTTTTGCGCG GCTGCCAGGC TGTGCAATC
351  CAAGTCGATG CGGTTGGAAG GCGTATCGGT TTCGACATCG AACGTTTGTT
401  TTGCCGACAA CTCTTCTTCA GATTCCCCAT CTAAGGCAAG TGTGTCGTTT
451  ACATCGTTTT TCGGAGCGGG TTCGGGCGTT GCCCGAGTTT CGACTTCGGC
501  AAAGGTGATT TCTATGCCGT CGTCTGCCGC GTCGTC AAG TCAGGCTCTT
551  CCTCAGGGAC GGATTCTTCG GTACGCGCGC GCGGTTTGGG TTGGGCAAGG
601  CGCAAAGCA GCAGCAGGGC GATCAATGCC GCCCTCCGC CGGCAAGCAG
651  CAAGGTGTAC GAACCGCCGA ACAGTCCGCT TTCGGTTTCT TCTTCGGCAG
701  AAACCTGTTT GACAGGTTCT GAAACGGCGT TACCGGTTTC GTCGGTCGGC
751  GTGTCGATGG CAGAAGCGGC GGCTTCTTGG GGGGCGGATT CGGCAGCGGT
801  TTCCGATGCG CAGTATTTG CAGCGGTAC AGGTTGGGT CGAACGGCCG
851  GTTTTCCGC TTTTGCTTCG GCGCGGCAA CTTTGTCTC AGGTTTTCTA
901  ACCGGTTTCT CTACCGTTGC CTGTTGGAC GGTTCGGAC GCATGGATGC
951  GGTTCGGCT TTGGGTTTCG CCGTTGCGG TTTGGGTTGT TCCGCTTTGA
1001 TCCTGTTTCA ATTCCGAATG TGA
```

This corresponds to the amino acid sequence <SEQ ID 1736; ORF 575.a>:

```
a575.pep
  1  MVSGEAEFRK PASPEGEAGF AEA VSSVPIW LFEGR LSEKS VSTVSGLFSA
 51  VWATDSGSGV SMTISTGLYG LKVS GSYTLS VDSMAFQSAS ARFWVSSSCV
101  SAPDKMPFCA AARLSKSKSM RLEGVSVSTS NVC FADNSSS DSPSKASVSF
151  TSFFGAGSGV AGVSTSAKVI SMPSSAASSR SGSSSGTDSS VRRARLDWAR
201  RKSSSRAINA APPPASSKVY EPPNSPLSVS SSAETCSTGS ETALPVSSVG
251  VSMAEAAASW GADSAAVSDA AVFAAGTGS RTAGFSAFAS GAATFASGFS
301  TGFSTVACLD GSDGMDAVSA LGFAVCGLGC SALILFRFGM *
```

889

m575/a575 98.8% identity in 344 aa overlap

	10	20	30	40	50	60
m575.pep	MVSGEEAFRKPASPEGEAGFAEAVSSVPIWLFEGRLSEKSVSTVSGLFSAVWATDSGSGV					
a575	MVSGEEAFRKPASPEGEAGFAEAVSSVPIWLFEGRLSEKSVSTVSGLFSAVWATDSGSGV					
	70	80	90	100	110	120
m575.pep	SMTISTGLYGLKVGSYTSLVDSMAFQSASARFWSSSCVSAAPDKMPFCAAARLSKSKSM					
a575	SMTISTGLYGLKVGSYTSLVDSMAFQSASARFWSSSCVSAAPDKMPFCAAARLSKSKSM					
	130	140	150	160	170	180
m575.pep	RLEGVSVSTSNVCFADNSSSDSPSKASVSFTSFFGAGSGVAGVSTSAKVISMPSAASSR					
a575	RLEGVSVSTSNVCFADNSSSDSPSKASVSFTSFFGAGSGVAGVSTSAKVISMPSAASSR					
	190	200	210	220	230	240
m575.pep	SGSSSGTDSSVRRARLDWARRKSSSRINAAPPPASSKVYEPNRPNSPLSVSSSAETC					
a575	SGSSSGTDSSVRRARLDWARRKSSSRINAAPPPASSKVYEPN----SPLSVSSSAETC					
	250	260	270	280	290	300
m575.pep	STGSETALPVSSVGVSMAEAAASWGADSAAVSDAAVFAAGTGSGRTAGFSAFASGAATFA					
a575	STGSETALPVSSVGVSMAEAAASWGADSAAVSDAAVFAAGTGSGRTAGFSAFASGAATFA					
	310	320	330	340		
m575.pep	SGFSTGFSTVACLDGSDGMDAVSALGFAVCGLCGCSALILFRFGMX					
a575	SGFSTGFSTVACLDGSDGMDAVSALGFAVCGLCGCSALILFRFGMX					
	300	310	320	330	340	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1737>:

g576.seq.. (partial)

```

1 ..atgggcgtgg acatcggacg ctccctgaaa caaatgaagg aacaggcgcg
51 ggaaatcgat ttgaaagtct ttaccgatgc catgcaggca gtgtatgacg
101 gcaaagaaat caaatgacc gaagagcag cccaggaagt gatgatgaaa
151 ttctctgcagg agcagcaggc taaagccgta gaaaaacaca aggcggatgc
201 gaagcccaac aaagaaaaag gcgaagcctt cctgaaggaa aatgcccgcg
251 aagacggcgt gaagaccact gttccggtc tgcagtacaa aatcaccaaa
301 cagggtgaag gcaaacagcc gacaaaagac gacatcgta ccgtggaata
351 cgaaggccgc ctgattgacg gtaccgtatt cgacagcagc aaagccaacg
401 gcggcccggc caccttcctt ttgagccaag tgattccggg ttggaccgaa
451 ggcgtagcgc ttctgaaaga aggcggcgaa gccacgttct acatcccgtc
501 caaccttgcc taccgcgaac aggtgcgagg cgaaaaaatc ggtccgaacg
551 ccactttggt atttgacgtg aaactgggtca aaatcggcgc acccgaaaaa
601 gcgcccgcca agcagccgga tcaagtcgac atcaaaaaag taaattaa

```

This corresponds to the amino acid sequence <SEQ ID 1738; ORF 576.ng>:

g576.pep.. (partial)

```

1 ..MGVDIGRSLK QMKEQGAIEID LKVFTDAMQA VYDGKEIKMT EEQAQEVNMK
51 FLQEQQAKAV EKHKADAKAN KEKGEAFLKE NAEEDGVKTT ASGLQYKITK
101 QGEGKQPTKD DIVTVEYEGR LIDGTVFDSS KANGGPATFP LSOVIPGWTE
151 GVRLLEKGG EATFYIPSNLA YREQGAGEKI GPNATLVFDV KLVKIGAPEN
201 APAKQPDQVD IKKVN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1739>:

m576.seq.. (partial)

```

1 ..ATGCAGCAGG CAAGCTATGC GATGGCGTG GACATCGGAC GCTCCCTGAA

```

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```

51   GCAAATGAAG GAACAGGGCG CGGAAATCGA TTTGAAAGTC TTTACCGAAG
101  CCATGCAGGC AGTGTATGAC GGCAAAGAAA TCAAATGAC CGAAGAGCAG
151  GCTCAGGAAG TCATGATGAA ATTCCTTCAG GAACAACAGG CTAAGCCGT
201  AGAAAAACAC AAGGCGGACG CGAAGGCCAA TAAAGAAAAA GGCGAAGCCT
251  TTCTGAAAGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGC
301  CTGCAATACA AAATACCAA ACAGGGCGAA GGCAAACAGC CGACCAAAGA
351  CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCGATTGAC GGTACGGTAT
401  TCGACAGCAG CAAAGCCAAC GCGGCCCGG TCACCTTCCC TTTAGCCAA
451  GTGATTCGGG GTTGGACCGA AGCGGTACAG CTTCTGAAAG AAGGCGGCGA
501  AGCCACGTC TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCGG
551  GCGACAAAAT CGGTCCGAC GCCACTTTGG TATTTGATGT GAAACTGGTC
601  AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG CTCAAGTCGA
651  CATCAAAAAA GTAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1740; ORF 576>:

m576.pep... (partial)

```

1   ..MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ
51  AOEVMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASG
101 LQYKITKQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
151 VIPGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVDVKLV
201 KIGAPENAPA KQPAQVDIKK VN*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m576/g576 97.2% identity in 215 aa overlap

	10	20	30	40	50	60
m576.pep	MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ AOEVMKFLQ					
g576	:					
	10	20	30	40	50	
	70	80	90	100	110	120
m576.pep	EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASGLQYKITKQEGKQPTKDDIV					
g576	:					
	60	70	80	90	100	110
	130	140	150	160	170	180
m576.pep	TVEYEGRLID GTVFDSSKANGGPVTFPLSQVIPGWTEGVQLLKEGGEATFYIPSNLAYRE					
g576	:					
	120	130	140	150	160	170
	190	200	210	220		
m576.pep	QGAGDKIGPNATLVFDVKLVKIGAPENAPAKQPAQVDIKKVN					
g576	:					
	180	190	200	210		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1741>:

a576.seq

```

1   ATGAACACCA TTTTCAAAT CAGCGCACTG ACCCTTCCG CCGCTTTGGC
51  ACTTTCGCC TGCGCAAAA AAGAAGCCGC CCCGCATCT GCATCCGAAC
101 CTGCCGCCG TTCTCCGCG CAGGGCGACA CCTCTCGAT CGGCAGCAGC
151 ATGCAGCAG CAAGCTATGC GATGGCGTG GACATCGAC GCTCCCTGAA
201 GCAAATGAAG GAACAGGGCG CGGAAATCGA TTTGAAAGTC TTTACCGAAG
251 CCATGCAGGC AGTGTATGAC GGCAAAGAAA TCAAATGAC CGAAGAGCAG
301 GCTCAGGAAG TCATGATGAA ATTCCTTCAG GAACAACAGG CTAAGCCGT
351 AGAAAAACAC AAGGCGGACG CGAAGGCCAA TAAAGAAAAA GGCGAAGCCT
401 TTCTGAAAGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGC
451 CTGCAATACA AAATACCAA ACAGGGCGAA GGCAAACAGC CGACCAAAGA
501 CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCGATTGAC GGTACGGTAT
551 TCGACAGCAG CAAAGCCAAC GCGGCCCGG TCACCTTCCC TTTAGCCAA

```

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```

601 GTGATTCTGG GTTGGACCGA AGGCGTACAG CTTCTGAAAG AAGGCGGCGA
651 AGCCACGTTT TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCGG
701 GCGACAAAAT CGGCCCGAAC GCCACTTTGG TATTTGATGT GAAACTGGTC
751 AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG CTCAAGTCGA
801 CATCAAAAAA GTAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1742; ORF 576.a>:

```

a576.pep
1  MNTIFKISAL TLSAALALSA CGKKEAAPAS ASEFAAASSA QGDTSSIGST
51  MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ
101 AQEVMKFLQ EQQAKAVEKH KADAKANKEK GEAFLEKNAE KDGVKTTASG
151 LQYKITKQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
201 VILGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVFDVKLV
251 KIGAPENAPA KQPAQVDIKK VN*

m576/a576 99.5% identity in 222 aa overlap

m576.pep
10 20 30
MQQASYAMGV DIGRSLKQMK EQGAEIDLKV
|||||
a576 CGKKEAAPAS ASEFAAASSA QGDTSSIGST MQQASYAMGV DIGRSLKQMK EQGAEIDLKV
30 40 50 60 70 80

m576.pep
40 50 60 70 80 90
FTEAMQAVYD GKEIKMTEEQ AQEVMKFLQ EQQAKAVEKH KADAKANKEK GEAFLEKNAE
|||||
a576 FTEAMQAVYD GKEIKMTEEQ AQEVMKFLQ EQQAKAVEKH KADAKANKEK GEAFLEKNAE
90 100 110 120 130 140

m576.pep
100 110 120 130 140 150
KDGVKTTASGL QYKITKQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
|||||
a576 KDGVKTTASGL QYKITKQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
150 160 170 180 190 200

m576.pep
160 170 180 190 200 210
VIPGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVFDVKLV KIGAPENAPA
|| |||||
a576 VILGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVFDVKLV KIGAPENAPA
210 220 230 240 250 260

m576.pep
220
KQPAQVDIKK VN*
|||||
a576 KQPAQVDIKK VN*
270

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1743>:

```

g576-1.seq
1 ATGAACACCA TTTTCAAAAT CAGCGCACTG ACCCTTTCCG CCGCTTTGGC
51 ACTTTCCGCC TGCAGCAAAA AAGAAGCCGC CCCCGCATCT GCATCCGAAC
101 CTGCCCAGCG TTCTGCCGCG CAGGCGGACA CCTCTTCAAT CGGCAGCAGC
151 ATGCAGCAGG CAAGCTATGC AATGGCGGTG GACATCGGAC GCTCCCTGAA
201 ACAAATGAAG GAACAGGGCG CGGAATCGA TTTGAAAGTC TTTACCGATG
251 CCATGCAGGC AGTGTATGAC GGCAAGAGAA TCARAATGAC CGAAGAGCAG
301 GCCCAGGAAG TGATGATGAA ATTCCTGCAG GAGCAGCAGG CTAAAGCCGT
351 AGAAAAACAC AAGGCGGATG CGAAGGCCAA CAAAGAAAAA GGCGAAGCCT
401 TCCTGAAGGA AATGCGCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGT
451 CTGCAGTACA AAATCACCAA ACAGGCTGAA GGCAAAACGC CGACAAAAGA
501 CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACCGTAT
551 TCGACAGCAG CAAAGCCAAC GGCGGCCCGC CCACCTTCCC TTTGAGCCAA
601 GTGATTCCGG GTTGGACCGA AGGCGTACGG CTTCTGAAAG AAGGCGGCGA
651 AGCCACGTTT TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCGG
701 GCGAAAAAAT CGGTCCGAAC GCCACTTTGG TATTTGACGT GAAACTGGTC
751 AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG ATCAAGTCGA
801 CATCAAAAAA GTAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1744; ORF 576-1.ng>:

```
g576-1.pep
1  MNTIFKISAL TLSAALALSA CGKKEAPAS ASEPAASAA QGDTSSIGST
51  MQQASYAMGV DIGRSLQMK EQGAEIDLKV FTDAMQAVYD GKEIKMTEEQ
101 AQEVMMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASG
151 LQYKITKQGE GKOPTKDDIV TVEYEGRLID GTVFDSSKAN GGPATFPLSQ
201 VIPGWTEGVR LLKEGGEATF YIPSNLAYRE QGAGEKIGPN ATLVFDVKLV
251 KIGAPENAPA KQPDQVDIKK VN*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1745>:

```
m576-1.seq
1  ATGAACACCA TTTTCAAAAT CAGCGCACTG ACCCTTCCG CCGCTTTGGC
51  ACTTTCGCCG TCGCGCAAAA AAGAAGCCGC CCCCCTCAT CTATCCGAAC
101 CTGCGGCCGC TTCTTCGCG CAGGCGGACA CCTCTTCGAT CGGCAGCAGC
151 ATGCAGCAGG CAAGCTATGC GATGGGCGTG GACATCGGAC GCTCCCTGAA
201 GCAAATGAAG GAACAGGGCG CGGAAATCGA TTTGAAAGTC TTTACCGAAG
251 CCATGCAGGC AGTGTATGAC GGCAAAGAAA TCAAATGAC CGAAGAGCAG
301 GCTCAGGAAG TCATGATGAA ATTCTTCAG GAACAACAGG CTAAAGCCGT
351 AGAAAAACAC AAGGCGGACG CGAAGGCCAA TAAAGAAAAA GGCGAAGCCT
401 TTTTGAAAGA AAATCCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGC
451 CTGCAATACA AAATCACCAA ACAGGGCGAA GGCAACACAG CGACCAAGA
501 CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACGGTAT
551 TCACAGCAGC CAAAGCCAAC GCGGCGCCGG TCACCTTCCC TTTGAGCCAA
601 GTGATTCGGG GTTGGACCGA AGCGGTACAG CTTCTGAAAG AAGGCGGCCG
651 AGCCACGTTT TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCGG
701 GCSACAAAT CGGTCCGAAC GCCACTTTGG TATTTGATGT GAAACTGGTC
751 AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG CTCAGTCCGA
801 CATCAAAAAA GTAAATTAA
```

This corresponds to the amino acid sequence <SEQ ID 1746; ORF 576-1>:

```
m576-1.pep
1  MNTIFKISAL TLSAALALSA CGKKEAPAS ASEPAASAA QGDTSSIGST
51  MQQASYAMGV DIGRSLQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ
101 AQEVMMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASG
151 LQYKITKQGE GKOPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
201 VIPGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVFDVKLV
251 KIGAPENAPA KQPAQVDIKK VN*
```

g576-1/m576-1 97.8% identity in 272 aa overlap

	10	20	30	40	50	60
g576-1.pep	MNTIFKISAL	TLSAALALS	SACGKKEA	PASASEPA	ASAAQGD	TSSIGSTM
m576-1	MNTIFKISAL	TLSAALALS	SACGKKEA	PASASEPA	ASAAQGD	TSSIGSTM
	70	80	90	100	110	120
g576-1.pep	DIGRSLQMK	EQGAEIDL	KVFTDAM	QAVYDGE	KIKMTEE	QAQEVMM
m576-1	DIGRSLQMK	EQGAEIDL	KVFTDAM	QAVYDGE	KIKMTEE	QAQEVMM
	130	140	150	160	170	180
g576-1.pep	KADAKANKE	KGAEFLK	ENAAKDG	VKTASGL	QYKITKQ	GEGKOPT
m576-1	KADAKANKE	KGAEFLK	ENAAKDG	VKTASGL	QYKITKQ	GEGKOPT
	190	200	210	220	230	240
g576-1.pep	GTVFDSSK	ANGGPAT	FPLSQVI	PGWTEGV	RLLKEGG	EATFYIP
m576-1	GTVFDSSK	ANGGPAT	FPLSQVI	PGWTEGV	RLLKEGG	EATFYIP
	250	260	270			
g576-1.pep	ATLVFDVK	LKIGAPEN	APAKQPD	QVDIKK	VNX	
m576-1	ATLVFDVK	LKIGAPEN	APAKQPD	QVDIKK	VNX	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1747>:

a576-1.seq

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```

1  ATGAACACCA TTTTCAAAT CAGCGCACTG ACCCTTTCGG CCGCTTTGGC
51  ACTTTCCGCC TCGGCAAAA AAGAAGCCGC CCCCGCATCT GCATCCGAAC
101 CTGCCGCCGC TTCTTCCGCG CAGGGCGACA CCTCTTCGAT CGGCAGCACG
151 ATGCAGCAGG CAAGCTATGC GATGGGCGTG GACATCGGAC GCTCCCTGAA
201 GCAAAATGAAG GAACAGGGCG CGGAAATCGA TTTGAAAGTC TTTACCGAAG
251 CCATGCAGGC AGTGTATGAC GGCAAAGAAA TCAAATGAC CGAAGAGCAG
301 GCTCAGGAAG TCATGATGAA ATTCCTTCAG GAACAACAGG CTAAGCCGT
351 AGAAAAACAC AAGGCGGACG CGAAGGCCAA TAAAGAAAAA GCGGAAGCCT
401 TTCTGAAAGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGC
451 CTGCAATACA AAATCACCAA ACAGGGCGAA GGCAACAGC CGACCAAGA
501 CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACGGTAT
551 TCGACAGCAG CAAAGCCAAC GCGGCGCCCG TCACCTTCCC TTTGAGCCAA
601 GTGATTCTGG GTTGGACCGA AGCGGTACAG CTTCTGAAAG AAGGCGGCGA
651 AGCCACGTTT TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGTTGCGG
701 GCGACAAAT CGGCCCGAAC GCCACTTTGG TATTGTATGT GAAACTGGTC
751 AAAATCGGCG CACCCGAAAA CGCGCCGCC AAGCAGCCGG CTCAGTCGA
801 CATCAAAAAA GTAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1748; ORF 576-1.a>:

a576-1.pep

```

1  MNTIFKISAL TSLAALALSA CGKKEAAPAS ASEPAASSA QGDTSSIGST
51  NMQASYAMGV DIGRSLKOMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ
101 AQEVMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASG
151 LQYKITKQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
201 VILGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVDVKLV
251 KIGAPENAPA KQPAQVDIKK VN*

```

a576-1/m576-1 99.6% identity in 272 aa overlap

	10	20	30	40	50	60
a576-1.pep	MNTIFKISALTSLAALALSACGKKEAAPASASEPAASSAQGDTSSIGSTMQOASAMGV					
m576-1	MNTIFKISALTSLAALALSACGKKEAAPASASEPAASSAQGDTSSIGSTMQOASAMGV					
	10	20	30	40	50	60
	70	80	90	100	110	120
a576-1.pep	DIGRSLKOMKEQGAIEDLVFTEAMQAVYDQKEIKMTEEQAEVMMKFLQEQQAKAVEKH					
m576-1	DIGRSLKOMKEQGAIEDLVFTEAMQAVYDQKEIKMTEEQAEVMMKFLQEQQAKAVEKH					
	70	80	90	100	110	120
	130	140	150	160	170	180
a576-1.pep	KADAKANKEKGEAFLENAAKDGVKTTASGLQYKITKQEGKQPTKDDIVTVEYEGRLID					
m576-1	KADAKANKEKGEAFLENAAKDGVKTTASGLQYKITKQEGKQPTKDDIVTVEYEGRLID					
	130	140	150	160	170	180
	190	200	210	220	230	240
a576-1.pep	GTVFDSSKANGGPVTFPLSQVILGWTEGVQLLKEGGEATFYIPSNLAYREQGAGDKIGPN					
m576-1	GTVFDSSKANGGPVTFPLSQVILGWTEGVQLLKEGGEATFYIPSNLAYREQGAGDKIGPN					
	190	200	210	220	230	240
	250	260	270			
a576-1.pep	ATLVFDVKLVKIGAPENAPAKQPAQVDIKKVN					
m576-1	ATLVFDVKLVKIGAPENAPAKQPAQVDIKKVN					
	250	260	270			

Expression of ORF 576

The primer described in Table 1 for ORF 576 was used to locate and clone ORF 576. ORF 576 was cloned in pET and pGex vectors and expressed in E.coli as above described. The products of protein expression and purification were analyzed by SDS-PAGE. Figure 3A shows the results of affinity purification and Figure 3B shows the expression in E.coli. Purified His-fusion protein was used to immunize mice, whose sera were used for ELISA (positive result), FACS analysis (Figure 3C), western blot (Figure 3D). These experiments confirm that ORF 576 is a surface-exposed protein and that it is a useful immunogen. The

hydrophilicity plots, antigenic index, and amphipatic regions of ORF 576 are provided in Figure 7. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 576 and the amino acid sequence encoded thereby is provided in Example 1.

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1749>:

```
g577.seq..
1   atggaagga gcggtgtatt tggtaaaatt gtcggcaatc gcatactccg
51  tatgccgtcc gaacacgctg ccgcattcta tccgaaaccg tgcaaatcgt
101 ttaactaac gcaatcttgg ttcagagtgc gaagctgtcc gtgcggcggtt
151 tttatttacg gagcaaacat gaaacttata tataccgtca tcaaaatcat
201 tatectgctg ctcttctctg tgcttgccgt cattaatatg gatgccgtta
251 ccttttccta tcttcggggg cagagtgtca atctgccgct gattgtcgta
301 ttgttcggcg cgtttgcgt cgcatcgtg ttcggaatgt ttgccctggt
351 cgggcggctg ctgtccttgc gcggcgaaaa cagccgcctg cgtgcggaag
401 tgaagaaaag tgcgcgcttg agcggacaga aattgactgc accgccgata
451 caaaatgctg ccgaatctgc caaacagcct taa
```

This corresponds to the amino acid sequence <SEQ ID 1750; ORF 577.ng>:

```
g577.pep
1   MERSGVFGKI VGNRI LRMPSEHAAAFYPKP CKSFKLQSW FRVRS PCGV
51  FIYGANMKLI YTVIKI ILL LFLLLAVINM DAVTF SYLPG QSVN PLIVV
101 LFGAFVVGIV FGMFALFGR LSLRGENSRL RAEVKKSARL SGQKL TAPPI
151 QNAAESAKQP *
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1751>:

```
m577.seq..
1   ATGGAAAGGA ACGGTGTATT TGGTAAAATT GTCGGCAATC GCATACTCCG
51  TATGTCGTCC GAACACGCTG CCGCATCCTA TCCGAAACCG TGCAAATCGT
101 TTAAGTACG GCAATCTTGG TTCAGAGTGC GAAGCTGTCT GGGCGGCGTT
151 TTTATTTACG GAGCAAACAT GAACTTATC TATACCGTCA TCAAAATCAT
201 TATCCTGCTG CTCTTCCTGC TGCTTGCCGT CATTAAATACG GATGCCGTTA
251 CCTTTTCCTA CCTGCGGGG CAAAATTCTG ATTGCGCGCT GATTGTGCTA
301 TTGTCGGCG CATTGTAGT CGGTATTATT TTTGGAATGT TTGCCTTGT
351 CGGACGGTTG TTGTCGTTAC GTGGCGAGAA CGGCAGGTG CGTGCCGAAG
401 TAAAGAAAAA TCGCGGTTT ACGGGGAAG AGCTGACCGC ACCACCGCG
451 CAAAATGCGC CCGAATCTAC CAAACAGCCT TAA
```

This corresponds to the amino acid sequence <SEQ ID 1752; ORF 577>:

```
m577.pep..
1   MERNGVFGKI VGNRI LRMSSEHAAASYPKP CKSFKLQSW FRVRS CLGGV
51  FIYGANMKLI YTVIKI ILL LFLLLAVINT DAVTF SYLPG QKFD PLIVV
101 LFGAFVVGII FGMFALFGR LSLRGENGRL RAEVKNARL TGKEL TAPPA
151 QNAPESTKQP *
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m577/g577 88.1% identity in 160 aa overlap

	10	20	30	40	50	60
m577.pep	MERN	GVFGKIVGNRI	LRMSSEHAAASYPKP	CKSFKLQSWFRVRS	CLGGVFIYGANMKLI	
g577	MERS	GVFGKIVGNRI	LRMPSEHAAAFYPKP	CKSFKLQSWFRVRS	PCGVFIYGANMKLI	
	10	20	30	40	50	60
	70	80	90	100	110	120
m577.pep	YTVIKI	ILLLFLLLAVINT	DAVTF SYLPGQKFD	PLIVVLF	GAFVVGII	FGMFALFGR

895

```

|||||
g577  YTVIKIIILLFLLAVINMDAVTFSYLPQSVNPLIVVLFGAFVVGIVFGMFALFGR
      70      80      90      100     110     120

      130      140      150      160
m577.pep LSLRGENGRLRAEVKKNARLTGKELTAPPAQNAPESTKQPX
      |||||:|||||:|||||:|||||:|||||
g577     LSLRGENSRLRAEVKKSARLSGQKLTAPPIQNAESAQKQPX
      130      140      150      160

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1753>:

```

a577.seq
1  ATGGAAAGGA ACGGTGTATT TGGTAAAATT GTCGGCAATC GCATACTCCG
51  TATGTCGTCC GAACACGCTG CCGCATCCTA TCCGAAACCG TGCAAATCGT
101 TTAAACTAGC GCAATCTTGG TTCAGAGTGC GAAGCTGTCC GGGCGGCGTT
151 TTTATTTACG GAGCAAACAT GAAACTTATC TATACCGTCA TCAAATCAT
201 TATCCTGCTG CTCTTCCTGC TGCTTGCTGT CATTAAATACG GATGCCGTTA
251 CCTTTTCCTA CCTGCCGGGG CAAAATTTCG ATTTGCCGCT GATTGTCGTA
301 TTGTTGCGCG CGTTTGTCTG CGGCATCGTG TTCGGAATGT TTGCCTTGTT
351 CGGACGGTTG TTGTCGTTAC GTGGCGAGAA CGGCAGGTTG CGTGCCGAAG
401 TAAAGAAAAA TGCGCGTTTG ACGGGGAAGG AGCTGACCGC ACCACCGGCG
451 CAAATGCGC CCGAATCTGC CAAACAGCCT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1754; ORF 577.a>:

```

a577.pep
1  MERNGVFGKI VGNRILRMSS EHAAASYPKP CKSEKLAQSW FRVRSCPGGV
51  FIYGANMKLI YTVIKIILL LFLLLAVINT DAVTFSYLPQ QKFDLPLIVV
101 LFGAFVVGIV FGMFALFGR LSLRGENGRL RAEVKKNARL TGKELTAPPA
151 QNAPESAKQP *

```

m577/a577 98.1% identity in 160 aa overlap

```

      10      20      30      40      50      60
m577.pep MERNGVFGKIVGNRILRMSSEHAAASYPKPCKSEKLAQSWFRVRSCLGGVFIYGANMKLI
      |||||
a577     MERNGVFGKIVGNRILRMSSEHAAASYPKPCKSEKLAQSWFRVRSCPGGVFIYGANMKLI
      10      20      30      40      50      60

      70      80      90      100     110     120
m577.pep YTVIKIILLFLLAVINTDAVTFSYLPQKFDLPLIVVLFGAFVVGIIFGMFALFGR
      |||||
a577     YTVIKIILLFLLAVINTDAVTFSYLPQKFDLPLIVVLFGAFVVGIVFGMFALFGR
      70      80      90      100     110     120

      130      140      150      160
m577.pep LSLRGENGRLRAEVKKNARLTGKELTAPPAQNAPESTKQPX
      |||||:|||||
a577     LSLRGENGRLRAEVKKNARLTGKELTAPPAQNAPESTKQPX
      130      140      150      160

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1755>:

```

g578.seq..
1  atgggaaagc tcgacatcgg gatattgttc gcgattttct tcaaagattt
51  cgcgccacag ttcggtggtt tccaaaacgt tggctttgcc tacggagcag
101 acttttttgc tgcgtttttg ggcggattgg aaggccacgt gggcgatgcg
151 ggcgatttcg cttecgctgt atttcattgt gttgtagcct tcgtgttcgc
201 cgtttttcaa aacacggatg ccgcgcggtt cgcgaaata aatatcgccg
251 gtaagttcgc gcacaatcaa aatatccaaa ccggcaacga tttcaggcct
301 gagcgtggag gcgttggtta a

```

This corresponds to the amino acid sequence <SEQ ID 1756; ORF 578.ng>:

```

g578.pep
1  MGKLDIGILF ADFFKDFAPQ FGGFQNVGFA YGADFFAAFL GGLEGHVGDA
51  ADFAFAVFHG VVAFVFAVFQ NTDAARFAEI NIAGKFAHNQ NIQTGNDFRL

```


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101 ERGGVG*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1757>:

```
m578.seq..
1  ATGGGAAAGC TCGACATCAG GGTACTCTTT GCCGATTCTT TCAAAGATTT
51  CGCGCCACAA TTCGGTGGTT TCCAAAACGT TGGCTTTGCC TACGGAACAG
101 ACTTTTTTGC TCGCTTTTTC GCGGATTGG  AAGCAACAT GGGCAATACG
151 GCGGATTTCG CTTTCGCTGT ATTTCATGGT GTTGTAGCCT TCGCGTTCCG
201 CGTTTTCAG AACCGGATG CCGCGCGTT CGCCGAAATA GATGTCGCCG
251 GTGAGTTCGC GCACAATCAA AATATCCAAA CCGCAACGA TTTCAGGCTT
```

This corresponds to the amino acid sequence <SEQ ID 1758; ORF 578>:

```
m578.pep..
1  MGKLDIRVLF ADFFKDFAPQ FGGFQNVGFA YGTDFFAFL GGLEGNMGNT
51  ADFAFVPHG VVAFAVVFQ NADAARFAEI DVAGEFAHNQ NIQTGNDFRL
101 QRGVG*
```

m578/g578 87.7% identity in 106 aa overlap

	10	20	30	40	50	60
m578.pep	MGKLDIRVLFADFFKDFAPQ	FGGFQNVGFAYGTDFFAFL	GGLEGNMGNTADFAFAVPHG			
		:			:	
g578	MGKLDIGILFADFFKDFAPQ	FGGFQNVGFAYGADFFAFL	GGLEGHVGDADFAFAVPHG			
	10	20	30	40	50	60

	70	80	90	100
m578.pep	VVAFAVVFQ NADAARFAEIDVAGEFAHNQ	NIQTGNDFRLQ RGGVGX		
		:		:
g578	VVAFVFAVFQNTDAARFAEINIAGKFAHNQ	NIQTGNDFRLERGGVGX		
	70	80	90	100

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1759>:

```
a578.seq
1  ATGGGAAAGC TCGACATCAG GGTATTCTTT GCCGATTCTT TCAAAGATTT
51  CGCGCCACAA TTCGGTGGTT TCCAAAACGT TGGCTTTGCC TACGGAGCAG
101 ACTTTTTTGC TCGCTTTTTC GCGGATTGG  AAGCGACGT GGGCAATACG
151 GCGGATTTCG CTTTCGCTGT ATTTCATGGT GTTGTAGCCT TCGCGTTCCG
201 CGTTTTCCAG AACACGGATG CCGCGCGTT CGCCGAAATA AATATCGCCG
251 GTGAGTTCGC GCACAATCAA AATATCCAAA CCCGCAACGA TTTCAGACTT
301 GAGCGTGGAG GCGTTGGCTA G
```

This corresponds to the amino acid sequence <SEQ ID 1760; ORF 578.a>:

```
a578.pep
1  MGKLDIRVFF ADFFKDFAPQ FGGFQNVGFA YGADFFAFL GGLEGDVGNT
51  ADFAFVPHG VVAFAVVFQ NTDAARFAEI NIAGEFAHNQ NIQTRNDFRL
101 ERGGVG*
```

m578/a578 91.5% identity in 106 aa overlap

	10	20	30	40	50	60
m578.pep	MGKLDIRVLFADFFKDFAPQ	FGGFQNVGFAYGTDFFAFL	GGLEGNMGNTADFAFAVPHG			
		:			:	
a578	MGKLDIRVFFADFFKDFAPQ	FGGFQNVGFAYGADFFAFL	GGLEGDVGNTADFAFAVPHG			
	10	20	30	40	50	60

	70	80	90	100
m578.pep	VVAFAVVFQ NADAARFAEIDVAGEFAHNQ	NIQTGNDFRLQ RGGVGX		
		:		:
a578	VVAFAVVFQNTDAARFAEINIAGEFAHNQ	NIQTRNDFRLERGGVGX		
	70	80	90	100

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1761>:

```
g579.seq..
1  ATGAGGCGG CGATGACGCG CGCGCAGGTC GATGCCACGC TGATTAGTTT
```

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```

51  TTTGTGTAAT GTTGCCAATA TCGGCTTATT GATTTTGGTG ATTATTGCCG
101 CATTGGGACG GTTGGGCGTT TCCACAACAT CCGTAACCGC CTTAATCGGC
151 GCGCGGGGTT TGGCGGTGGC GTTGTCTTA AAAGACCAGC TGTCCAATTT
201 TGCCGCCGGC GCGCTGATTA TCCTGTTCG CCCGTTCAAA GTCGGCGACT
251 TTATCCGTGT CGGCGGTTT GAAGGATATG TCCGGGAAAT CAAAATGGTG
301 CAGACTTCTT TCGGACGAC CGACAACGAA GAAGTCGTGC TGCCCAACAG
351 CGTGGTGATG GGCAACAGCA TCGTCAACCG TTCCAGCTG CCGCTTTGCC
401 GCGCCCAAGT GATAGTCGGC GTCGATTACA ACTGCGATT GAAAGTGGCG
451 AAAGAGGCGG TGTGAAAGC CGCCGCGAA CACCCCTGA GCGTTCAAAA
501 CGAAGAGCGG CAGCCCGCG CTTACATCAC CGCCTTGGG GACAATGCCA
551 TCGAAATCAC ATTATGGGCT TGGGCAAACG AAGCAGACCG CTGGACGCTG
601 CAATGCGACT TGAACGAACA AGTGGTCGAA AACCTCCGA AGTCAATAT
651 CAACATCCCG TTCCCGCAAC GCGACATACA CATCATCAAT TCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1762; ORF 579.ng>:

g579.pep..

```

1  MRAAMTRAQV DATLISFLCN VANIGLLILV IIAALGRLGV STTSVTALIG
51  GAGLAVALSL KDQLSNFAAG ALIILFRPFK VGDFIRVGGF EGYVREIKMV
101 QTSRLRTDNE EVVLPNSVVM GNSIVNRSSL PLCRAQVIVG VDYNCDLKVA
151 KEAVLKAAAE HPLSVQNEER QPAAYITALG DNAIEITLWA WANEADRWTL
201 QCDLNEQVVE NLRKVNINIP FPQRDIHIIN S*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1763>:

m579.seq..

```

1  ATGAGGGCGG CGATGACGCG CGCGCAGGTC GATGCCACGC TGATTAGTTT
51  TTTGTGTAAT GTTGCCAATA TCGGCTTATT GATTTTGGTG ATTATTGCCG
101 CATTGGGACG ATTGGGCGTT TCCACAACAT CCGTAACCGC CTTAATCGGC
151 GCGCGGGGTT TGGCGGTGGC GTTGTCTTA AAAGACCAGC TGTCCAATTT
201 TGCCGCCGGC GCACTGATTA TCCTGTTCG CCCGTTCAAA GTCGGCGACT
251 TTATCCGTGT CGGCGGTTT GAAGGATATG TCCGAGAGAT TAAAATGGTG
301 CAGACTTCTT TCGGACGAC CGACAACGAA GAAGTCGTGC TGCCCAACAG
351 CGTGGTGATG GGCAACAGCA TCGTCAACCG TTCCACACTG CCGCTGTGCC
401 GCGCCCAAGT GATAGTCGGC GTCGATTACA ACTGCGATT GAAAGTGGCG
451 AAAGAGGCGG TGTGAAAGC CGCCGCGAA CACCCCTGA GCGTTCAAAA
501 CGAAGAGCGG CAGGCTGCCG CTTACATCAC CGCCTTGGG GACAATGCCA
551 TCGAAATCAC ATTATGGGCT TGGGCAAACG AAGCAGACCG CTGGACGCTG
601 CAATGCGACT TGAACGAACA AGTGGTCGAA AACCTCCGA AGTCAATAT
651 CAACATCCCG TTCCCGCAAC GCGACATACA CATCATCAAT TCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1764; ORF 579>:

m579.pep..

```

1  MRAAMTRAQV DATLISFLCN VANIGLLILV IIAALGRLGV STTSVTALIG
51  GAGLAVALSL KDQLSNFAAG ALIILFRPFK VGDFIRVGGF EGYVREIKMV
101 QTSRLRTDNE EVVLPNSVVM GNSIVNRSSL PLCRAQVIVG VDYNCDLKVA
151 KEAVLKAAAE HPLSVQNEER QAAAYITALG DNAIEITLWA WANEADRWTL
201 QCDLNEQVVE NLRKVNINIP FPQRDIHIIN S*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m579/g579 98.7% identity in 231 aa overlap

	10	20	30	40	50	60
m579.pep	MRAAMTRAQVDATLISFLCNVANIGLLILVIAALGRLGVSTTSVTALIGGAGLAVALSL					
g579	MRAAMTRAQVDATLISFLCNVANIGLLILVIAALGRLGVSTTSVTALIGGAGLAVALSL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m579.pep	KDQLSNFAAGALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLRTDNEEVVLPNSVVM					
g579	KDQLSNFAAGALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLRTDNEEVVLPNSVVM					
	70	80	90	100	110	120

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	130	140	150	160	170	180
m579.pep	GNSIVNRSTLPLCRAQVIVGVVDYNCDLKVAKEAVLKAAVEHPLSVQNEERQAAAYITALG					
	: : : : : :					
g579	GNSIVNRSSLPLCRAQVIVGVVDYNCDLKVAKEAVLKAAAEHPLSVQNEERQPAAYITALG					
	130	140	150	160	170	180

	190	200	210	220	230
m579.pep	DNAIEITLWAWANEADRWTLCQDLNEQVVENLRKVNINIPFPQRDIHIINSX				
	: : : : :				
g579	DNAIEITLWAWANEADRWTLCQDLNEQVVENLRKVNINIPFPQRDIHIINSX				
	190	200	210	220	230

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1765>:

```
a579.seq
1  ATGAGGGCGG CGATGACGCG CGCGCAGGTC GATGCCACGC TGATTAGTTT
51  TTTGTGTAAT GTTGCCAATA TCGGCTTATT GATTTGGTG ATTATGCCG
101 CATTGGGCAG ATTGGGCGTT TCCACAACAT CCGTAACCGC CTTAATCGGC
151 GCGCGCGGGT TGGCGGTGGC GTTGTCTTG AAAGACCAGC TGTCCAATTT
201 TGCCGCCGGC GCGCTGATTA TCCTGTCCG CCCGTTCAA GTCGGCGATT
251 TTATCCGCGT CGGCGGTTTT GAAGGATATG TCCGAGAGAT TAAATGGTG
301 CAGACTTCTT TGCGGACGAC CGACAACGAA GAAGTCGTGC TGCCCAACAG
351 CGTGGTGATG GGCAACAGCA TCGTCAACCG TTCCACACTG CCGCTGTGCC
401 GCGCCCAAGT GATAGTCGGC GTCGATTACA ACTGCGATTT GAAAGTGGCG
451 AAAGAGGCGG TGTGAAAGC CGCCGTCGAA CACCCCTTGA GCGTCAAAA
501 CGAAGAGCGG CAGGCCGCCG CCTACATCAC CGCCTGGGC GACAATGCCA
551 TCGAAATCAC ATTATGGGCT TGGGCAAACG AAGCAGACCG CTGGACGCTG
601 CAATGCGACT TGAACGAACA AGTGGTCGAA AACCTCCGCA AAGTCAATAT
651 CAACATCCCG TTCCCGCAAC GCGACATACA CATCATCAAT TCTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1766; ORF 579.a>:

```
a579.pep
1  MRAAMTRAQV DATLISFLCN VANIGLLILV IIAALGRLGV STTSVTALIG
51  GAGLAVALSL KDQLSNFAAG ALIILFRPFK VGDFIRVGGF EGYVREIKMV
101 QTSRLRTDNE EVVLPNSVVM GNSIVNRSTL PLCRAQVIVG VDYNCDLKVA
151 KEAVLKAAVE HPLSVQNEER QAAAYITALG DNAIEITLWA WANEADRWTL
201 QCDLNEQVVE NLRKVNINIP FPQRDIHIIN S*
```

m579/a579 100.0% identity in 231 aa overlap

	10	20	30	40	50	60
m579.pep	MRAAMTRAQVDATLISFLCNVANIGLLILVIAALGRLGVSTTSVTALIGGAGLAVALSL					
	: : : : :					
a579	MRAAMTRAQVDATLISFLCNVANIGLLILVIAALGRLGVSTTSVTALIGGAGLAVALSL					
	10	20	30	40	50	60

	70	80	90	100	110	120
m579.pep	KDQLSNFAAGALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLRTDNEEVVLPNSVVM					
	: : : : :					
a579	KDQLSNFAAGALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLRTDNEEVVLPNSVVM					
	70	80	90	100	110	120

	130	140	150	160	170	180
m579.pep	GNSIVNRSTLPLCRAQVIVGVVDYNCDLKVAKEAVLKAAVEHPLSVQNEERQAAAYITALG					
	: : : : :					
a579	GNSIVNRSTLPLCRAQVIVGVVDYNCDLKVAKEAVLKAAVEHPLSVQNEERQAAAYITALG					
	130	140	150	160	170	180

	190	200	210	220	230
m579.pep	DNAIEITLWAWANEADRWTLCQDLNEQVVENLRKVNINIPFPQRDIHIINSX				
	: : : : :				
a579	DNAIEITLWAWANEADRWTLCQDLNEQVVENLRKVNINIPFPQRDIHIINSX				
	190	200	210	220	230

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1767>:

g579-1.seq

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```

1  ATGGACTTCA AACAATTGA TTTTTTACAC CTGATCAGTG TTTCCGGTTG
51  GCGGCATCTG GCTGAAAAGG CGTGGGCGGT CGGGCTGAAC CTTGCCGCCG
101 CGCTGCTTAT TTTCTTGGTC GGGAAATGGG CGGCGAAACG CATTGTCGCC
151 GTAATGAGGG CGGCGATGAC GCGCGCGCAG GTCGATGCCA CGCTGATTAG
201 TTTTTTGTGT AATGTTGCCA ATATCGGCTT ATTGATTTTG GTGATTATTG
251 CCGCATTTGGG ACGGTTGGGC GTTCCACAA CATCCGTAAC CGCCTTAATC
301 GCGGCGCGGG GTTGGCGGT GCGGTTGTCC TTAAAGACC AGCTGTCCAA
351 TTTTGCCGCC GCGCGCTGA TTATCCTGTT CCGCCCGTTC AAAGTCGGCG
401 ACTTTATCCG TGTCGGCGGT TTTGAAGGAT ATGTCGGGGA AATCAAPATG
451 GTGCAGACTT CTTTGGCGAC GACCGACAAC GAAGAAGTCG TGCTGCCCAA
501 CAGCGTGGTG ATGGGCAACA GCATCGTCAA CCGTTCACG CTGCCGCTTT
551 GCGCGCCCCA AGTGATAGTC GCGGTCGATT ACAACTGCCA TTTGAAAGTG
601 GCGAAAGAGG CGGTGTTGAA AGCCGCGGCC GAACACCCCT TGAGCGTTCA
651 AAACGAAGAG CCGCAGCCCG CCGCCTACAT CACCGCCTTG GCGGACAATG
701 CCATCGAAAT CACATTATGG GCTTGGGCAA ACGAAGCAGA CCGCTGGACG
751 CTGCAATGCG ACTTGAACGA ACAAGTGGTC GAAAACCTCC GCAAAGTCAA
801 TATCAACATC CCGTTCCCGC AACGCGACAT ACACATCATC AATTCCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1768; ORF 008.ng>:

g579-1.pep

```

1  MDFKQDFDLH LISVSGWGHL AEKAWAFGLN LAAALLIFLV GKWAAKRIVA
51  VMRAAMTRAQ VDATLISFLC NVANIGLLIL VIIAALGRLG VSTTSVIALI
101 GGAGLAVALS LKDQLSNFAA GALIILFRPF KVGDFIRVGG FEGYVREIKM
151 VQTSLRLTTDN EEVVLPNSV MGNSIVNRSS LPLCRAQVIV GVDYNCDLKV
201 AKEAVLKAAA EHPLSVQNEE RQAAAYITAL GDNAIEITLW AWANEADRWT
251 LQCDLNEQVV ENLRKVNINI PFPQRDIHII NS*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1769>:

m579-1.seq

```

1  ATGGACTTCA AACAATTGA TTTTTTACAC CTGATCAGTG TTTCCGGTTG
51  GGAGCATCTG GCTGAAAAGG CGTGGGCGGT CGGGCTGAAC CTTGCCGCCG
101 CGCTGCTTAT TTTTTTGGTC GGGAAATGGG CGGCGAAACG CATTGTCGCT
151 GTGATGAGGG CGGCGATGAC GCGCGCGCAG GTCGATGCCA CGCTGATTAG
201 TTTTTTGTGT AATGTTGCCA ATATCGGCTT ATTGATTTTG GTGATTATTG
251 CCGCATTTGGG CAGATTGGGC GTTCCACAA CATCCGTAAC CGCCTTAATC
301 GCGGCGCGGG GTTGGCGGT GCGGTTGTCC CTGAAAGACC AGCTGTCCAA
351 TTTTGCCGCC GCGCGACTGA TTATCCTGTT CCGCCCGTTC AAAGTCGGCG
401 ATTTTATCCG CGTCGGCGGT TTTGAAGGAT ATGTCGGAGA GATTAAAATG
451 GTGCAGACTT CTTTGGCGAC GACCGACAAC GAAGAAGTCG TGCTGCCCAA
501 CAGCGTGGTG ATGGGCAACA GCATCGTCAA CCGTTCACA CTGCCGCTGT
551 GCGCGCCCCA AGTGATAGTC GCGGTCGATT ACAACTGCCA TTTGAAAGTG
601 GCGAAAGAGG CGGTGTTGAA AGCCGCGGTC GAACACCCCT TGAGCGTTCA
651 AAACGAAGAG CCGCAGGCTG CCGCCTACAT CACCGCCTTG GCGGACAATG
701 CCATCGAAAT CACATTATGG GCTTGGGCAA ACGAAGCAGA CCGCTGGACG
751 CTGCAATGCG ACTTGAACGA ACAAGTGGTC GAAAACCTCC GCAAAGTCAA
801 TATCAACATC CCGTTCCCGC AACGCGACAT ACACATCATC AATTCCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1770; ORF 579-1>:

m579-1.pep

```

1  MDFKQDFDLH LISVSGWEHL AEKAWAFGLN LAAALLIFLV GKWAAKRIVA
51  VMRAAMTRAQ VDATLISFLC NVANIGLLIL VIIAALGRLG VSTTSVIALI
101 GGAGLAVALS LKDQLSNFAA GALIILFRPF KVGDFIRVGG FEGYVREIKM
151 VQTSLRLTTDN EEVVLPNSV MGNSIVNRSS LPLCRAQVIV GVDYNCDLKV
201 AKEAVLKAAA EHPLSVQNEE RQAAAYITAL GDNAIEITLW AWANEADRWT
251 LQCDLNEQVV ENLRKVNINI PFPQRDIHII NS*

```

m579-1/g579-1 98.6% identity in 282 aa overlap

	10	20	30	40	50	60
m579-1.pep	MDFKQDFDLH	LISVSGWEHLAEKAWAFGLN	LAAALLIFLV	GKWA A KRIVAVMRAAMTRAQ		
g579-1	MDFKQDFDLH	LISVSGWGH L AEKAWAFGLN	LAAALLIFLV	GKWA A KRIVAVMRAAMTRAQ		
	70	80	90	100	110	120
m579-1.pep	VDATLISFLCNVANIGLLILVIIAALGR	GVSTTSVIALIGGAGLAVALS	LKDQLSNFAA			
g579-1	VDATLISFLCNVANIGLLILVIIAALGR	GVSTTSVIALIGGAGLAVALS	LKDQLSNFAA			
	130	140	150	160	170	180
m579-1.pep	GALIILFRPF	KVGDFIRVGGFEGYVREIKM	VQTS L RLTTDNEEVVL	PNSVVMGNSIVNRST		

900

```

|||||
g579-1  GALIILFRPFKVGDFIRVGGFESYVREIKMVQTSRLRTDNEEVVLPNSVVMGNSIVNRSS
          130      140      150      160      170      180
          190      200      210      220      230      240
m579-1.pep LPLCRAQVIVGVVDYNDLKVAKFAVLKAAVEHPLSVQNEERQAAAYITALGDNAIETTLW
          190      200      210      220      230      240
g579-1  LPLCRAQVIVGVVDYNDLKVAKFAVLKAAEHPLSVQNEERQPAAYITALGDNAIETTLW
          190      200      210      220      230      240
          250      260      270      280
m579-1.pep AWANEADRWTLQCDLNEQVVENLRKVNINIPFPQRDIHIINSX
          |||||
g579-1  AWANEADRWTLQCDLNEQVVENLRKVNINIPFPQRDIHIINSX
          250      260      270      280

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1771>:

a579-1.seq

```

1  RTGGACTTCA AACAAATTTGA TTTTTCAC CTGATAAGTG CTTCCGGCTG
51  GGAGCATCTG GCTGAAAAGG CGTGGCGCTT CGGGCTGAAC CTTGCCGCGG
101 CGCTGCTTAT TTTTGTGGT GGAATAAGG CGGCGAAGC CATTGTCGCC
151 GTGATGAGGG CGGCGATGAC GCGCGCGCAG GTCGATGCCA CGTGATTAG
201 TTTTGTGTGT AATGTTGCCA ATATCGGCTT ATTGATTTTG GTGATTATTG
251 CCGCATTTGG CAGATTGGGC GTTCCACAA CATCCGTAAC CGCCTTAATC
301 CGCGGCGCGG GTTGGCGGT GCGCTGTGCC TTGAAAGACC AGCTGTCCAA
351 TTTTCCCGCC GCGCGCGCTG TTATCCTGTT CCGCCCGTTC AAAGTCGGCG
401 ATTTTATCCG CGTCGGCGGT TTTGAAGGAT ATGTCCGAGA GATTAAATG
451 GTGCAGACTT CTTTGGCGAC GACCGACAAC GAAGAAGTCG TGCTGCCCAA
501 CAGCGTGGTG ATGGGCAACA GCATCGTCAA CCGTCCACA CTGCCGCTGT
551 CCGCGCGCCA AGTGATAGTC GCGCTCGATT ACAACTGCGA TTTGAAAGTG
601 CCGAAAGAGG CGGTGTTGAA AGCGCGCGTC GAACACCCCT TGAGCGTTCA
651 AAACGAAGAG CGGCAGGCGC CCGCTACAT CACCGCCTTG GCGGACAATG
701 CCATCGAAT CACATTATGG GCTTGGGCAA ACGAAGCAGA CCGTGGACG
751 CTGCAATGCG ACTTGAACGA ACAAGTGGTC GAAACCTCC GCAAAGTCAA
801 TATCAACATC CCGTCCCGC AACCGGACAT ACACATCATC AATCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1772; ORF 579-1.a>:

a579-1.pep

```

1  MDFKQDFDLH LISASGWEHL AEKAWAFGLN LAAALLIFLV GKWAARKRIVA
51  VMRAAMTRAQ VDATLISFLC NVANIGLLIL VIALGRLG VSTTSVTALI
101 GGAGLAVALS LKDQLSNFAA GALIILFRPF KVGDFIRVGG FEGYVREIKM
151 VQTSRLRTDN EEVVLPNSV VMGNSIVNRST LPLCRAQVIV GVDYNDLKV
201 AKEAVLKAAV EHPLSVQNEE RQAAAYITAL GDNAIETLW AWANEADRWT
251 LQCDLNEQVV ENLRKVNINI PFPQRDIHII NS*

```

a579-1/m579-1 99.6% identity in 282 aa overlap

```

          10      20      30      40      50      60
a579-1.pep MDFKQDFDLHLISASGWEHLAEKAWAFGLNLAAALLIFLVGKWAARKRIVAVMRAAMTRAQ
          |||||
m579-1  MDFKQDFDLHLISVSGWEHLAEKAWAFGLNLAAALLIFLVGKWAARKRIVAVMRAAMTRAQ
          10      20      30      40      50      60
          70      80      90      100     110     120
a579-1.pep VDATLISFLCNVANIGLLILVIAALGRLGVSTTSVTALIGGAGLAVALSLKDQLSNFAA
          |||||
m579-1  VDATLISFLCNVANIGLLILVIAALGRLGVSTTSVTALIGGAGLAVALSLKDQLSNFAA
          70      80      90      100     110     120
          130     140     150     160     170     180
a579-1.pep GALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLRTDNEEVVLPNSVVMGNSIVNRST
          |||||
m579-1  GALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLRTDNEEVVLPNSVVMGNSIVNRST
          130     140     150     160     170     180
          190     200     210     220     230     240
a579-1.pep LPLCRAQVIVGVVDYNDLKVAKFAVLKAAVEHPLSVQNEERQAAAYITALGDNAIETTLW
          |||||
m579-1  LPLCRAQVIVGVVDYNDLKVAKFAVLKAAVEHPLSVQNEERQAAAYITALGDNAIETTLW
          190     200     210     220     230     240
          250     260     270     280
a579-1.pep AWANEADRWTLQCDLNEQVVENLRKVNINIPFPQRDIHIINSX

```

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m579-1 |||||
 AWANEADRWTLQCDLNEQVVENLRKVNINIPFPQRDIHIINSX
 250 260 270 280

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1773>:

g580.seq
 1 atggattcgc ccaaggtcgg gtgcgggtgg atggttttgc cgatgtctgc
 51 cgcgctcgag ccatttcga tggcaaggca gacttcgccg atcatgtcgc
 101 caccgttcgg accgacaatg ccgccgccga tgatgcggcc ggtttcggca
 151 tcgaaaatca gcttggtaaa gccgtgtcgc caaccgttgg caatcgcacg
 201 accggaagcc gcccatggga agttggcttt ggtaattttg cggcctgatg
 251 ctttggcaga caattcggtt tcaccgaccc atgccacttc gggggaagtg
 301 tag

This corresponds to the amino acid sequence <SEQ ID 1774; ORF 580.ng>:

g580.pep..
 1 MDSFKVGCGW MVLPMASASQ PISMARQTSP IMSPPFGPTM PPPMMRPVSA
 51 SKISLVKPLS QPLAIARPEA AHGKLALVIL RPDALADNSV SPTHATSGEV
 101 *

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1775>:

m580.seq..
 1 ATGGATTTCG CCAAGGTCGG GTGCGGGTGG ATGGTTTTCG CGATGTCTGC
 51 CGCGTCGCAG CCCATTTCGA TGGCAAGGCA GACTTCGCCG ATCATATCGC
 101 CACCGTTCGG ACCGACAATG CCGCCGCCGA TGATGCGGCC GGTTCGGCA
 151 TCAAAAATCA GCTTGGTAAA GCCGTGTGCG CAACCGTTGG CAATCGCACG
 201 GCCGGAAGCC GCCCAGGGA AGTTGGCTTT GGTGATTTTG CGGCCGAGG
 251 CTTTGGCGGA CAGTTCGGTT TCGCCACCCC ACGCCACTTC GGGGGAAGTG
 301 TAG

This corresponds to the amino acid sequence <SEQ ID 1776; ORF 580>:

m580.pep..
 1 MDSFKVGCGW MVLPMASASQ PISMARQTSP IISPPFGPTM PPPMMRPVSA
 51 SKISLVKPLS QPLAIARPEA AHGKLALVIL RPEALADSSV SPTHATSGEV
 101 *

m580/g580 97.0% identity in 100 aa overlap

	10	20	30	40	50	60
m580.pep	MDSFKVGCGWMVLPMASASQPISMARQTSP IISPPFGPTM PPPMMRPVSASKISLVKPLS					
g580	MDSFKVGCGWMVLPMASASQPISMARQTSP IMSPPFGPTM PPPMMRPVSASKISLVKPLS					
	10	20	30	40	50	60
	70	80	90	100		
m580.pep	QPLAIARPEAAHGKLALVILRPEALADSSVSPTHATSGEVX					
g580	QPLAIARPEAAHGKLALVILRPDALADNSVSPTHATSGEVX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1777>:

a580.seq
 1 ATGGATTTCG CCAAGGTCGG GTGCGGGTGG ATGGTTTTCG CGATGTCTGC
 51 CGCGTCGCAG CCCATTTCGA TGGCAAGGCA GACTTCGCCG ATCATGTCCG
 101 CACCGTTCGG ACCGACAATG CCGCCGCCGA TGATGCGGCC GGTTTCAGCA
 151 TCAAAAATCA GCTTGGTGA ACCATTGTGCG CAACCGTTGG CAATCGCACG
 201 GCCGGAAGCA GCCCATG3GA AGTTGGCTTT GGTGATTTTG CGGCCGAGG
 251 CTTTGGCAGA CAATTCG3TT TCGCCACCCC ATGCCACTTC AGGAGAAGTG
 301 TAA

This corresponds to the amino acid sequence <SEQ ID 1778; ORF 580.a>:

a580.pep
 1 MDSFKVGCGW MVLPMASASQ PISMARQTSP IMSPPFGPTM PPPMMRPVSA
 51 SKISLVKPLS QPLAIARPEA AHGKLALVIL RPEALADNSV SPTHATSGEV

902

101 *

m580/a580 98.0% identity in 100 aa overlap

	10	20	30	40	50	60
m580.pep	MDSPKVGCGWMVLPMSAASQPISMARQTSPIISPPFGPTMPPPMRVSASKISLVKPLS					
a580	MDSPKVGCGWMVLPMSAASQPISMARQTSPIISPPFGPTMPPPMRVSASKISLVKPLS					
	10	20	30	40	50	60

	70	80	90	100
m580.pep	QPLAIARPEAAHGKLALVILRPEALADSSVSPHATSGEVX			
a580	QPLAIARPEAAHGKLALVILRPEALADNSVSPHATSGEVX			
	70	80	90	100

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1779>:

g581.seq..

```

1  atgcacttcg cccagcttgt gggtaaacc ggtatagaac aaaatacgtt
51  ctgtcgtcgt ggttttaccg gcatcgatat gggcggaat accgatgttg
101 cggtacaggg tgatcggggt cttacgagcc attttattag cttttcaaaa
151 ttgaaaacgg aagtggagaga atgctttgtt ggcttcagcc atacgggtga
201 cttcttcacg ttttttcaac gcaccgccac ggcttcgga cgcataatc
251 aactcgctcg ccaaacgcag atccatggat ttctcaccac gtttgcgggc
301 cgcgtcgcca acccaacgca ttgccaagc cagacggcgt ga

```

This corresponds to the amino acid sequence <SEQ ID 1780; ORF 581.ng>:

g581.pep..

```

1  MHFAQLVGQT GIEQNTFCRR GFTRIDMGGN TDVAVQADRG LSHFISLSK
51  LETEVRECFV GFSHTVYFFT FFQRTATAFG RINQLACQTQ IHGFLTTFAG
101 RVANPTHCS QTA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1781>:

m581.seq..

```

1  ATGCACTTCG CCCAGCTTGT GGTCAAACC GGTATAGAAC AAAATACGTT
51  CTGTCGTCGT GGTTTTACCC GCGTCAATAT GGGCGGAAT ACCGATGTTA
101 CGGTACAGGC TGATCGGGGT CTTACGAGCC ATTTTATTAG CCTTTCAAAA
151 TTGAAAACGG AAGTGAGAGA ATGCTTTGTT GGCTTCAGCC ATACGGGTGA
201 CTTCTTCACG TTTTTTCAAC GCACCGCCAC GGCTTCGGA CGCATCAATC
251 AATTCGCCTG CCAAACGCAG GTCCATGGAT TTCTCACCAC GTTTCGGGCG
301 CGCATCGCGA ACCCAGCGCA TTGCCAAGC CAAACGGCGT GA

```

This corresponds to the amino acid sequence <SEQ ID 1782; ORF 581>:

m581.pep..

```

1  MHFAQLVGQT GIEQNTFCRR GFTRVNMGGN TDVTQADRG LSHFISLSK
51  LETEVRECFV GFSHTVYFFT FFQRTATAFG RINQFACQTQ VHGFLLTFAG
101 RIANPAHCQS QTA*

```

m581 / g581 93.8% identity in 113 aa overlap

	10	20	30	40	50	60
m581.pep	MHFAQLVGQTGIEQNTFCRRGFTRVNMGGNTDVTQADRG LSHFISLSKLETEVRECFV					
g581	MHFAQLVGQTGIEQNTFCRRGFTRIDMGGNTDVTQADRG LSHFISLSKLETEVRECFV					
	10	20	30	40	50	60

	70	80	90	100	110
m581.pep	GFSHTVYFFTFFQRTATAFGRINQFACQTQVHGFLTTFAGRANPAHCQSQTAX				
g581	GFSHTVYFFTFFQRTATAFGRINQLACQTQIHGFLTTFAGRANPAHCQSQTAX				
	70	80	90	100	110

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1783>:

903

```

a581.seq
1  ATGCACTTCG CCCAGCTTGT GGTCAAAACC GGTATAGAAC AAAATACGTT
51  CTGTCGTCGT GGTTTTACCC GCATCGATAT GGC CGGAAAT ACCGATGTTA
101 CGGTACAGGC TGATCGGGGT CTTACGAGCC ATTTTATTAG CTTTCAAAA
151 TTAGAAACGG AAGTGAGAGA ATGCTTTGTT GGCTTCAGCC ATACGGTGTA
201 CTTCTTCACG TTTTTC AAC GCACCGCCAC GGCCTTCGGA CGCATCAATC
251 AATTCGCCTG CCAAACG CAG GTCCATGGAT TTCTCACCAC GTTTCGGGGC
301 CGCATCGCGA ACCCAGCGCA TTGCCAAAGC CAAACGGCGT GA

```

This corresponds to the amino acid sequence <SEQ ID 1784; ORF 581.a>:

```

a581.pep
1  MHFAQLVGQT GIEQNTFCRR GFTRIDMGGN TDVTVQADRC LTSHFISLSK
51  LETEVRECFV GFSHTVYFFT FFQRTATAFG RINQFACQTQ VHGFLLTFAG
101 RINPAHCQS QTA*

```

m581/a581 98.2% identity in 113 aa overlap

	10	20	30	40	50	60
m581.pep	MHFAQLVGQTGIEQNTFCRRGFTRVNMGGNTDVTVQADRG	LTSHFISLSKLETEVRECFV				
a581	MHFAQLVGQTGIEQNTFCRRGFTRIDMGGNTDVTVQADRG	LTSHFISLSKLETEVRECFV				
	10	20	30	40	50	60
	70	80	90	100	110	
m581.pep	GFSHTVYFFTFQRTATAFGRINQFACQTQVHGFLTTFAGRIANPAHCQSQTAX					
a581	GFSHTVYFFTFQRTATAFGRINQFACQTQVHGFLTTFAGRIANPAHCQSQTAX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1785>:

```

g582.seq..
1  atgcgctata ttcttttgac aggactgttg ccgacggcat ccgcttttgg
51  agagaccgcg ctgcaatgcg ccgctttgac ggacaatggt acgcgtttgg
101 cgtgttacga caggattttt gcggcacagc ttccgtcttc ggcagggcag
151 gaagggcagg agtcgaaagc cgtactcaat ctgacggaaa ccgtccgcag
201 cagcttggat aaggggcagg cggtcattgt tgttgaaaaa ggcggggatg
251 cgcttcctgc cgacagtgcg ggcgaaacgc ccgatctcta tacgccttgc
301 agcctgatgt acgacttggc caaaaacgat ttgcgcgggc tgttggcggt
351 acgcgaacac aatccgatgt accttatgcc gttttggtat aacaattcgc
401 ccaactatgc cccgagttcg ccgacgcgcg gtacgactgt acaggaaaaa
451 ttccggacagc agaaaacgtgc ggaaaccaaa ttgcaggttt cgttcaaaag
501 caaaattgcc gaaaatttgc ttaaaaccgc cgcggtatctg tggttcggct
551 acaccctaaag atccgattgg cagatttaca accaaggcag gaaatccgcg
601 ccgttcgcga atacggatta caaacctgaa atttccctga cccagcctgt
651 gaaggcggtat ttgccgttcg gcggcaggct gcgtatgctc ggtgcggtt
701 ttgtccacca gtccaacgga cagagcgcgc ccgaatcgcg ttcggtgaac
751 aggatttatg ccatggcagg catggaatgg ggcaaatgga cggtgattcc
801 gcgcgtgtgg gtgcgtgcgt tcgatcagag cggcgataaa aacgacaatc
851 ccgatattgc cgactatatg gggtatggcg acgtgaagct gcagtaccgc
901 ctgaacgaca ggcagaatgt gtattccgta ttgcgtaca accccaaaac
951 gggctacggc gcgattgaag ccgcctacac gtttcgatt aaggggcaaac
1001 tcaaaaggcgt ggtacgcgga ttccacggtt acggcgagag cctgatcgac
1051 tacaaccaca agcagaacgg tatcggtatc gggttgatgt tcaacgactg
1101 ggacggcatc tga

```

This corresponds to the amino acid sequence <SEQ ID 1786; ORF 582.ng>:

```

g582.pep ..
1  MRYILLTGLL PTASAFGETA LQCAALTDNV TRLACYDRIF AAQLPSSAGQ
51  EQQESKAVLN LTETVRSSLD KGEAVIVVEK GGDALPADSA GETADIYTPL
101 SLMYDLKND LRGLLGVRH NPMYLMFPWY NNSPNYAPSS PTRGTTVQEK
151 FGQQRABTK LQVSFKSKIA ENLPKTRADL WFGYTORSDW QIYNQGRKSA
201 PFRNTDYKPE IFLTQPVKAD LPFGGRLRML GAGFVHQSNQ QSRPESRSWN
251 RIYAMAGMEW GKLTVI PRVW VRAFDQSGDK NDNPDIAIDY GYGDVVKLYR
301 LNDRONVYSV LRYNPKTYG AIEAAYTPPI KGKLGKVVVRG FHGYGESLID
351 YNHKQNGIGI GLMPNDWDGI *

```


The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1787>:

```
m582.seq ..
1  ATGCGCTATA TTCTTTTGAC AGGACTGTG CCGATGGCAT CCGCTTTTGG
51  AGAGACCGCG CTGCAATGCG CCGCTTTGAC GGACAATGTT ACGCGTTTGG
101 CGTGTACAGA CAGGATTTT GCGGCACAGC TTCCGTCTTC GGCAGGGCAG
151 GAAGGGCAGG AGTCGAAAGC CGTACTCAAT CTGACGAAA CCGTCCGCAG
201 CAGCCTGGAT AAGGGCGAGG CCGTCATGT TGTGAAAAA GGCGGGGATG
251 CGCTTCCTGC CGACAGTGG GCGGAAACCG CCGACATCTA TACGCCTTGG
301 AGCCTGATGT ACGACTTGA CAAAAACGAT TTGCGCGGGC TGTGGGGCGT
351 ACGCGAACAC AATCCGATGT ACCTTATGCC GCTCTGGTAC AACAAATCGC
401 CCAACTATGC CCCGGGTTGC CCGACGCGCG GTACGACTGT ACAGGAAAAA
451 TTCGGACAGC AGAAACGTGC GGAACCAAA TTGCAGTTT CGTTCAAAAG
501 CAAAATTGCC GAAGATTGT TAAAACCCG CCGGATCTG TGTTCGGCT
551 ACACCCAAAG ATCCGATTGG CAGATTACA ACCAAGCAG GAAATCCGCG
601 CCGTTCGCA ATACGGATTA CAAACCTGAA ATTTCTCTGA CCCAGCCTGT
651 GAAGGCGGAT TTGCCGTTGC GCGGCAGGCT GCGTATGCTC GGTGCGGGTT
701 TTGTCCACCA GTCCAACGGA CAGAGCCGTC CCGAATCGCG TTCGTGGAAC
751 AGGATTACG CCATGGCAGG CATGGAATGG GSCAAATTGA CGGTGATTCC
801 GCGCGTGTGG GTGCGTGGT TCGATCAGAG CCGCGATAAA AACGACAATC
851 CCGATATTGC CGACTATATG GGTATGGCG ACGTGAAGCT GCAGTACCGC
901 CTGAACGACA GGCAGAATGT GTATTCCGTA TTGCGCTACA ACCCCAAAAC
951 GGGCTACGGC GCGATTGAAG CCGCCTACAC GTTCCGATT AAGGGCAAC
1001 TCRAAGGCGT GGTACGCGGA TTCCACGGTT ACGGCGAGAG CCTGATCGAC
1051 TACAACCACA AGCAGAACGG TATCGGTATC GGGTTGATGT TCAACGACTT
1101 GGACGGCATC TGA
```

This corresponds to the amino acid sequence <SEQ ID 1788; ORF 582>:

```
m582.pep
1  MRYILLTGLL PMASAFGETA LQCAALTDNV TRLACYDRIF AAQLPSSAGQ
51  EGQESKAVLN LTETVRSSLD KGEAVIVVEK GGDALPADSA GETADIYTPL
101 SLMYDLKND LRLLGVREH NPMYLMPLWY NNSPNYAPGS PTRGTTVQEK
151 FGQKRAETK LQVSFKSKIA EDLFKTRADL WFGYTRSDW QIYNQGRKSA
201 PFRNTDYKPE IFLTQPVKAD LPPGGRRLML GAGFVHQSNQ QSRPESRSWN
251 RIYAMAGMEW GKLTVI PRVW VRAFDQSGDK NDNPDADYM GYGDVKLQYR
301 LNDQNVYSV LRYNPKTGYG AIEAAYTFPI KGKLKGVVRG PHGYGESLID
351 YNHKQNGIGI GLMFNDLOGI *
```

m582 / g582 98.6% identity in 370 aa overlap

m582.pep	10	20	30	40	50	60
m582.pep	MRYILLTGLLPMASAFGETALQCAALTDNVTRLACYDRIFAAQLPSSAGQEGQESKAVLN					
g582	MRYILLTGLLPTASAFGETALQCAALTDNVTRLACYDRIFAAQLPSSAGQEGQESKAVLN					
	10	20	30	40	50	60
m582.pep	70	80	90	100	110	120
m582.pep	LTETVRSSLDKGEAVIVVEKGGDALPADSAGETADIYTPSLMYDLKNDLRLLGVREH					
g582	LTETVRSSLDKGEAVIVVEKGGDALPADSAGETADIYTPSLMYDLKNDLRLLGVREH					
	70	80	90	100	110	120
m582.pep	130	140	150	160	170	180
m582.pep	NPMYLMPLWYNNSPNYAPGSPTRGTTVQEKFGQKRAETKLQVSFKSKIAEDLFKTRADL					
g582	NPMYLMPLWYNNSPNYAPGSPTRGTTVQEKFGQKRAETKLQVSFKSKIAENLFKTRADL					
	130	140	150	160	170	180
m582.pep	190	200	210	220	230	240
m582.pep	WFGYTRSDWQIYNQGRKSAPFRNTDYKPEIFLTQPVKADLPFGGRRLMLGAGFVHQSNQ					
g582	WFGYTRSDWQIYNQGRKSAPFRNTDYKPEIFLTQPVKADLPFGGRRLMLGAGFVHQSNQ					
	190	200	210	220	230	240
m582.pep	250	260	270	280	290	300
m582.pep	QSRPESRSWNRIYAMAGMEWGKLTVI PRVWVRAFDQSGDKNDNPDADYMGYGDVKLQYR					
g582	QSRPESRSWNRIYAMAGMEWGKLTVI PRVWVRAFDQSGDKNDNPDADYMGYGDVKLQYR					
	250	260	270	280	290	300
	310	320	330	340	350	360

905

```

m582.pep  LNDQRNVYSVLRYPKTYGYAIEAAYTFPIKGLKGVVRGFHGYGESLIDYNHKQNGIGI
          |||||
g582      LNDQRNVYSVLRYPKTYGYAIEAAYTFPIKGLKGVVRGFHGYGESLIDYNHKQNGIGI
          310      320      330      340      350      360

          370
m582.pep  GLMFNDLDGIX
          |||||
g582      GLMFNDWDGIX
          370

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1789>:

```

a582.seq
1  ATGCGCTATA TTCTTTTGAC AGGACTGTTG CCGATGGCAT CCGCTTTTGG
51  AGAGACCGCG CTGCAATGCG CCGCTTTGAC GGACAATGTT ACGCGTTTGG
101 CGTGTACGA CAGGATTTT GCGGCACAGC TTCCGTCTTC GGCAGGGCAG
151 GAAGGGCAGG AGTCGAAAGC CGTACTCAAT CTGACGGAAA CCGTCCGCAG
201 CAGCCTGGAT AAGGGCGAGG CGGTCATTGT TGTGAAAAA GGCGGGGATG
251 CGCTTCCTGC CGACAGTGCG GCGGAAACCG CCGACATCTA TACGCCTTTG
301 AGCCTGATGT ACGACTTGA CAAAAACGAT TTGCGCGGGC TGTGGGCGT
351 ACGCGAACAC AATCCGATGT ACCTTATGCC GCTCTGGTAC AACAAATTCG
401 CCAACTATGC CCCGGGTTCG CCGACGCGCG GTACGACTGT ACAGGAAAAA
451 TTCGGACAGC AGAAACGTGC GGAACCAAA TTGCAGGTTT CGTTCAAAAG
501 CAAAATTGCC GAAGATTGT TAAAACCCG CGCGGATCTG TGGTTCGGCT
551 ACACCCAAAG ATCCGATTGG CAGATTACA ACCAAGGCAG GAAATCCGCG
601 CCGTTCGCA ATACGGATTA CAAACCTGAA ATTTCTCTGA CCCAGCCTGT
651 GAAGCGGAT TTGCCGTTG GCGGCAGGCT GCGTATGCTC GGTGCGGGTT
701 TTGTCCACCA GTCCAACGGA CAGAGCCGTC CCGAATCGCG TTCGTGGAAC
751 AGGATTACG CCATGGCAGG CATGGAATGG GGCAAATTGA CCGTGATTCC
801 GCGCGTGTGG GTGCGTGCCT TCGATCAGAG CCGCGATAAA AACGACAATC
851 CCGATATTGC CGACTATATG GGTATGGCG ACGTAAGCT GCAGTACCGC
901 CTGAACGACA GGCAGAATGT ETATCCGTA TTGCGCTACA ATCCCAAAAC
951 GCGCTACGCG GCGATTGAAG CCGCTACAC GTTCCGATT AAGGGCAAAC
1001 TCAAAGGCGT GGTACGCGGA TTCCACGGT ACGGCGAGAG CCTGATCGAC
1051 TACAACCACA AGCAGAACGG TATCGGTATC GGTGTGATGT TCAACGACTT
1101 GGACGCGATC TGA

```

This corresponds to the amino acid sequence <SEQ ID 1790; ORF 582.a>:

```

a582.pep
1  MRYILLTGLL PMASAFGETA LQCAALTDNV TRLACYDRIF AAQLPSSAGQ
51  EGQESKAVLN LTETVRSSLD KGEAIVVEK GGDALPADSA GETADIYTPL
101 SLMYDLKND LRGLLGVRH NPMYLMPLWY NNSPNYAPGS PTRGTTVQEK
151 FGQQRKRAETK LQVSFKSKIA EDLEKTRADL WFGYTQRSW QIYNQGRKSA
201 PFRNTDYKPE IFLTQPVKAD LPFGGRLRML GAGFVHQSNQ QSRPESRSWN
251 RIYAMAGMEW GKLTVIPRVW VRAFDQSGDK NDNPOIADYM GYGDVKLQYR
301 LNDQRNVYSV LRYNPKTSYG AIEAAYTFPI KGLKGVVRG FHGYGESLID
351 YNHKQNGIGI GLMFNDLDGI *

m582/a582 100.0% identity in 370 aa overlap

          10      20      30      40      50      60
m582.pep  MRYILLTGLLPMASAFGETALQCAALTDNVTRLACYDRIFAAQLPSSAGQEGQESKAVLN
          |||||
a582      MRYILLTGLLPMASAFGETALQCAALTDNVTRLACYDRIFAAQLPSSAGQEGQESKAVLN
          10      20      30      40      50      60

          70      80      90      100     110     120
m582.pep  LTETVRSSLDKGEAIVVEKGGDALPADSAGETADIYTPLSLMYDLKNDLRGLLGVRH
          |||||
a582      LTETVRSSLDKGEAIVVEKGGDALPADSAGETADIYTPLSLMYDLKNDLRGLLGVRH
          70      80      90      100     110     120

          130     140     150     160     170     180

```

906

```

m582.pep      NPMYLMPLWYNNSPNYAPGSPTRGTTVQEKFGQKRAETKLQVSFKSKIAEDLFKTRADL
               |||
a582          NPMYLMPLWYNNSPNYAPGSPTRGTTVQEKFGQKRAETKLQVSFKSKIAEDLFKTRADL
               13C      140      150      160      170      180

               190      200      210      220      230      240
m582.pep      WFGYTQSRSDWQIYNQGRKSAPFRNTDYKPEIFLTQPVKADLPFGGRLRMLGAGFVHQSN
               |||
a582          WFGYTQSRSDWQIYNQGRKSAPFRNTDYKPEIFLTQPVKADLPFGGRLRMLGAGFVHQSN
               190      200      210      220      230      240

               250      260      270      280      290      300
m582.pep      QSRPESRSWNRIYAMAGMEWGKLTVIPRVWVRAFDQSGDKNDNPDIADYMGYGDVKLQYR
               |||
a582          QSRPESRSWNRIYAMAGMEWGKLTVIPRVWVRAFDQSGDKNDNPDIADYMGYGDVKLQYR
               250      260      270      280      290      300

               310      320      330      340      350      360
m582.pep      LNDRQNVYSVLRYNPKTGYGAIEAAYTFPIKGLKGVVRGFHGYGESLIDYNHKGQNGIGI
               |||
a582          LNDRQNVYSVLRYNPKTGYGAIEAAYTFPIKGLKGVVRGFHGYGESLIDYNHKGQNGIGI
               310      320      330      340      350      360

               370
m582.pep      GLMFNDLDGIX
               |||
a582          GLMFNDLDGIX
               370

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1791>:

g583.seq..

```

1  atgataattg accaaagcca aatatttacc catcttgccct tctgtgccct
51  ttgcgggatt ggagccgtaa ctgccggcaa tcgactgcat aatcggatgt
101 ataatgccgc cgccgcgcgc ggtattggaa ggggtaacgg gagccagcag
151 cagtccggaa agagcgagac tgtaaccgat gccacgcgtt tttcttccaa
201 aaacggcgat aaacaaatat ccgatacgca tccccagccc tgttttgagc
251 aaaccgcgct aaatcataac tgcgatggca atcagccaaa tcaacggatt
301 ggcgaacgca ctcaacgcat cgctcatcgc cgcgccgggt ttgtcggcgg
351 ttacgcgggt tactgagacc aaccgcgagg caataatcga cagcgcgccc
401 aacggcataa ccttgccgat aatggcgcca atcacaccga caaacatagc
451 cagcagcgtc caagcctgag gcttgacccc gtcgggtacg ggcagtgcca
501 aaaccagggc gcacaatact gcggcaatgg cgaggggtat cggtttgaaa
551 cccaatttca tcatattgac ctccgtaaaa aagaccgtcc cgaaaaatcg
601 gaaaaataa

```

This corresponds to the amino acid sequence <SEQ ID 1792; ORF 583.ng>:

g583.pep..

```

1  MIIDQSIFT HLAFCAPCGI GAVTAGNRLH NRMYNAAAAR GIGRNGSQQ
51  QFGKSETVTD AQRFSKNGD KQISDTHPQP CFEQTARNHN CDGNQPNQRI
101 GERTQRIHR RARFVGGYAG YCDQPDGNNR QRAQRHNLAD NGGNHTDKHS
151 QQRPSLRLLD VGYGQCQNGG AQYCGNGEGY RFETQFHHID LRKKDRPEKS
201 EK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1793>:

m583.seq..

```

1  ATGATAGITG ACCAAAGCCA AATATTTACC CATCTTGCCCT TCTGTGCCCT
51  TTGCGGGATT GGAGCCGTAA CTGCCGGCAA TCGACTGCAT AATCGGATGT
101 ATATATGCCG CGCCGCGCGC GGTATTGGAA GGGGTAACGG GAGCCAGCAG
151 CAGTTCGGAA AGAGCGAGAC TGTAAACCGAT GCCCAGCGTT TTTCTTCCAA
201 AAACGGCGAT AAACAAATAT CCGATACGCA TCCCCAGCCC TGTTTTGAGC
251 AAACGGCGCG AAATCATAAC TGCGATGGCA ATCAGCCAAA TCAACGGATT
301 GCGGAACGCA CTCAACGCAT CGCTCATCGC CGCGCCCGGT TTGTCGGCGG
351 TTACGCGGGT TACTGCGACC AACCAGCGG CAATAATCGA CAGCGCGCCC
401 AACGGCATGG CCTTGCCGAT AATGGCGGCA ATCACACCGA CAAACATGGC
451 CAGCAGCGTC CAAGCCTGAG GCTTGACCCC GTCGGGTACG GGCAGTGCCA
501 AAACAGGGC GCACAATACT GCGCAATGG CGAGGGGTAT CGGTTTGAAA

```

907

551 CCCAATTTCATCATATTGACCTCCGTAAAAAAGACCGTCCCGAAAAATCG
 601 GAAAAATAA

This corresponds to the amino acid sequence <SEQ ID 1794; ORF 583>:

m583.pep..

1 MIVDQSQIFT HLAFCAFCGI GAVTAGNRLH NRMYNAAAAARGIGRNGSQQ
 51 QFGKSETVTD AQRFSKNGD KQISDTHPQP CFEQTARNHN CDGNQPNQRI
 101 GERTQRIHR RARFVGGYAG YCDQPDGNNR QRAQRHGLAD NGGNHTDKHG
 151 QQRPSLRLDP VGYGQCQNQG AQYCGNGEGY RFETQFHHID LRKKDRPEKS
 201 EK*

m583 / g583 98.5% identity in 202 aa overlap

	10	20	30	40	50	60
m583.pep	MIVDQSQIFT HLAFCAFCGI GAVTAGNRLH NRMYNAAAAARGIGRNGSQQ QFGKSETVTD					
g583	MIIDQSQIFT HLAFCAFCGI GAVTAGNRLH NRMYNAAAAARGIGRNGSQQ QFGKSETVTD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m583.pep	AQRFSKNGDKQISDTHPQPCFEQTARNHNC DGNQPNQRI GERTQRIHR RARFVGGYAG					
g583	AQRFSKNGDKQISDTHPQPCFEQTARNHNC DGNQPNQRI GERTQRIHR RARFVGGYAG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m583.pep	YCDQPDGNNR QRAQRHGLAD NGGNHTDKHG QQRPSLRLDP VGYGQCQNQGAQYCGNGEGY					
g583	YCDQPDGNNR QRAQRHGLAD NGGNHTDKHG QQRPSLRLDP VGYGQCQNQGAQYCGNGEGY					
	130	140	150	160	170	180
	190	200				
m583.pep	RFETQFHHID LRKKDRPEKSEKX					
g583	RFETQFHHID LRKKDRPEKSEKX					
	190	200				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1795>:

a583.seq

1 ATGATAGTTG ACCAAAGCCA AATATTTACC CATCTTGCCCT TCTGTGCCTT
 51 TTGCGGGATT GGAGCCGTAA CTGCCGGCAA TCGACTGCAT AATCGGATGT
 101 ATAATGCCGC CGCCGCGCGC GGTATTGGAA GGGTAACGG GAGCCAGCAG
 151 CAGTTCGGAA AGAGCGAGAC TGTAAACGAT GCCCAGCGTT TTTCTTCCAA
 201 AAACGCGCAT AAACAAATAT CCGATACGCA TCCCCAGCCC TGTTTTGAGC
 251 AAACGCGCGC AAATCATAAC TGCGATGGCA ATCAGCCAAA TCAACGGATT
 301 GGCGAACGCA CTCAACGCAT CGCTCATCGC CGCACCCGGT TTGTCGCGCG
 351 TTACGCGCGT TACTGCGACC AACCCGACGG CAATAATCGA CAGCGCACCC
 401 AACGCGCATGG CCTTGCCGAT AATGGCGGCA ATCACACCGA TAAACATGGC
 451 CAGCAGCGTC CAAGCCTGAG GCTTGACCCC GTCGGGTACG GGCAGTGCCA
 501 AAACCAAGGC GCACAATACT GCGGCAATGG CGAGGGGTAT CGGTTTGAAA
 551 CCCAATTTCATCATATTGACCTCCGTAAAAAAGACCGTCCCGAAAAATCG
 601 GAAAAATAA

This corresponds to the amino acid sequence <SEQ ID 1796; ORF 583.a>:

a583.pep

1 MIVDQSQIFT HLAFCAFCGI GAVTAGNRLH NRMYNAAAAARGIGRNGSQQ
 51 QFGKSETVTD AQRFSKNGD KQISDTHPQP CFEQTARNHN CDGNQPNQRI
 101 GERTQRIHR RTRFVGGYAG YCDQPDGNNR QRTQRHGLAD NGGNHTDKHG
 151 QQRPSLRLDP VGYGQCQNQG AQYCGNGEGY RFETQFHHID LRKKDRPEKS
 201 EK*

m583/a583 99.0% identity in 202 aa overlap

	10	20	30	40	50	60
m583.pep	MIVDQSQIFT HLAFCAFCGI GAVTAGNRLH NRMYNAAAAARGIGRNGSQQ QFGKSETVTD					

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```

a583      MIVDQSQIFTHLAFCAFCGIGAVTAGNRLHNRMYNAAAARGIGRNGSQQFGKSETVTD
           10      20      30      40      50      60
           70      80      90      100     110     120
m583.pep  AQRFSKNGDKQISDTHPQPCFEQTARNHNCNQPQRIGERTQRIAHRRARFVGGYAG
           |||||
a583      AQRFSKNGDKQISDTHPQPCFEQTARNHNCNQPQRIGERTQRIAHRRTRFVGGYAG
           70      80      90      100     110     120
           130     140     150     160     170     180
m583.pep  YCDQPDGNNRQRAQRHGLADNGGNHTDKHGQQRPSLRLDPVGYGQCQNQGAQYCGNGEGY
           |||||
a583      YCDQPDGNNRQRTQRHGLADNGGNHTDKHGQQRPSLRLDPVGYGQCQNQGAQYCGNGEGY
           130     140     150     160     170     180
           190     200
m583.pep  RFETQFHHIDLKKDRPEKSEKX
           |||||
a583      RFETQFHHIDLKKDRPEKSEKX
           190     200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1797>:

```

g584.seq..
1  atgtctgcgtt ctattttggc ggcttcctcg ctggcggtat cttttccggc
51  ggcggctgag gcattgaatt acaatattgt cgaattttcc gaatcggcgg
101 gtatcgaggt ggctcagcat acaatgtccg cgcgtttcca ggtggcggcg
151 gaaggacggg acaaaaatgc cgtcaatgcc gagtttgta aaaaattcaa
201 caatttcacc agaaaatcga aaaatggtag ctttaaaacc gaattggtat
251 cgcgcagtcg gatgccgcgc tatcaatata ccaacggcag acgcattcaa
301 acaggctggg aggagcgtgc ggaatttaag gcggaggcca gggattttga
351 tgccttaaac cgttttattg ctgatgttca gacggatgct tcgcttgaag
401 ataccgattt cagcgtgtcg cgcgaacgcc gaaacgaggt catcgatcag
451 gtcagcaagg atgccgtttt gcgtttcaag gcgcgtgccg aaaaactggc
501 gggcgcttcg ggtgcgtccg gttataaaat cgtcaaatg aattttgggc
551 aaatcggcag ccatattgcg ggcgatgggg ctgttcgggc aaaaatgctg
601 cgcgcgatgc cgatggcggc aagcgtcaat atgaagggt aegattcagc
651 cgcacgggtg gtggaggaaa tcagcatcag catcaatggg acggttcagt
701 tctaa

```

This corresponds to the amino acid sequence <SEQ ID 1798; ORF 584.ng>:

```

g584.pep Length:..
1  MLRSILAASL LAVSFPAARE ALNYNIVEFS ESAGIEVAQD TMSARFQVAA
51  BGRDKNVNA EFKKFNFT RSKNGSFKT ELVSRSAMPR YQYNGRRRIQ
101 TGWEERAEFK AGRDFDALN RFIADVQTD SLEDTDFSVS RERRNEVIDQ
151 VSKDAVLRFK ARAEKLAVL GASGYKIVKL NFGQIGSHIA GDGAVRAKML
201 RAMPMAASVN MKGTDSAAPG VEEISISING TVQP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1799>:

```

m584.seq..
1  ATGTTGCGTC TTGTTTGGC GGCTTGGCTG TCGGCGGTAT CTTTCCGGC
51  AGCGGCTGAA GCATIGAATT ACAATATTGT CGAATTTTCC GAATCGGCGG
101 GTGTCAGGAT GGCTCAGGAT ACAATGTCCG CACGTTTCCA AGTGACGGCG
151 GAAGGACGGG AAAAAATGC CGTCAATGCT GAGTTTGTTA AAAAAATCAA
201 CAAGTTCATC AGAAAATCGA AAAATGGTAG CTTTAAACC GAATTGGTAT
251 CGCGCAGTGC GATGCCGCGC TATCAATATA CCAACGGCAG ACGCATTCAA
301 ACAGGCTGGG AGGAGCGTGC GGAATTTAAG GTCGAAGGTA GAGATTTTGA
351 TGAGTTAAAC CGTTTATTG CCGATATTCA AGCAGATGCC CGCTTGGMAT
401 ATACGGATTT CCATGTGTCG CGCGAACGCC GCAACGAGGT CATCkATCAG
451 GTCAGCAAGG ATGCCGTTT GCGTTTCAAG GCGCGTCCG AAAAGTTGGC
501 GGGCGTTTTG GGTGCGTCCG GTTATAAAAT CGTCAAATG AATTGGGAC
551 ACATCGGCAG CCATATCGCG GGAGGGGAG CTGCTCAGGC AAAAAATGCTT
601 CGTGCCATGC CGATGGCGGC AAGCGTCAAT ATGGAGGGTG CGGATTCCGC
651 CGCGCTGGT GTGGAGGAAA TCAGCATCAG CGTCAATGGG ACGGTTCACT
701 TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1800; ORF 584>:

909

m584.pep..

```

1  MLRLVLAASL SAVSFPAAAE ALNYNIVEFS ESAGVEVAQD TMSARFQVTA
51  EGRDKNVNA EFVKKFNKFI RKSKNGSFKT ELVSRSAMPR YQYTNRRRIQ
101 TGWEERAEFK VEGRDFDELN RFIADIQADA ALXYTDFHVS RERRNEVIXQ
151 VSKDAVLRFK ARAEKLAVL GASGYKIVKL NLGHIGSHIA GGGAAQAKML
201 RAMPMAASVN MEGADSAAPG VEEISISVNG TVQF*

```

m584 / g584 89.7% identity in 234 aa overlap

```

              10      20      30      40      50      60
m584.pep  MLRLVLAASLSAVSFPAAAEALNYNIVEFS ESAGVEVAQDTMSARFQVTABGRDKNVNA
          ||| :||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g584      MLRSILAASLLAVSFPAAAEALNYNIVEFS ESAGIEVAQDTMSARFQVAEGRDKNVNA
              10      20      30      40      50      60

              70      80      90     100     110     120
m584.pep  EFVKKFNKFI RSKNGSFKTELVSRSAMP RYQYTNRRRIQTGWEEARAEFKVEGRDFDELN
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g584      EFVKKFNFT RSKNGSFKTELVSRSAMP RYQYTNRRRIQTGWEEARAEFKAEGRDFDALN
              70      80      90     100     110     120

              130     140     150     160     170     180
m584.pep  RFIADIQADAALXYTDFHVSRRERRNEVIXVSKDAVLRFKARA EKLAVLGASGYKIVKL
          ||||| :||| :| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g584      RFIADVQTDASLEDTFVSRRERRNEVIDQVSKDAVLRFKARA EKLAVLGASGYKIVKL
              130     140     150     160     170     180

              190     200     210     220     230
m584.pep  NLGHIGSHIAGGGAAQAKMLRAMPMAASVNMEGADSAAPGV EEEISISVNGTVQFX
          ||| :||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g584      NFGQIGSHIAGDGAVRAKMLRAMPMAASVNMKGTD SAAPGV EEEISISINGTVQFX
              190     200     210     220     230

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1801>:

```

a584.seq
1  ATGTTGCGTT CTATTTTGGC GGCTTCCCTG CTG.....
51  .....ATTGT CGAATTTTCT GAATCGGCGG
101 GTGTCGAGGC GGTTCAGGAT ACAATGTCCG CACGTTTCCA AGTGACGGCG
151 GAAGGACGGG AAAAAATGC CGTCAATGCC GAGTTTGTTA AAAAATTCAA
201 CAATTTCAAC AGAAAATCAA AAAATGGTAG CTTTAAARACC GAATTGGTAT
251 CGCGCAGTGC GATGCCGCGC TATCAATATA CCAACGGCAG ACGCATTCAA
301 ACAGGTTGGG AGGAGCGTGC GGAATTTAAG GTCGAGGGTA GGAATTTTGA
351 TCGGTTGAAC CGTTTTATG CCGATGTTCA GGCAGATGCC GCGTTGGAAT
401 ATACGGATTT CCATGTGTCG CGCGAACGCC GCAACGAGGT CATCGATCAG
451 GTCAGCAAGG ATGCCGTTT GCGTTTCAAG GCGCGTGCCG AAAAGTTGGC
501 GGGCGTTTGG GGTGCGTCCG GTTATAAAAT CGTCAAATTG AATTTGGGAC
551 ACATCGGCAG CCATATCGCG GGAGGGGGAG CTGCTCAGGC AAAAATGCTT
601 CGTGCCATGC CGATGGCGGC AAGCGTCAAT ATGGAGGGTG CGGATTCGCG
651 CGCGCCTGGT GTGGAGGAAA TCAGCATCAG CGTCAATGGG ACGGTTCACT
701 TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1802; ORF 584.a>:

```

a584.pep
1  MLRSILAASL L..... IVEFS ESAGVEAVQD TMSARFQVTA
51  EGRDKNVNA EFVKKFNFT RKSKNGSFKT ELVSRSAMPR YQYTNRRRIQ
101 TGWEERAEFK VEGRNFDALN RFIADVQADA ALEYTDFHVS RERRNEVIDQ
151 VSKDAVLRFK ARAEKLAVL GASGYKIVKL NLGHIGSHIA GGGAAQAKML
201 RAMPMAASVN MEGADSAAPG VEEISISVNG TVQF*

```

m584/a584 88.9% identity in 234 aa overlap

```

              10      20      30      40      50      60
m584.pep  MLRLVLAASLSAVSFPAAAEALNYNIVEFS ESAGVEVAQDTMSARFQVTAEGRDKNVNA
          ||| :||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a584      MLRSILAASL-----IVEFS ESAGVEAVQDTMSARFQVTAEGRDKNVNA
              10      20      30      40

```

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	70	80	90	100	110	120
m584.pep	EFVKKFNKFIRKSKNGSFKTELVSRSAMPYQYTNGRRIQTGWEERAEFKVEGRDFDELN					
a584	EFVKKFNKFIRKSKNGSFKTELVSRSAMPYQYTNGRRIQTGWEERAEFKVEGRNFDALN					
	50	60	70	80	90	100
	130	140	150	160	170	180
m584.pep	RFIADIQADAALXYTDFHVSRRERNEVIXQVSKDAVLRFKARAELAGVLGASGYKIVKL					
a584	RFIADVQADAALXYTDFHVSRRERNEVIDQVSKDAVLRFKARAELAGVLGASGYKIVKL					
	110	120	130	140	150	160
	190	200	210	220	230	
m584.pep	NLGHIGSHIAGGGAAQAKMLRAMPMAASVNMEGADSAAPGVVEEISISVNGTVQFX					
a584	NLGHIGSHIAGGGAAQAKMLRAMPMAASVNMEGADSAAPGVVEEISISVNGTVQFX					
	170	180	190	200	210	220

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1803>:

g585.seq..

```

1  atgaaactgt  tccaacgcac  tttegccaca  ttttgccgag  ttatcgctcg
51  cgcaatcttt  gtggcgagtt  tttctttttg  gctgggtgag  aacacccttg
101  ccgaaaacca  attcaaccaa  cgccgcacca  tcgaaaccac  attgatgggc
151  agcattatgt  ccgcattcaa  gacacggggc  gacaacggcg  cgcgcgaaat
201  cctgaccgaa  tggaaaaaca  gcccgctctc  atccgcgctt  tacgtcatac
251  agggcgacga  gaaaaaagac  atcttaaaac  gctatatcga  caattacacc
301  atagaacgag  ccgggctgtt  tgccgccaac  aacccccatt  ccaaccttgt
351  ccgcacgcaa  tacgacgggt  tcggcggaag  atacctgttc  ttcattaaag
401  gctgggacaa  ccaccaggca  caacgcctgc  ccagcccgct  gtttatcccg
451  ggctcgccgc  ttgccccgat  ttggcacgaa  ttcacatccc  tctccttcat
501  catcattgtc  ggactgctga  tggcatatat  ccttgccggc  aacattgcca
551  aacccatcag  aatcttaggc  aacggcatgg  acagggtggc  agaacgagaa
601  ctggaagacc  gcgtttgcca  acaggttcgc  gaccgcgacg  acgaattggc
651  cgatgttgcc  atgcaattcg  acacaatggt  ggaaaaactg  gaataa

```

This corresponds to the amino acid sequence <SEQ ID 1804; ORF 585.ng>:

g585.pep..

```

1  MKLFORIFAT  FCAVIVCAIF  VASFSFWLVQ  NTLAENQFNQ  RRTIETLMG
51  SIISAFKTRG  DNGAREILTE  WKNSPVSSAV  YVIQDEKED  ILNRYIDNYT
101  IERARLFAAN  NPHSNLVRIE  YDRFGEEYLF  PIKGDNDHQA  QRLPSPLFIP
151  GLPLAPIWHE  FIILSFIIIV  GLLMAYILAG  NIAKPIRILG  NGMDRVAERE
201  LEDRVCCQVR  DRDELADVA  MQPDTMVEKL  E*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1805>:

m585.seq..

```

1  ATGAAACTGT  TCCAACGCAT  TTTCGCCACA  TTTTGGCGGG  TTATCGTCTG
51  TGCAATCTTT  GTGGCGAGTT  TTCTTTCTG  GCTGGTGCAG  AACACCCCTG
101  CCGAAAACCA  GTTCAACCAA  CGCCGCACCA  TCGAAACCAC  TTTGATGGGC
151  AGCATCATTT  CCGCATTCCG  GGCACGCGGG  GACGCGGGTG  CGCGCGAAAT
201  CCGACGGGAA  TGGAAAGACA  GCCCCGTCTC  ATCGGGCGTG  TACGTTATAC
251  AGGGCGACGA  GAAAAAGAT  ATCCTGAACC  GGTATATCGA  CAGCTATACC
301  ATCGAACGCG  CCGGCTTTT  CGCCGCCGGA  CACCCGCATT  CCAACCTCGT
351  CCATATCGAA  TACGACGCT  TCGGCGAAGA  ATACCTGTTC  TTCACCAAAG
401  ACTGGGACAA  ACTCCAAGCC  CGCCGCTGCG  CCAGCCCCCT  GTTGATCCCC
451  GGCTGCGCCG  TCGCCCGAT  TTGGCACGAA  CTCATCATAT  TGTCTTCAT
501  CATCATGCTC  GGAATGCTGA  TGGCATATAT  CCTCGCCGGC  AACATTGCCA
551  AACCCATCAG  AATCTTAGGC  AACGGCATGG  ACAGGCTGGC  AAACGGAGAA
601  CTGAAACCC  GTATCTCCCA  ACAGGTCGAC  GACCGCGACG  ACGAATTGTC
651  CCATCTTGCC  ATCCAATTCC  ACAAAATGGT  GGAAGAACTC  GAAAAACTCG
701  TTGCCAAGA  ACGCCACCTG  CTCCATCAG  TCTCCATGA  AATGCGTCTT
751  CCCCTTGCGC  GCATGCAGGC  AATTGTCGGA  CTGATTACAG  CGCAGCCCA
801  AAAACAGGAG  CAATATCTCA  AACGGCTGGA  AGGCGAACTG  ACCGCGATGG
851  ATACGCTGGC  CGGGGAAGTG  TTAACCTGT  CCCGTCTCGA  AACTTCCAAT
901  ATGGCTTTGG  AAAAAAGAA  CCTGAAACTC  CTGCCCTTCC  TGGGCAACCT
951  GGTAGAAGCA  AATCAAAGCA  TTGCCAGAA  AAACGGACAA  ACGTTACCC
1001  TGTCTGCCGA  CGGAAAAATC  CCCGAAAAA  CAACCATCCT  TGCCAACGAA

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1051 AGCTACCTGT ACCGCGCCTT CGACAACGTC ATCCGCAACG CCGTCAACTA
1101 CAGTCCCCAA GGCAGCACCA TCCTGATCAA CATCGGACAA GACCACAAAC
1151 ACTGGATAAT CGACGTTACC GACAAAGGCC CCGCGGTGGA CGAAATGCAG
1201 CTCCCGCACA TCTTCACCGC TTTCTACCGT GCAGACTCCA GTGCCAACAA
1251 ACCCGGAACA GGAAGTGGGC TTGCATTGAC CCAACATATT ATTGAACAGC
1301 ACTGCGGCAA AATCATCGCC GAAAACATCA AACCGAACGG TCTGCGGATG
1351 CGCTTTATCC TGCCCAAGAA AAAAACCGGT TCCAAACAG AAAAAAGTGC
1401 GAACTGA

```

This corresponds to the amino acid sequence <SEQ ID 1806; ORF 585>:

m585.pep..

```

1 MKLFQRI FAT FCAVIVCAIF VASFSFWLVQ NTLAENQFNQ RRTIETTLMG
51 SIISAFRARG DAGAREILTE WKDSPVSSGV YVIQGEKKD ILNRYIDSYT
101 IERARLFAAG HPHSNLVHIE YDRFGEYLF FTKDWDKLQA RRLPSPLLIIP
151 GLPLAPIWHE LIILSFIIIV GLLMAYILAG NIAKPIRILG NGMDRVANGE
201 LETRISQQVD DRDELSHLA IQFDKMVEKL EKLVAERHL LHHVSHMRS
251 PLARMQAIIV LIQAQPKQE QYLRLEGE LTRMDTLAGE LTLRLETSN
301 MALEKESLKL LPFLGNLVED NQSIQKNCQ TVTSLADGKI PENTTILANE
351 SYLYRAFQNV IRNAVNYSP EGTILINICQ DHKHWIIDVT DNGPCVDEM
401 LPHIFTAFYR ADSSANKPGT GLGLALTQHI IEQHCCKIIA ENIKPNGLRM
451 RFILPKKKTG SKTEKSAN*

```

m585 / g585 88.3% identity in 231 aa overlap

	10	20	30	40	50	60
m585.pep	MKLFQRI FAT FCAVIVCAIF VASFSFWLVQ NTLAENQFNQ RRTIETTLMG SIISAFRARG					
g585	MKLFQRI FAT FCAVIVCAIF VASFSFWLVQ NTLAENQFNQ RRTIETTLMG SIISAFKTRG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m585.pep	DAGAREILTEWKDSPVSSGVYVIQGEKKDILNRYIDSYTIERARLFAAGHPHNSNLVHIE					
g585	DNGAREILTEWKNSPVSSAVYVIQGEKKDILNRYIDNYTIERARLFAANNPHNSNLVRIE					
	70	80	90	100	110	120
	130	140	150	160	170	180
m585.pep	YDRFGEYLF FTKDWDKLQARRLPSPLLIIPGLPLAPIWHELIILSFIIIVGLLMAYILAG					
g585	YDRFGEYLF FFIKGDNDHQAQR LPSPLFIPLGLPLAPIWHEFIILSFIIIVGLLMAYILAG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m585.pep	NIAKPIRILGNGMDRVANGELETRISQQVDDRDELSHLA IQFDKMVEKLEKLVAERHL					
g585	NIAKPIRILGNGMDRVAERELEDRVCQVDRDELADVAMQFDTMVEKLEX					
	190	200	210	220	230	
	250	260	270	280	290	300
m585.pep	LHHVSHMRSPLARMQAIIVGLIQAQPKQE QYLRLEGE LTRMDTLAGE LTLRLETSN					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1807>:

a585.seq

```

1 ATGAAACTGT TCCAACGCAT CTTCGCCACA TTTTGCGCGG TTATCGTCTG
51 TGCAATCTTT GTGGCGAGTT TTTCTTCTG GCTGGTGCGAG AACACCCTTG
101 CCGAAAACCA GTTCAACCAA CGCCGCACCA TCGAAACCAC TTTGATGGGC
151 AGCATCATT CCGCATTCCG GGCACGCGGG GACGCGGGTG CGCGCGAAAT
201 CCTGACGGAA TGGAAAGACA GCCCGTCTC ATCGGGCGTG TACGTTATAC
251 AGGGCGACGA GAAAAAGAT ATCCTGCACC GGTATATCGA CAGCTACACC
301 ATCGAACGCG CCCGCTTTT CGCCGCCGGA CACCCGCATT CCAACCTCGT
351 CCATATCGAA TACGACCGCT TCGGCGAAGA ATACCTGTTT TTCACCAAG
401 ACTGGGACAA ACTCCAAGCC CGCCGCTGC CCAGCCCCCT GTTGATCCCC
451 GGCCTGCCGC TCGCCCGGAT TTGGCAGGAA CTCATCATAT TGTCCTTCAT
501 CATCATCGTC GGAAGTCTGA TGGCGTACAT CCTCGCCGGC AACATTGCCA
551 AACCCATCAG AATCTTAGGC AACGGCATGG ACAGGGTGGC AAACGGAGAA
601 CTTGAAACCC GTATCTCCA ACAGGTCGAC GACCGCGACG ACGAATTGTC

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651 CCATCTTGCC ATCCAATTCG ACAAATGGT GGAAAACTC GAAAACTCG
701 TTGCCAAAGA ACGCCACCTG CTCCATCACG TCTCCCATGA AATGCGTTCT
751 CCCCTTGCGC GCATGCAGGC AATTGTCGGA CTGATTCAGG CGCAGCCCCA
801 AAAACAGGAG CAATATCTCA AACGGCTGGA AGGCGAACTG ACCCGCATGG
851 ATACGCTGGC CGGGGAACTG TTAACCTGT CCCGTCTCGA AACTTCCAAT
901 ATGGCTTTGG AAAAAGAAAG CCTGAAACTC CTGCCCTTCC TGGGCAACCT
951 GGTAGAAGAC AATCAAAGCA TTGCCAGAA AAACGGACAA ACGGTTACCC
1001 TGTCTGCCGA CGGAAAAATC CCGGAAAACA CAACCATCCT TGCCAACGAA
1051 AGCTACCTGT ACCGCGCCTT CGACAACGTC ATCCGCAACG CCGTCAACTA
1101 CAGTCCCGAA GGCAGACCA TCCTGATCAA CATCGGACAA GACCACAAAC
1151 ACTGGATAAT CGACGTTACC GACAACGGCC CCGGCGTGA CGAAATGCAG
1201 CTCCGCACA TCTTACCGC TTTCTACCGT GCAGACTCCA GTGCCAACAA
1251 ACCCGGAACA GGAAGTGGGC TTGCATTGAC CCAACATATT ATTGAACAGC
1301 ACTCGGCA AATCATCGCC GAAAACATCA AACCGAACGG TCTGCGGATG
1351 CGCTTTATCC TGCCAAGAA AAAAACCGGT TCCAAACAG AAAAAAGTGC
1401 GAACTGA

```

This corresponds to the amino acid sequence <SEQ ID 1808; ORF 585.a>:

```

a585.pep
1  MKLFQRI FAT FCAVIVCAIF VASFSFWLVQ NTLAENQFNQ RRTIETTLMG
51  SIISAFRARG DAGAREILTE WKDSPVSSGV YVIQGDEKDD ILHRYIDSYT
101 IERARLFAAG HPHSNLVHIE YDRFGEEYLF FTKDWDKLQA RRI,PSPELLIP
151 GLPLAPIWHE LIILSFIIIV GLLMAYILAG NIAKPIRILG NGMDRVANGE
201 LETRISQVDD DRDDELSHLA IQFDKMVEKL EKLVAKEERHL LHHVSHEMRS
251 PLARMQAIVG LIQAQPQKQE QYLKRLEGEL TRMDTLAGEL LTLSRLETSN
301 MALEKESLKL LPFLGNLVED NQSIAQKNGQ TVTLSADGKI PENTTILANE
351 SYLYRAFNDV IRNAVNSYPE GSTILINIQ DHKHWIIDVT DNGPGVDEMQ
401 LPHIFTAFYR ADSANKPGT GLGLALTQHI IEQHCCKIIA ENIKPNGLRM
451 RFILPKKKTG SKTEKSAN*

m585/a585 99.8% identity in 468 aa overlap

          10      20      30      40      50      60
m585.pep  MKLFQRI FATFCAVIVCAIFVASFSFWLVQNTLAENQFNQRRRTIETTLMGSIISAFRARG
a585      MKLFQRI FATFCAVIVCAIFVASFSFWLVQNTLAENQFNQRRRTIETTLMGSIISAFRARG
          10      20      30      40      50      60

          70      80      90      100     110     120
m585.pep  DAGAREILTEWKDSPVSSGVYVIQGDEKDDILNRYIDSYTIERARLFAAGHPHSNLVHIE
a585      DAGAREILTEWKDSPVSSGVYVIQGDEKDDILHRYIDSYTIERARLFAAGHPHSNLVHIE
          70      80      90      100     110     120

          130     140     150     160     170     180
m585.pep  YDRFGEEYLF FTKDWDKLQARRLPSPLLIPGLPLAPIWHELIILSFIIIVGLLMAYILAG
a585      YDRFGEEYLF FTKDWDKLQARRLPSPLLIPGLPLAPIWHELIILSFIIIVGLLMAYILAG
          130     140     150     160     170     180

          190     200     210     220     230     240
m585.pep  NIAKPIRILGNMGMDRVANGELETRISQVDDRDDELSHLAIQFDKMVEKLEKLVAKEERHL
a585      NIAKPIRILGNMGMDRVANGELETRISQVDDRDDELSHLAIQFDKMVEKLEKLVAKEERHL
          190     200     210     220     230     240

          250     260     270     280     290     300
m585.pep  LHHVSHEMRSP LARMQAIVGLIQAQPQKQEYQLKRLEGELTRMDTLAGELLTSLRLETSN
a585      LHHVSHEMRSP LARMQAIVGLIQAQPQKQEYQLKRLEGELTRMDTLAGELLTSLRLETSN
          250     260     270     280     290     300

          310     320     330     340     350     360
m585.pep  MALEKESLKL LPFLGNLVEDNQSIAQKNGQTVTLSADGKIPENTTILANESYLYRAFNDV
a585      MALEKESLKL LPFLGNLVEDNQSIAQKNGQTVTLSADGKIPENTTILANESYLYRAFNDV

```

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	310	320	330	340	350	360
	370	380	390	400	410	420
m585.pep	IRNAVNYSPEGSTILINIGQDHKHWIIDVTDNGPGVDEMQLPHIFTAFYRADSSANKPGT					
a585	IRNAVNYSPEGSTILINIGQDHKHWIIDVTDNGPGVDEMQLPHIFTAFYRADSSANKPGT					
	370	380	390	400	410	420
	430	440	450	460	469	
m585.pep	GLGLALTQHIIEQHCGKIIAENIKPNGLRMRFILPKKKTGSKTEKSANX					
a585	GLGLALTQHIIEQHCGKIIAENIKPNGLRMRFILPKKKTGSKTEKSANX					
	430	440	450	460		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1809>:

g586.seq..

```

1 atggcagccc atctcgaaga acaacaagag ttagacaact ttaaatattt
51 ttggaaaacc acgggcaaat ggctgtttgc cctgctgatt ttggcggcac
101 tccgctactt gggatacacg gtttaccaaa accgtgcggc ttcccaaaat
151 caggaaagcgg cggcgggtgct ggcaaacatc gtggaaaagg cgcaaaacaa
201 agccccgcaa agcgaaatca atgccgaact gtccaaactc caacaaagct
251 acccccattc catttccgcc gcccaagcca cgctgatggc ggcggaacc
301 gaatttgacg cgcagcggtta cgatgttgcc gaaggtcatt tgaaatgggt
351 gttgtccaac caaaaagaca gcctgattca ggcgttgccg gcgcagcgctc
401 tggcgcttgt gttgttgcaa caaaaaaat acgatgccgc gcttgccgca
451 ctgcacacgc cgggttgaggc ggacttcgcc cccctgctga tggaaactaa
501 aggcgatggt tatgccgcac agggaaaaag ccagggaagc ttaaaaaact
551 acggacaggc ttggaaaaa atgectcaag attctgtcgg tcgcgaattg
601 ctcaaatga aactcgattc gctgaaataa

```

This corresponds to the amino acid sequence <SEQ ID 1810; ORF 586.ng>:

g586.pep..

```

1 MAAHLEEQQE LDNFKYFWKT TGKWLFALLI LAALGYLGYT VYONRAASON
51 QEAAAVLANI VEKAQNKAPQ SEINAELSKL QQSYPHSISA AQATLMAAAT
101 EFDQRYDVA EGHLLKWVLSN QKDSLIQALA AQLRGVLLQ QKKYDAALAA
151 LDTFVEADFA PLLMETKGDV YAAQKSQEA LKNYQALEK MPQDSVGREL
201 LQMKLDSLK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1811>:

m586.seq

```

1 ATGCGAGCCC ATCTCGAAGA ACAACAAGAG TTAGACAAC TTAATATTT
51 TTGGAACACC ACGGGCAAT GGCTGTTTGC CTTGCTGATT TTGGCGGCAC
101 TCGGCTACTT GGGATACACG GTTACCAAAA ACCGTAAAGT TTCCCAAAAT
151 CAGGAAGCGG CCGCGGTGCT GGCAAAATC GTAGAAAAGG CGCAAAGCAA
201 AGCCCCGCAA AGCGAAATCA ATGCCGAATT GACCAAACT CAACAAAGCT
251 ACCCGCATTC CATTTCCGCC GCCCAAGCCA CACTGATGGC GCGGCAACC
301 GAATTTGACG CGCAGCGTTA CGATGTTGCC GAAGGCCATT TGAAATGGGT
351 GTTGTCACAC CAAAAAGACA GCCTGATTCA AGCGTTGGCG GCGCAGCGTC
401 TGGGCGTTGT GTTGTGCAA CAAAAAAAT ACGATGCCGC GCTTGCCGCG
451 CTCGATACGC CGGTGAAGC GGACTTCGCC CCCCTGCTGA TGGAAACCAA
501 AGGCGATGTC TATGCCGCAC AGGGAAAAAG CCAGGAAGCC TTAATAAACT
551 ACGGACAGGC TTTAGAAAAA ATGCCTCAAG ATTCTGTCGG TCGCGAATTG
601 GTTCAATGA AACTTGATTC GCTGAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1812; ORF 586>:

m586.pep

```

1 MAAHLEEQQE LDNFKYFWKT TGKWLFALLI LAALGYLGYT VYQNRKVSQN
51 QEAAAVLANI VEKAQSKAPQ SEINAELTKL QQSYPHSISA AQATLMAAAT
101 EFDQRYDVA EGHLLKWVLSN QKDSLIQALA AQLRGVLLQ QKKYDAALAA
151 LDTFVEADFA PLLMETKGDV YAAQKSQEA LKNYQALEK MPQDSVGREL
201 VQMKLDSLK*

```

m586 / g586 97.1% identity in 209 aa overlap

	10	20	30	40	50	60
m586.pep	MAAHLEEQQELDNFKYFWKTTGKWLFAALLILAALGYLGYTVYQNRKVSQNQEAAAVLANI					

914

```

g586      MAAHLEEQQE LDNFKYFWKT TGKWLFAVLI LAALGYLGYT VYQNRAASQNQEAAAVLANI
           10      20      30      40      50      60

m586.pep  70      80      90      100     110     120
VEKAQSKAPQSEINAELTKLQQSYPHSISAAQATLMAAAATEFDAQRYDVAEGHLKWVLSN
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g586      70      80      90      100     110     120
VEKAQNKAPQSEINAELSKLQQSYPHSISAAQATLMAAAATEFDAQRYDVAEGHLKWVLSN

m586.pep  130     140     150     160     170     180
QKDSLIIQALAAQRLGVVLLQKKYDAALAALDTPVEADFAPLLMETKGDVYAAQGSQEA
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g586      130     140     150     160     170     180
QKDSLIIQALAAQRLGVVLLQKKYDAALAALDTPVEADFAPLLMETKGDVYAAQKSQEA

m586.pep  190     200     210
LKNYGQALEKMPQDSVGREL VQMKLDSLKX
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g586      190     200     210
LKNYGQALEKMPQDSVGRELLQMKLDSLKX
           190     200     210

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1813>:

```

a586.seq
1   ATGGCAGCCC ATTTGGAAGA ACAACAAGAG TTGGACAAC TTAATATTT
51  TTGGAAAACC ACGGGCAAAT GGCTGTTTGC CGTGCTGATT TTGGCGGCAC
101 TCGGCTACTT GGGATACACG GTTTACCAA ACCGTGCGGC TCCCCAAAT
151 CAGGAAGCGG CGGCGGTGCT GGCAAACATC GTGGAAAAGG CGCAAACAA
201 AGCCCCGCAA AGCGAAATCA ATGCCGAATT GGCCAAGCTC CAACAAAGCT
251 ACCCCCATTC CATTTCGCCG GCCCAAGCCA CGCTGATGGC GGCAGCAACC
301 GAATTTGACG CGCAGCGTTA CGATGTTGCC GAAGGCCATT TGAATGGGT
351 ATTGTCACAC CAAAAAGACA GCCTGATCCA GGCCTTGGCG SCGCAGCGTC
401 TGGCGGTTGT GTTGTTCGAA CAAAAAAT ACGATGCCGC SCTTGCCGCA
451 CTCGACACGC CGGTTGAAGC GGACTTCGCC CCCCTGCTGA TGGAAACCAA
501 AGGCGATGTC TATGCCGCAC AGGGAAAAG CCAGGAAGCC TTAATAAACT
551 ACGGACAGGC TTAGAAAAA ATGCCTCAAG ATTCTGTCGG TCGCGAATTG
601 GTTCAAATGA AACTTGATTG GCTGAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1814; ORF 586.a>:

```

a586.pep
1   MAAHLEEQQE LDNFKYFWKT TGKWLFAVLI LAALGYLGYT VYQNRAASQN
51  QEAAAVLANI VEKAQNKAPQ SEINAELAKL QSYPHSISA AQATLMAAAT
101 EFDAQRYDVA EGHKLVLSN QKDSLIIQALA AQLGVVLLQ QKKYDAALAA
151 LDTPVEADFA PLLMETKGDV YAAQGSQEA LKNYGQALEK MPQDSVGREL
201 VQMKLDSLK*

```

m586/a586 97.6% identity in 209 aa overlap

```

m586.pep  10      20      30      40      50      60
MAAHLEEQQE LDNFKYFWKT TGKWLFAVLI LAALGYLGYT VYQNRAASQNQEAAAVLANI
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a586      10      20      30      40      50      60
MAAHLEEQQE LDNFKYFWKT TGKWLFAVLI LAALGYLGYT VYQNRAASQNQEAAAVLANI

m586.pep  70      80      90      100     110     120
VEKAQSKAPQSEINAELTKLQQSYPHSISAAQATLMAAAATEFDAQRYDVAEGHLKWVLSN
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a586      70      80      90      100     110     120
VEKAQNKAPQSEINAELAKLQQSYPHSISAAQATLMAAAATEFDAQRYDVAEGHLKWVLSN

m586.pep  130     140     150     160     170     180
QKDSLIIQALAAQRLGVVLLQKKYDAALAALDTPVEADFAPLLMETKGDVYAAQGSQEA
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a586      130     140     150     160     170     180
QKDSLIIQALAAQRLGVVLLQKKYDAALAALDTPVEADFAPLLMETKGDVYAAQGSQEA
           130     140     150     160     170     180

```

915

	190	200	210
m586.pep	LKNYGQALEKMPQDSVGRELVMKLDLKLX		
a586	LKNYGQALEKMPQDSVGRELVMKLDLKLX		
	190	200	210

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1815>:

g587.seq..

1	atgaaacgta	tctttttgcc	cgcccttgccc	gccatcctgc	ctttatccgc
51	ttatgccgac	ctgcccttga	cgattgaaga	cataatgacc	gacaagggaa
101	aatggaaact	ggaaacttcc	cttacctatc	tgaatagcga	aaacagccgc
151	gccgcacttg	ccgcaccggt	ttacattcaa	accggcgcaa	cctcgtttat
201	ccccattccg	accgaaattc	aagaaaacgg	cagcaatacc	gatatgctcg
251	ccggcacgct	cggtttgcgc	tacggactga	ccggcaatac	cgacatttac
301	ggcagcggca	gctatctgtg	gcacgaagaa	cgcaaaactcg	acggcaacgg
351	caaaacccgc	aacaaacgga	tgtccgacat	atccgccggc	atcagccaca
401	ccttccttaa	agacggcaaa	aaccccgccc	taatcagctt	tcttgaaagc
451	acggtttacg	aaaaatcgcg	caacaaagcc	tcgttaatac	aaaaaagggg
501	gctttgcccc	ttttataact	taaggataaa	ttatgaatat	taa

This corresponds to the amino acid sequence <SEQ ID 1816; ORF 587.ng>:

g587.pep..

1	MKRIFLPALP	AILPLSAYAD	LPLTIEDIMT	DKGKWKLETS	LTYLNSNSNR
51	AALAAPVYIQ	TGATSFIP	TEIQENGST	DMLAGTLGLR	YGLTGNTDIY
101	SGSYLWHEE	RKLDGNKTR	NKRMSDISAG	ISHTFLKDGK	NPALISFLES
151	TVYEKSRNKA	SLIKRGLCP	FYNLRINYEY	*	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1817>:

m587.seq..

1	ATGAAGCGCA	TCTTTTGGCC	CGCCTTGCCC	GCCATCCTGC	CTTTATCCAC
51	TTATGCCGAC	CTGCCCTTGA	CGATTGAAGA	CATAATGACC	GACAAGGGAA
101	AATGGAACCT	GGAACTTCC	CTTACCTACC	TGAACAGCGA	AAACAACCGC
151	GCCGAACCTG	CCGCACCGGT	TTACATTCAA	ACCGGCGCAA	CCTCGTTTAT
201	CCCCATTCCG	ACCGAAATCC	AAGAAAACGG	CAGCAATACC	GATATGCTCG
251	TCGGCACGCT	CGGTTTGCGC	TACGGACTGA	CCGGGAATAC	CGACATTTAC
301	GGCAGCGGCA	GCTATCTGTG	GCACGAAGAA	CGCAAACTCG	ACGGCAACAG
351	CAAAACCCGC	AACAAACGGA	TGTCCGACGT	ATCCCTCGGC	ATCAGCCACA
401	CTTTCCTTAA	AGACGACAAA	AACCCCGCCC	TAATCAGCTT	TCTTGAAAGC
451	ACGGTTTACG	AAAAATCGCG	CAACAAAGCC	TCGTCGGGAA	AATCCTGGCT
501	CATCGGCGCC	ACCACCTACA	AAGCCATAGA	TCCGATTGTC	CTTTCCTCA
551	CCGCCGCCTA	CCGCATCAAC	GGCAGCAAAA	CCCTTTCAGA	CGGCATCCGC
601	TACAAATCGG	GCAACTACCT	GCTGCTCAAC	CCCAACATCT	CATTGCTGTC
651	CAACGACAGA	ATCAGCCTGA	CCGGAGGCAT	CCAATGGCTG	GGCAGGCAGC
701	CCGACCGGAC	GGACGGCAAA	CGGGAATCCT	CCAGAAACAC	ATCCACCTAC
751	GCCCATTTTC	GCGCAGGTTT	CGGTTTCACC	AAAACACCGG	CTTTAAACGC
801	ATCCGCACGT	TTCAACGTTT	CAGGGCAAAG	CAGTTCGGAA	CTGAAATTTG
851	CGGTACAGCA	TACATTTTAA			

This corresponds to the amino acid sequence <SEQ ID 1818; ORF 587>:

m587.pep..

1	MKRIFLPALP	AILPLSTYAD	LPLTIEDIMT	DKGKWKLETS	LTYLNSNNR
51	AELAAPVYIQ	TGATSFIP	TEIQENGST	DMLVGTGLR	YGLTGNTDIY
101	SGSYLWHEE	RKLDGNSKTR	NKRMSDVSLG	ISHTFLKDDK	NPALISFLES
151	TVYEKSRNKA	SSGKSWLIGA	TTYKAIDPIV	LSLTAAAYRIN	GSKTLSDGIR
201	YKSGNYLLN	PNISFAANDR	ISLTGGIQWL	GRQPDRTDGK	RESSRNTSTY
251	AHFGAGFGFT	KTALNASAR	FNVSGQSSSE	LKFGVQHTF*	

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m587 / g587 95.0% identity in 161 aa overlap

10 20 30 40 50 60

```
a587.seq
1 ATGAAGCGCA TCTTTTGGCC CGCCTTGCCC GCCATCCTGC CTTTATCCGC
51 TTATGCGCGC CTGCCCTTGA CGATTGAAGA CATAATGACC GACAACGGCA
101 AATGGAACCT GGAAACCTTC CTTACTTACC TGAACGACGA AAACAACCGC
151 GCCGAACCTG CCGCACCGGT TTACATCCAA ACCGGCGCAA CCTCGTTTAT
201 CCCCATTCCG ACCGAAATCC AAGAAAAACG CAGCAATACC GATATGCTCG
251 TTGGCAGCGT CGGTTTGCCT TACGCACTGA CCGGGAATAC CGACATTTAC
301 GGCAGCGCGA GCTATCTGTG GCACGAAGAA CGCAAACTCG ACGGCAACGG
351 CAAAACCCGA AACAAACGGA TGTCCGACGT ATCCCTCGG ATCAGCCACA
401 CTTTCTTAA AGACGACAAA AACCCTCGCT TAATCAGTT TCTTTAAAGC
451 ACGGTTTACG AAAAATCGCG CAACAAAGCC TCGTCGGGAA AATCTCGGCT
501 CACTGGCGCC ACCACCTACA AAGCATCGA CCCCGTCGT CTCCTATTGA
551 CCGCTGCCTA CCGTATCAAC GCGAGCAAAA CCTTTCAAG CAACACCAAA
601 TACAAAGCAG GCAATTTACTG GATGCTGAAT CCCAATATAT CCTTCGCGCC
651 CAACGACAGA ATCAGCTCA CGGCGGCAT CCAATGGCTG GCGAAGCAGC
701 CCGACCGTCT GGACGGCAAA AAAGAATCCG CAAGAAACAC ATCCACCTAT
751 GCCCATTTCG GCGCAGGTTT CGGTTTCACC AAAACCAGG CTTTAAACGC
801 ATCCGCACGT TTCAACGTTT CAGGGCAAAG CAGTTCGGAA CTGAAATTTG
851 GCGTACAGCA TACGTTTAA
```

a587.pep

1	MKRIFLPALP	AILPLSAYAD	LPLTIEDIMT	DKGKWKLETS	LTYLNSENNK
51	AELAAPVYIQ	TGATSFPIPI	TEIQENGSNV	DMLVGTLGLR	YGLTGNTDIY
101	GGSGYLWHEE	RKLDGNGKTR	NKRMSDVSLG	ISHTFLKDDK	NPLNISFLES
151	TYYEKS RNKA	SSGKSWLIGA	TTYKAIDPVV	LSLTAAYRIN	GSKTLSSNTK
201	YKAGNYWMLN	PNISFAANDR	ISLTGGIQWL	GKQPDRLDGK	KESARNTSTY
251	AHFGAGVFGE	KTTALNASAR	FNVSGOSSSE	LKFGVOHTF*	

m587/a587 95.2% identity in 289 aa overlap

	10	20	30	40	50	60
m587.pep	MKRIFLPALPAILPLSTYADLPLTIEDIMTDKGKWKLETSLTYLNSENNRAELAAPVYIQ					
	:					
a587	MKRIFLPALPAILPLSAYADLPLTIEDIMTDKGKWKLETSLTYLNSENNRAELAAPVYIQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
m587.pep	TGATSFIPITPEIQENGSNITDMLVGTGLRLYGLTGNTDIYSGSGSYLWHEERKLDGNSKTR					
	:					
a587	TGATSFIPITPEIQENGSNITDMLVGTGLRLYGLTGNTDIYSGSGSYLWHEERKLDGNGKTR					
	70	80	90	100	110	120

917

	130	140	150	160	170	180
m587.pep	NKRMSDVSLGISHTFLKDDKNPALISFLESTVYEKSRNKASSGKSWLIGATTYKAIDPIV					
a587	NKRMSDVSLGISHTFLKDDKNPALISFLESTVYEKSRNKASSGKSWLIGATTYKAIDPVV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m587.pep	LSLTAAAYRINGSKTLSDGIRYKSGNYLLNPNISFAANDRISLTGGIQWLGRQPDRTDGK					
a587	LSLTAAAYRINGSKTLSSNTKYKAGNYWMLNPNISFAANDRISLTGGIQWLGRQPDRLDGK					
	190	200	210	220	230	240
	250	260	270	280	290	
m587.pep	RESSRNTSTYAHFGAGFGFTKTTALNASARFNVSGQSSSELKFGVCHTFX					
a587	KESARNTSTYAHFGAGFGFTKTTALNASARFNVSGQSSSELKFGVCHTFX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1821>:

```

g588.seq
1  atgcttaaac atctcgcat cctactgccc gccatgatgt tcgccctccc
51  cgcccagacc gccgtcctaa gcccctatca ggaaaccggc tgcacctacg
101 aaggcgggat cggaaaagac gggcttcctt caggcaaagg catatggcgt
151 tgccgggatg ggcgcgctta taccggttca ttcaaaaacg gcaaattcga
201 cgggcaaggc gtttataccg ttgccgccgg ccgcgaagta tttctcgagc
251 cgttcaattc cgacagtacc aaattccgca atatggcatt gtcgggcacg
301 ttcaaaacag gcttggcaca cggcagggtt gccgcctcgc aaaacggcga
351 aaccctcttt tattatgaaa tgcaaacacg gcatgattaa

```

This corresponds to the amino acid sequence <SEQ ID 1822; ORF 588.ng>:

```

g588.pep..
1  MLKHLAFLLP AMMFALPAQT AVLSPYQETG CTYEGGIGKD GLPSGKGIWR
51  CRDGRGYTGS FKNGKFDGQG VYTVAAGREV FLEPFNSDST KFRNMALSGT
101 FKQGLAHGRF AASQNGETLF YYEMRTRHD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1823>:

```

m588.seq..
1  ATGCTTAAAC ATCTCGCATT CCTACTGCCC GCCATGATGT TCGCCCTCCC
51  CACTTCGGCC GCCGTCTGA CTTCCTATCA AGAACCAGGC TGCACCTACG
101 ACGGCAATGT CGGCAAAGAC GGTAACCCG CCGGCAAAGG CACATGGCGC
151 TGCCAAGACG GCGCAACTA TACCGGTTCT TTTAAAAACG GCAAATTCGA
201 CGGGCAAGGC GTTTATACCG TTGCCGCCAA CCGCGAAATA TTTATCGAAC
251 CGTTCAATTC CGACAGTACC AAATCCGCA ACATGGTACT CTCGGGCACG
301 TTCAAAAAG GCTTGGCACA CCGCAGATTT ACCGTCTCGC AAAACGGCGA
351 AACCCTCTTC ATTATGAAAT GCGAAAACGG CATGATTAAA GAAGTGAAAC
401 TGCCCCAAAA CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1824; ORF 588>:

```

m588.pep..
1  MLKHLAFLLP AMMFALEPSTA AVLTSYQEPG CTYDGNVGKD GKPAKGKTWR
51  QDGRNYTGS FKNGKFDGQG VYTVAANREI FIEPFNSDST KFRNMVLSGT
101 FFKGLAHGRF TVSQNGETLF IMKCENGMK EVKLPKNK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m588 / g588 82.5% identity in 120 aa overlap

10 20 30 40 50 60

918

```

m588.pep    MLKHLAFLLPAMMFALPTSAAVLTSYQEPGCTYDGNVGKDGKPKAGKGTWRCQDGRNYTGS
g588        MLKHLAFLLPAMMFALPAQTAVLSPYQETGCTYEGGIGKDGLP SGKGIWRCRDGRGYTGS
              10      20      30      40      50      60

              70      80      90      100     110     120
m588.pep    FKNGKFDGQGVYTVAAANREIFIEPFNSDSTKFRNMVLSGTFKKGLAHGRFTVSQNGETLF
g588        FKNGKFDGQGVYTVAAAGREVFLEPFNSDSTKFRNMALSGTFKQGLAHGRFAASQNGETLF
              70      80      90      100     110     120

              130     139
m588.pep    IMKCENGMKEVKLPKNKX
g588        YYEMRTRHDX
              130

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1825>:

```

a588.seq
1  ATGCTTAAAC ATCTCGCATT CCTACTGCCC GCCATGATGT TCGCCCTCCC
51 CGCCGCGTCC GCCGTTCTGA CTTCTATCA AGAACCCGGC TGCACCTACG
101 AAGGCGATGT CGGCAAAGAC GGTAAACCCG CCGGCAAAGG CACATGGCGC
151 TGCCAAGACG GCGCAACTA TACCGGTTCTG TTTAAAAATG GCAAATTCGA
201 CGGACAAGGC GTTTATACCG TTGCCGCCAA CCGCGAAATA TTTATCGAAC
251 CGTTCAATTC CGACAGTACC AAATTCGCA ACATGGTACT CTCGGGCACA
301 TTCAAAAAAG GCTTGGCACA CGGCAGATTT ACCGTCTCGC AAAACGGCGA
351 AACCCTCTTC ATTATGAAAT GCGAAAACGG CATGATTAA GAAGTGAAGC
401 TGCCCCAAAA CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1826; ORF 588.a>:

```

a588.pep
1  MLKHLAFLLP AMMFALPAAS AVLTSYQEPG CTYEGDVGKD GKPKAGKTWR
51  CQDGRNYTGS FKNGKFDGQG VYTVAAANREI FIEPFNSDST KFRNMVLSGT
101 FKKGLAHGRF TVSQNGETLF IMKCENGMK EVKLPKNK*

```

m588/a588 96.4% identity in 138 aa overlap

```

              10      20      30      40      50      60
m588.pep    MLKHLAFLLPAMMFALPTSAAVLTSYQEPGCTYDGNVGKDGKPKAGKGTWRCQDGRNYTGS
a588        MLKHLAFLLPAMMFALPAASAVLTSYQEPGCTYEGDVGKDGKPKAGKGTWRCQDGRNYTGS
              10      20      30      40      50      60

              70      80      90      100     110     120
m588.pep    FKNGKFDGQGVYTVAAANREIFIEPFNSDSTKFRNMVLSGTFKKGLAHGRFTVSQNGETLF
a588        FKNGKFDGQGVYTVAAANREIFIEPFNSDSTKFRNMVLSGTFKKGLAHGRFTVSQNGETLF
              70      80      90      100     110     120

              130     139
m588.pep    IMKCENGMKEVKLPKNKX
a588        IMKCENGMKEVKLPKNKX
              130

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1827>:

```

g589.seq..
1  atgcaacaaa aaatccgttt ccaaatcgag gcgatgacct gtcaggcatg
51  tgcttcgcgc attgaaaaag tgttgaaaca aaaagatttt gtcgaatcgg
101 cgggagtga ctttgccagt gaggaagcgc aggttacgtt tgacggcagc
151 aaaacctcgg ttgccgacat tgccaaaatc attgagaaaa ccggttacgg
201 cgccaaggaa aaaacggaag atacattgcc gcaacctgaa gcagaacacc
251 atatcggtcg gcggttggtg cttttgctga ccatcaatat cccgttcctt

```

```

301 atcggatgtag tagggatgat gctaaaaggg ctgaattgga caccggcacga
351 ttggatgatt ccgcctgtat ggcaagttgt actggcaagc atagtgaac
401 ttggctggc aatcccgttt tacaaaagcg cgtgggcaag cattaaaggc
451 gggctggcga atatggacgt actcgttacc atcggcacg tgctgattta
501 cctgtattcc gtttatatgc tgtttttcag ttcgcatcg gcgcacggta
551 tggcgcatgt gtattttgaa gcgggcgtga tggatcgcg ttttgtgtcg
601 ctgggtaagt ttttgaaca ccgcaccaa aaatccagcc tgaacagctt
651 gggcttactg ctaaaactca cggcgaccca agtcaacgtg caacgcaacg
701 gcgaatggaa acaactgccc atcgaccaag tgcaaatcgg cgaccttatc
751 cgcaccaacc acggcgaaac catcgtgccc gacggcatta tcgaaagcgg
801 cagcgggttg gcggacgaaa gccaccttac cggcgaatcc aatcccgaag
851 agaaaaaggg gggcgcaaaa gtgttggcgg gcgcgctgat gaccgaaggg
901 agcgtggtgt accgcgccgc gcagctcgcc agccaaaccc tgctcggcga
951 catgatgaac gcgctctctg aagcacaagg cagtaaagca ccgattgcgc
1001 gcgtggccga taaagcggcg gcggtatttg tgccaactgt cgtgggcac
1051 gcgcttctga cttttatcgt tgcttggctg attaagggcg attggacggg
1101 cgcactgatg cagcgcgttg ccgttttggg gattgcctgc ccgtgcgcgc
1151 tcggctctggc gaccctgccc gcgattatgg tcggcatggg caaagcgggtg
1201 aaacacggca tttggtttaa agacgcggcg gcaatggagg aagcagccca
1251 cgtcgatgcc gtcgtattgg acaaaaccgg tacgctgacc gaaggcaggc
1301 cgcaggttgc cgccgtttat tacgttcccc acagcggcct tgacgaagac
1351 gctttgtacc gcatcgccgc cgccgtcgag caaaacgccg cccaccgcgt
1401 cgcccgccgc atcgtctccc cgcaacaagc gcgcggttgg gagattcccc
1451 ctgcacaaaa tgcgcaaac gttgtcggag caggcattac cgcgaagtg
1501 gaagcgtgg gtttggtgaa atcaggcaaa gccgaatttg ccgaactgac
1551 cttgcgaag ttttcagacg gcgtttggga aatcgccagt gcggttaccg
1601 tatctgtaaa cggcaaacgc atcgcgcgat tcgcactctc cgacgcgttg
1651 aaagccgata ccgccgaagc catagggcgt ctgaaaaaac acaatatcga
1701 tgtctatatt atgagcggcg ataaccaaag tacggtcgaa tacgtcgcca
1751 aacaactggg catcgcacac gccttcggta atatgagtcg gtgcgacaaa
1801 gccgccgaag tgcagaaact caaagccgcc ggcaaaaccg tggcgatggg
1851 gggcgacggc atcaacgacg cgcccgccgt tgcccgccgc aacgtcagct
1901 tcgccatgaa aggcggtgcg gacgttgccg aacacaccgc ctccgccacg
1951 ctgatgcagc attcgggtcaa tcagctcgcc gatgccctgc tgatatcgca
2001 ggcaacggtt gaaaaatca agcaaaacct atttttcgcc ttcttctaca
2051 atatatggg cattccgctc gccgcgctcg gctttttaa tcccgtcata
2101 gcaggcgcg caatggcggc aagctcggtt tcggtatttg gcaatgccct
2151 gcgcctgaaa tgggtaaaaa tcgattga

```

This corresponds to the amino acid sequence <SEQ ID 1828; ORF 589.ng>:

g589.pep..

```

1  MQQKIRFQIE AMTCQACASR IEKVLNKKDF VESAGVNFAS EEAQVTFDGS
51  KTSVADI AKI IEKTYGAK EKTEDLPQPE AEHHIGWRLW LLLTINIPFL
101 IGMVGMMLKG LNWTRHDMI PPVWQFVLAS IVQLWLAI PF YKSAWASIKG
151 GLANMDVLVT IGTVSIYLYS VYMLFFSSHA AHGMAHVYFE AGVMVIGFVS
201 LGKFLEHRTK KSSLNSLGLL LKLTPTQVNV QRNGEWKQLP IDQVQIGDLI
251 RTNHGERIAA DGIIESGSGW ADESHLTGES NPEEKKAGSK VLAGALMTEG
301 SVVYRAAQLG SQTLLGDMMN ALSEAQGSKA PIARVADKAA AVFVPTVVGI
351 ALLTFIVAWL IKGDWTVALM HAVAVLVIA PCALGLATPA AIMVGMGKAV
401 KHGIWEKDAA AMEEAAHVDA VVLDKTGTLT EGRPOVAAYV YVPDSGFDED
451 ALYRIAAAVE QNAAHPLARA IVSAAQARGL EIPAAQNAQT VVGAGITAEV
501 EGVGLVKSGK AEFAELTLPK FSDGVWEIAS AVTVSVNGKP IGAFALSDAL
551 KADTAEAIGR LKKHNIDVYI MSGDNQSTVE YVAKQLGIAH AFGNMSPCDK
601 AAEVQKLKAA GKTVMVGDG INDAPALAAA NVSFAMKGG A DVAEHTASAT
651 LMQHSVNQLA DALLISQATL ENIKQNLFFA FFYNILGIPL AALGFLNPVI
701 AGAAMAASSV SVLGNALRLK WVKID*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1829>:

m589.seq..

```

1  ATGCAACAAA AAATCCGTTT CCAAATCGAA GGCATGACCT GCCAGGCCTG
51  CGCTTCGCGC ATTGAAAAAG TGTGAACAA AAAAGATTTT GTCGAATCGG
101 CGGGGGTAAA CTTCCGCCAGC GAAGAGGCGC AGGTAGTGTG TGACGACAGC
151 AAAACCTCAG TAGCCGACAT TGCCAAAATC ATTGAGAAAA CCGGTTACGG
201 CGCGAAGGAA AAAACGGAAG ATACATTGCC GCAACCCGAA GCAGAACACC
251 ATATCGGCTG GCGCTGTGG CTGCTGTTCA CCATCAACGT CCCGTTTCCTT

```


This corresponds to the amino acid sequence <SEQ ID 1830; ORF 589>:

1	MQQKIRFOIE	GMTCQACASR	IEKVLNKKDF	VESAGVNFAS	EEAQVVFDD
51	KTSVADIAEI	IEKTYGYAKE	KTEDTLPQPE	AEHHIGWRWL	LLFTINVVEL
101	<u>IGMAGMMIGR</u>	HOWMIPPLGW	FALASVVQLW	LAIFPIYKSAV	ASIKGGLGNL
151	DLVLTGTGVS	IYLYSVYMLF	FSPHAAVQMA	HVYFEVGVMV	IGFVSLKFLM
201	EHRTKKSSLN	SLGLLKLTP	TQVNVQRNGE	WKQLPIDQVQ	IGDLIRANHG
251	ERIAADGIIIE	SGSGWADESH	LQSGENPEEK	KAGGKVLAGA	LMTEGSSVYR
301	ATQLGSQTQL	GDDMMNALSE	QTSGKAPIARV	ADKAAAEVFP	AVVGIALTLT
351	IVTWLTKGDW	TVALMHAVAV	LVIACPCALG	LATPAAINVG	MGKAVKHGIW
401	<u>FKDAAAMEEA</u>	AHVDAVVLDK	TGTLTEGSPQ	VAAVYCVPDS	GFEDCALYRI
451	AAAEVQNAAH	PLARIVSAA	QARGLDIPAA	QNAQTUVGAG	ITAEVEGVGL
501	VKAGKAEFAE	LALPKFLDGV	WDIASIVAS	VDNKPIGAVA	LADALKADTA
551	EAIRGLKKHN	IDVYIMSGDN	QGTVEYVAKQ	LGTAHAFGNM	SPRDKAAEVQ
601	KLKAAGKTVA	MVGDDGNDAP	ALAAANVSFA	MKGGADVAEH	TASATLMQHS
651	VNQLADALLV	SQATLKNIKP	NLFFAFFYNI	LGIPLAALGF	LNPVIAGAAM
701	AASSVSVLSN	ALRLKRVKID	*		

Homology with a predicted ORF from *N. gonorrhoeae*

m589.pep MQQKIRFQIEGMTCCACASRIEKVLNKKDFVESAGVNFASEEAQVVFDSDSKTSVADIAKI
||||| : |||||

921

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g589      MQQKIRFQIEAMTCQACASRIEKLNNKKDFVESAGVNFASEEAQVTFDGSKTSVADI AKI
           10      20      30      40      50      60

           70      80      90      100     110
m589.pep  IEKTGYGAKEKTEDILPQPEAEHHIGWRLWLLFTINV PFLIGMAGMMIG-----RHDWMI
           |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g589      IEKTGYGAKEKTEDILPQPEAEHHIGWRLWLLLTINIPFLIGMVGMMMLKGLNWRH D WMI
           70      80      90      100     110     120

           120     130     140     150     160     170
m589.pep  PPLWQFALASVVQLWLAIPFYKSAWASIKGGLANMDVLVTIGTVSIYLYSVYMLFFSPHA
           ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g589      PPVWQFVLASIVQLWLAIPFYKSAWASIKGGLANMDVLVTIGTVSIYLYSVYMLFFSSHA
           130     140     150     160     170     180

           180     190     200     210     220     230
m589.pep  AYGMAHVYFEVGMVIGFVSLGKFLEHRTKKSSLNSLGLLLKLTPTQVNVQRNGE WKQLP
           |:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g589      AHGMAHVYFEAGVMVIGFVSLGKFLEHRTKKSSLNSLGLLLKLTPTQVNVQRNGE WKQLP
           190     200     210     220     230     240

           240     250     260     270     280     290
m589.pep  IDQVQIGDLIRANHGERIAADGIIESGSGWADESHLTGESNPEEKKAGGKVLAGALMTEG
           |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g589      IDQVQIGDLIRTNHGERIAADGIIESGSGWADESHLTGESNPEEKKAGGKVLAGALMTEG
           250     260     270     280     290     300

           300     310     320     330     340     350
m589.pep  SVVYRATQLGSQTQLGDMMNALSEAQGSKAPIARVADKAAAVFVPAVVGIALLT FIVTWL
           |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g589      SVVYRAAQLGSQTLLGDMMNALSEAQGSKAPIARVADKAAAVFVPTVVGIALLT FIVAWL
           310     320     330     340     350     360
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922

	360	370	380	390	400	410
m589.pep	IKGDWTVALMHAVAVLVIA PCALGLATPAAIMVGMGKAVKHGIWFKDAAAMEEAAHVDA 					
g589	IKGDWTVALMHAVAVLVIA PCALGLATPAAIMVGMGKAVKHGIWFKDAAAMEEAAHVDA 					
	370	380	390	400	410	420
	420	430	440	450	460	470
m589.pep	VVLDKTGTLTEGSPQVAAYVCVPDSGFDEDALYRIAAAVEQNAAHPLARAIVSAAQARGL 					
g589	VVLDKTGTLTEGRPQVAAYVYVPDSGFDEDALYRIAAAVEQNAAHPLARAIVSAAQARGL 					
	430	440	450	460	470	480
	480	490	500	510	520	530
m589.pep	DIPAAQNAQTVVGAGITAEEVGVGLVKAGKAEFAELALPKFLDGVDIASIVAVSVDNKP : : : : : :					
g589	EIPAAQNAQTVVGAGITAEEVGVGLVKS GKAEFAELTLPKFSDGVWEIASAVTVSVNGKP : : : : : :					
	490	500	510	520	530	540
	540	550	560	570	580	590
m589.pep	IGAFALADALKADTAEAI GR LKKHNIDVYIMSGDNQGTVEYVAKQLGIAHAFGNMSPRDK : : : : :					
g589	IGAFALSDALKADTAEAI GR LKKHNIDVYIMSGDNQSTVEYVAKQLGIAHAFGNMSPCDK : : : : :					
	550	560	570	580	590	600
	600	610	620	630	640	650
m589.pep	AAEVQKLKAAGKTVAMVGDGINDAPALAAANVSFAMKGGADVAEHTASATLMQHSVNQLA 					
g589	AAEVQKLKAAGKTVAMVGDGINDAPALAAANVSFAMKGGADVAEHTASATLMQHSVNQLA 					
	610	620	630	640	650	660
	660	670	680	690	700	710
m589.pep	DALLVSQATLKNIKQNLFFAFFYNILGIPLAALGFLNPVIAGAAMAASSVSVLGNALRLK : : : : : :					
g589	DALLISQATLENIKQNLFFAFFYNILGIPLAALGFLNPVIAGAAMAASSVSVLGNALRLK : : : : : :					
	670	680	690	700	710	720
	720					
m589.pep	RVKIDX 					
g589	WVKIDX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1831>:

```

a589.seq
1  ATGCAACAAA AAGTCCGTTT CCAAAATCGAA GGCATGACCT GCCAGGCATG
51  TGCTTCGCGC ATTGAAAAAG TGTGAACAA AAAAGATTTT GTCGAATCGG
101 CGGGGGTAAA CTTGCCAGC GAAGAGGCTC AGGTAGTGT TGACGACAGC
151 AAAACCTCAG TAGCCGACAT TGCCAAAATC ATTGAGAAAA CCGGTTACGG
201 CGCGAAGGAA AAAACGGAAG ATACATTGCC GCAACCCGAA GCAGAACACC
251 ATATCGGCTG GAGGTTGTGG CTTTGTCTGG CCATCAATAT CCCGTTCTCT
301 ATCGGTATGG TAGGGATGAT GCTAAAAGGG CTGAATTGGA CACGGCATGA
351 TTGGATGTTG TCGCCCTTGT TGCAGTTTGC ATTGGCGAGT GTGGTGCAGC
401 TTTGGCTGGC GGTGCCATT TACAAAAGCG CGTGGGCGAG CATTAAAGGC
451 GGGCTGGCGA ATATGGACGT ACTCGTTACC ATCGGCACGG TCTCGATTTA
501 CCTGTATTCC GTCTATATGC TGTTTTTCAG CCCGCACGCG GCGTACGGTA
551 TGGCGCATGT GTATTTTGAA GTAGGCATAA TGGTGATTGG TTTTGTGTCA
601 CTGGGTAAAT TTTTGGAACA CCGCACCAAA AAATCCAGCC TGAACAGCTT
651 GGGCTTGCTG CTCAAATCA CGCCAACCCA AGTCAACGTG CAACGCGATG
701 ACGAATGGCG GCAGCTACCC ATCGACCAAG TGCAATCGG GCACCTAATC
751 CGCGCCAATC ACGCGCAACG CATTGCCGCC GACGGCATCA TAGAAAGCGG
801 CAGCGGCTGG GCGGACGAAA GCCATCTTAC CGCGGAATCC AATCCCGAAG
851 AGAAAAAGGC AGGCGGCAAA GTATTGGCGG GCGCGCTGAT GACTGAAGGC
901 ACGTGGTGT ACCGCGCCGC GCAGCTCGGC AGCCAAACCC TCGTCGGCGA
951 CATGATGAAC GCGCTCTCCG AAGCGCAAGG CAGTAAACCA CCGATTGCGC
1001 GTGTGGCGGA CAAGGCGGCG GCGGTATTCTG TCCTGCGGT GTGGGCATC
1051 GCACTTTTGA CTTTATATCG TACTTGGCTG ATTAAGGCGG ATTGGACGCT
1101 CGCATTGATG CACGCCGTCG CCGTTTGGT GATTGCCTGC CCGTGTGCAC

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923

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1151 TCGGTTTGGC AACCCCTGCT GCGATTATGG TCGGTATGGG CAAAGCGGTT
1201 AAACACGGTA TTTGGTTTAA AGACGCGGCA GCAATGGAAG AAGCCGCCCA
1251 CGTTGATGCC GTCGTGCTGG ACAAACCGG CACGCTGACC GAAGGCAAGC
1301 CGCAGGTTGC CGCCGTTTAT TGTGTTCCCG ACAGCGGCTT TGACGAAGAC
1351 GCTTTGTACC GCATCGCCGC CGCCGTCGAA CAAAACGCCG CCCATCCGCT
1401 CGCCCGTGCC ATCGTCTCCG CCGCCAGGC GCGCGGTTTG GAGATTCCCA
1451 CCGCACAAAA TGCCCAAACC ATTGTCGGCG CGGGCATTAC CGCCGAAGTA
1501 AAAGGCGCGG GTTTGGTAAA AGCAGGCAAA GCCGAATTTG CCGAACTGAC
1551 CTTGCCGAAG TTTTCAGACG GCGTTTGGGA AATCGCCAGT GTGGTTGCCG
1601 TATCTGTAAA CGGCAACCT ATCGGCGCAT TCGCACTCGC CGACGCGTTG
1651 AAAGCCGATA CCGCCGAAGC CATAGGCCGT CTGAAAAAAC ACAATATCGA
1701 TGTCTATATT ATGAGCGGCG ATAACCAAGG CACGCTCGAG TACGTGCCCA
1751 AACAACTGGG CATCGCACAC GCCTTCGGTA ATATGAGTCC GCGCGACAAA
1801 GCCGCCGAAG TGCAGAACT CAAAGCGGCC GCGAAAACCG TGGCGATGGT
1851 CGCGGACGGC ATCAACGACG CGCCCGCGCT CGCCGCCGCC AACGTCAGCT
1901 TCGCCATGAA AGGCGGTGCA GACGTTGCCG AACACACCGC ATCCGCCACA
1951 CTGATGCAGC ATTCGGTCAA CCAGCTCGCC GATGCGCTAT CGGTATCGCG
2001 AGCGACGTTG AAAAACATCA AGCAAAACCT GTTTTTCGCC TTCTTCTACA
2051 ATATTTTGGG CATTCCGCTC GCCGCGCTCG GCTTTTAAAA CCCCCTCATC
2101 GCAGGCGCGG CAATGGCGGC AAGCTCGGTT TCCGTGTTGA GCAACGCCTT
2151 GCGCCTGAAA CGGGTAAAAA TCGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 1832; ORF 589.a>:

```

a589.pep
1  MQQKVRFQIE GMTQCACASR IEKVLNKKDF VESAGVNFAS EEAQVVFDDSD
51  KTSVADI AKI IEKTGYGAKE KTEDTLQPE AEHHIGWRLW LLLAINIPFL
101 IGMVGMMLKG LNWTRHDWML SPLLQFALAS VVQLWLAVPF YKSAWASIKG
151 GLANMDVLVT IGTVSIYLYS VYMLFFSPHA AYGMHVYFE VGIMVIGFVS
201 LGKFELEHRTK KSSLNSLGLL LKLTPTQVNV QRDGEWRQLP IDQVQIGDLI
251 RANHGERIAA DGIIESGSGW ADESHLTGES NPEEKKAGGK VLAGALMTEG
301 SVVYRAAQLG SQTLLGDMMN ALSEAQGSKA PIARVADKAA AVFVPAVVGI
351 ALLTFIATWL IKGDWTLALM HAVAVLVIA PCALGLATPA AIMVGMGKAV
401 KHGIWFKDAA AMEEAAHVDA VVLDKTGTLT EGKPQVAAY CVPDGDFDED
451 ALYRIAAAVE QNAAHPLARA IVSAAQARGL EIPTAQNAQT IVGAGITAEV
501 KGAGLVKAGK AEFaelTLpk FSDGVWEIAS VVAVSVNGKP IGAFALADAL
551 KADTAEAIR LKKNHIDVYI MSGDNQGTVE YVAKQLGIAH AFGNMSPRDK
601 AAEVQKLKAA GKTVMVGDG INDAPALAAA NVSFAMKGGG DVAHTASAT
651 LMQHSVNQLA DALSVSRATL KNIKQNLFFA FFYNILGIPL AALGFLNPVI
701 AGAAMAASSV SVLSNALRLK RVKID*

m589/a589 94.9% identity in 725 aa overlap

          10      20      30      40      50      60
m589.pep  MQQKIRFQIEGMTQCACASRIEKVLNKKDFVESAGVNFASEEAQVVFDDSKTSVADI AKI
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a589      MQQKVRFQIEGMTQCACASRIEKVLNKKDFVESAGVNFASEEAQVVFDDSKTSVADI AKI
          10      20      30      40      50      60

          70      80      90      100     110
m589.pep  IEKTGYGAKEKTEDTLQPEAEHHIGWRLWLLFTINVPFLIGMAGMMIG-----RHDWMI
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a589      IEKTGYGAKEKTEDTLQPEAEHHIGWRLWLLAINIPFLIGMVGMMMLKGLNWTRHDWML
          70      80      90      100     110     120

          120     130     140     150     160     170
m589.pep  PPLWQFALASVVQLWLAIPFYKSAWASIKGGLANMDVLVTIGTVSIYLYSVYMLFFSPHA
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a589      SPLLQFALASVVQLWLAVPFYKSAWASIKGGLANMDVLVTIGTVSIYLYSVYMLFFSPHA
          130     140     150     160     170     180

          180     190     200     210     220     230
m589.pep  AYGMHVYFEVGMVIGFVSLGKFELEHRTKSSLSLSLGLLLKLTPTQVNVQRNGEWRQLP
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a589      AYGMHVYFEVGIMVIGFVSLGKFELEHRTKSSLSLSLGLLLKLTPTQVNVQRNGEWRQLP
          190     200     210     220     230     240

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924

	240	250	260	270	280	290
m589.pep	IDQVQIGDLIRANHGERIAADGII	ESGSGWADESHLTGESNPEEKKAGGKVL	AGALMTEG			
a589	IDQVQIGDLIRANHGERIAADGII	ESGSGWADESHLTGESNPEEKKAGGKVL	AGALMTEG			
	250	260	270	280	290	300
	300	310	320	330	340	350
m589.pep	SVVYRATQLGSQTQLGDMMNALSEAQGS	KAPIARVADKAAAVFVP	AVVGIALLTFFIVTWL			
a589	SVVYRAAQLGSQTLLGDMMNALSEAQGS	KAPIARVADKAAAVFVP	AVVGIALLTFFIATWL			
	310	320	330	340	350	360
	360	370	380	390	400	410
m589.pep	IKGDWTVALMHAVAVLVIA	CPALGLATPAAIMVGMGKAVKHGIWFKDAAAMEEAHVDA				
a589	IKGDWTLALMHAVAVLVIA	CPALGLATPAAIMVGMGKAVKHGIWFKDAAAMEEAHVDA				
	370	380	390	400	410	420
	420	430	440	450	460	470
m589.pep	VVLDKTGTLTGEGSPQVA	AVYCVPSGDFEDALYRIAAVEQNAAHPLARAIVSAAQARGL				
a589	VVLDKTGTLTGEGKPQVA	AVYCVPSGDFEDALYRIAAVEQNAAHPLARAIVSAAQARGL				
	430	440	450	460	470	480
	480	490	500	510	520	530
m589.pep	DIPAAQNAQTVVAGITA	EVGGLVKAGKAFAELALPKFLDGVWDIASIVAVSVDNKP				
a589	EIPTAQNAQTVVAGITA	EVGGLVKAGKAFAELALPKFSDGVWEIASVVAVSVNGKP				
	490	500	510	520	530	540
	540	550	560	570	580	590
m589.pep	IGAFALADALKADTAEA	IGRLKKHNIDVYIMSGDNQGTVEYVAKQLGIAHAFGNMSPRDK				
a589	IGAFALADALKADTAEA	IGRLKKHNIDVYIMSGDNQGTVEYVAKQLGIAHAFGNMSPRDK				
	550	560	570	580	590	600
	600	610	620	630	640	650
m589.pep	AAEVQKLKAAGKTVAMV	GDGINDAPALAAANVSFAMKGGADVAEHTASATLMQHSVNQLA				
a589	AAEVQKLKAAGKTVAMV	GDGINDAPALAAANVSFAMKGGADVAEHTASATLMQHSVNQLA				
	610	620	630	640	650	660
	660	670	680	690	700	710
m589.pep	DALLVSQATLKNIKQNL	FFAFFYNILGIPLAALGFLNPVIAGAAMAASSVSVLSNALRLK				
a589	DALSVSQATLKNIKQNL	FFAFFYNILGIPLAALGFLNPVIAGAAMAASSVSVLSNALRLK				
	670	680	690	700	710	720
	720					
m589.pep	RVKIDX					
a589	RVKIDX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1833>:

g590.seq..

```

1  atgaaaaaac ctttgatttc agttgcggca gtattgctcg gcggttgcctt
51  ggggtacacct tattatttgg gtgtcaaaagc agaagaaagt ctgacgcagc
101 agcaaaaaat attgcagaaa acgggctttt tgaccgtcga atcgaccag
151 tatgatcgag gctggtttac ctctacggaa acgacggtea tccgtctgaa
201 acccgagttg ctgcataatg cgcagaaata cctgccggat aacttgaaaa
251 tagtggttga acagccgggt acgctggtta accatatcac gcacggccct
301 ttcgccggcg gattcggcac gcaggcgcac attgaaaccg agttcaaata
351 cgcgcctgaa acggaaaaag ttttggaaag cttttttggg aaacaagttc
401 cggtttccct tgccaatacc gtttatttca acggcagcgg taaaatggaa
451 gtcagtgttc cgcctttcga ttatgaagaa ctgtcgggca tcaggctgca

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925

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501 ctgggaaggc ctgacggggg aaacgggtta tcaaaaaggt ttcaaaagct
551 accgcaacag ctatgatgcg cccttggtca aaatcaagct ggcagacaaa
601 ggcgatgccc cgtttgaaaa agcgcatctc gattcggaaa cttcagacgg
651 catcaatccg cttgctttgg gcagcagcaa tctgactttg gaaaaatctt
701 cgctcgaaag gaaagagggg gtcgattaca acgtcaaat gaacgaactg
751 gtcaacctcg ttaccgatct gcagatcggc gcgtttatca atcccaacgg
801 cagcatcgca ccttccaaaa tcgaagtcgg caagctggct ttttcaacca
851 agaccggggg atcgggcgcg tttatcgaca ggaaggggcg gttccgtttc
901 gatacgttgg tgtacggcga tgaataatc ggcgcgctgg acatccatat
951 cgctgcccga cacctcgatg cttctgcctt aacggtattg aaacgcaagt
1001 ttgcacaaat ttctgccaaa aaaatgactg aggaacaaat ccgcaatgat
1051 ttgattggcg cagtcacagg cgatgcttcc ggattattta cccatgaccc
1101 ggtactaaat atcaaaatct tccgtttcac cctgcctcag ggaaaaattg
1151 atgtggggcg aaaaatcatg tttaaaggca tgaagaagga agatttgaac
1201 caattgggag tgatgttaa gaaaccgag gcaaacatca gaatgagtat
1251 tctcaaaaa atgttggaag atttggcggt aagtcaggct ggaaatattt
1301 tcagtgtaaa tgccgaagat gaggcggaag ccagagcaag cattgccgat
1351 attaatgaaa cattgcgctt gatggtggac agtacggtcc aaagtatggc
1401 aagggaaaaa tatcttactt tagacggtaa tcagattgat acggtcattt
1451 cccttaaaaa caacgccctg aagttaaacg ggaacgct gcaaatgaa
1501 cccgatcctg attttgacga gggagatatg gtttccggcc agccgcatta
1551 a

```

This corresponds to the amino acid sequence <SEQ ID 1834; ORF 590.ng>:

g590.pep..

```

1 MKKPLISVAA VLLGVALGTP YYLGVKAEES LTQQQKILQK TGFLTVESHQ
51 YDRGWFTSTE TTVIRLKPFL LHNAQKYLDP NLKIVLEQPV TLVNHITHGP
101 FAGGFGTAQH IETEFKYAPE TEKVLERFFG KQVPVSLANT VYFNGSGKME
151 VSVPAFDYEE LSGIRLHWEG LTGETVYQKG FKSyrNSYDA PLFKIKLADK
201 GDAAFEKAHF DSETSDGINP LALGSSNLT LKFSLEWKEG VDYNVKLNEL
251 VNLVTDLQIG AFINPNSIA PSKIEVGKLA FSTKTGESGA FIDSEGRFRF
301 DTLVYGDKEY CPLDIHIAAE HLDASALTVL KRKFAQISAK KMTTEQIRND
351 LIAAVKGDAS GLFTHDPVLN IKIFRFTLPQ GKIDVGGKIM FKGMKKEDLN
401 QLGLMLKKTE ANIRMSIPQK MLEDLAVSQA GNIFSVNAED EAEARASIAID
451 INETLRLMVD STVQSMAREK YLTLDGNQID TVISLKNAL KLNGKTLQNE
501 PDPDFDEGDM VSGQPH*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1835>:

m590.seq (partial) ..

```

1 ..TGGTTTACCT CTATGGAAC GACGGTCATC CGTCTGAAAC CCGAGTTGCT
51 GAATAATGCC CGAAATACC TGCCGGATAA CCTGAAACA GTGTGGAAC
101 AGCCGGTTAC GCTGGTTAAC CATATCACGC ACGGCCCTTT CGCCGGCGGA
151 TTCGCACGCG AGGCGTACAT TGAAACCGAG TTCAAATACG CGCCTGAAAC
201 GGAAAAAGTT CTGGAACGCT TTTTGGAAA ACAAGTCCCG GCTTCCCTTG
251 CCAATACCGT TTATTTTAA GGCAGCGGTA AAATGGAAGT CAGTGTTCCT
301 GCCTTCGATT ATGAAGAGCT GTCGGGCATc AG . CTGCACT GGGAAKGCCT
351 GACGGGAGAA ACGGTTTATC AAAAAGGTTT CAAAAGCTAC CGGAACGGCT
401 ATGATGCCCC CTTGTTTAAA ATCAAGCTGG CAGACAAAGG CGATGCCGCG
451 TTTGAAAAAG TGCATTTCGA TTCGGAAACT TCAGACGGCA TCAATCCGCT
501 TGCTTTGGGC AGCAGCAATC TGACCTTGGA AAAATTCTCC CTAGAATGGA
551 AAGAGGGTGT CGATTACAAC GTCAAGTTAA ACGAACTGGT CAATCTTGTT
601 ACCGATTTCG AGATTGGCGC GTTTATCAAT CCCAACGGCA GCATCGCACC
651 TTCCAAATC GAAGTCGCA AACTGGCTTT TTCAACCAAG ACCGGGGAAT
701 CAGGCGCGTT TATCAACAGT GAAGGGCAGT TCCGTTTCGA TACACTGGTG
751 TACCGGATG AAAAATACCG CCCGCTGGAC ATCCATATCG CTGCCGAACA
801 CCTCGATGCT TCTGCCTTAA CCGTATTGAA ACGCAAGTTT GCACAAATTT
851 CCGCCAAAAA AATGACCGAG GAACAAATCC GCAATGATTG GATTGCCGCC
901 GTCAAAGGAG AGGCTTCCGG ACTGTTCCAC AACAAATCCC TATTGGACAT
951 TAAAACCTTC CGATTACGCG TGCCATCGGG AAAAATCGAT GTGGGCGGAA
1001 AAATCATCTT TAAACACATG AAGAAGGAAG ATTTGAATCA ATTGGGTTTG
1051 ATGCTGAAGA AAACCGAAGC CGACATCAGA ATGACTATTG CCCAAAAAT
1101 GCTGGAAGAC TTGGCGGTCA GTCAGCAGG CAATATTTTC AGCGTCAATG
1151 CCGAAGATGA GGCGGAAGGC AGGGCAAGTC TTGACGACAT CAACGAGACC
1201 TTGCCCTTGA TGGTGGACAG TACGTTTCAG AGTATGGCAA GGGAAAAATA
1251 TCTGACTTTG AACGGCGACC AGATTGATAC TGCCATTTC TGA AAAACA
1301 ATCAGTTGAA ATTGAACGCT AAAACGTTGC AAAACGAACC GGAGCCGGAT
1351 TTTGATGAAG GCGGTATGCT TTCAGAGCCG CAGCAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1836; ORF 590>:

1	WFTSMETTVI	RLKPELLNNA	RKYLPDNLKT	VLEQPVTLVN	HITHGPFAGG
51	FGTQAYIETE	EKYAPETEKV	LERFFGKQSV	ASLANTVYFN	GSCKHEVSPV
101	AFDYVEELSE	XLHWLXLGTG	TVYQKGKQPV	RNGYDAPLFK	IKLADKGDAA
151	EKFWHDFSET	SDGINLPLALG	SSNLTLLEKFS	LEWKEGVVDYN	VKLNLVNLVL
201	TDLQIGAFIN	PNGSIAPSKI	EVGKLAFSTK	TGESAGAKFN	EGQFRTDVLV
251	YGDEKYGFID	IIHAAEHLDA	SALTVLTKRKF	AQISAKMTE	EQIRNDLIAA
301	VKGASGLFT	NNPVLDDIKT	FTFLPSGKID	VGGKIMFKDM	KKEDINQLGL
351	MLKKTEADIR	MSIPQKMLED	LAVSQAGNIF	SVNAEDEAEG	RASLDDINET
401	LRLMVDSTVP	SMAREKYLTL	NGDQIDTAIS	LKNNQLKLNG	KTLQNEPEPD
451	FDEGGMSTEQ	QO*			

m590 / g590 93.1% identity in 462 aa overlap

[illegible]

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1837>:

```
a590.seq
1   ATGAAAAAAC CTTTGATTTC GGTTCGCGCA GCATTGCTCG GCGTTGCTTT
51  GGGCAGCCCT TATTATTTGG GTGTCAAAGC CGAAGAAAGC TTGACGCAGC
101 AGCAAAAAAT ATTGCAGGAA GCGGGCTTCT TGACCGTCGA ATCGCACCAG
151 TATGAGCGCG GCTGGTTTAC CTCTACGGAA ACGACGGTCA TCCGCTTGAA
201 ACCCGAGTTG CTGCATAATG CGCAGAAATA CCTGCCGGAT AACCTGAAAA
251 CAGTGTGGGA ACAGCCGGTT ACGCTGGTAA ACCATATCAC GCACGGTCCT
301 TTTGCCGGCG GATTGCGCAC GCAGGCGTAC ATTGAAACCG AGTTCAAATA
351 CGCGCCTGAA ACGGAAAAAG TTCTGGAACG CTTTTTTGGA AAACAAGTCC
401 CGGTTTCCCT TGCCAATACC GTTATTTTA ACGGCAGCGG TAAATGGAA
451 GTCAGTGTTT CCGCCTTCGA TTATGAAGAG CTGTGCGGCA TCAGGCTGCA
501 CTGGGAAGGC CTGACGGGAG AAACGGTTTA TCAAAAAGGT TTCAAAAGCT
551 ACCGGAACGG CTATGATGCC CCCTTGTTTA AAATCAAGCT GGCAGACAAA
601 GCGGATGCCG CGTTTGAAAA AGTGCATTTC GATTGCGAAA CTTCAGACGG
651 CATCAACCCG CTTGCTTTGG GCAGCAGCAA TCTGACCTTG GAAAAATTTT
701 CCTTAGAATG GAAAGAGGGT GTCGATTACA ACGTCAAGTT AAACCAACTG
751 GTCAATCTTG TTACCGATTG GCAGATTGGC GCGTTTATCA ATCCCAACGG
801 CAGCATCGCA CCTTCCAAAA TCGAAGTCGG CAAGCTGGCT TTTTCAACCA
851 AGACCGGGGA ATCGGGCGCG TTTATCGATA GCGAAGGCGA GTTCCGTTTT
901 GGCACGCTGG TTACGGCGCA TGAAAAATAC GGCCCTCTGG ACATCCATAT
951 CGGTGCCGAA CACCTCGATG CTCTGCTT AACCCTATTG AAACGCAAGT
1001 TTGCACGAAT TTCTGCCAAA AAAATGACTG AAGAACAAAT CCGCAATGAT
1051 TTGATTGCGG CAGTCAAAGG CGAGGCTTCC GGATTATTTA CCCATAACCC
1101 AGTATTGGAC ATTAAACTTT TCCGATTACG GCTGCCATCG GGAAAAATCG
1151 ATGTGGGCGG AAAAATCATG TTAAAGACA TGAAGAAGGA AGATTGTAAC
1201 CAATTGGGTT TGATGCTGAA GAAAACCGAA GCCGACATCA GAATGAGTAT
1251 TCCCCAAAAA ATGCTGGAAG ACTTGCGGTT CAGTCAAGCA GCAATATTTT
1301 TCAGCGTCAA TGCCGAAGAT GAGGCGGAAG GCAGGGCAAG TCTTGACGAC
1351 ATCAACGAGA CCTTGCCTCT GATGGTGGAC AGTACGGTTC AGAGTATGGC
1401 AAGGGAAAAA TATCTGACTT TGAACGGCGA CCAGATTGAT ACTGCCATTT
1451 CTCTGAAAAA CAATCAGTTG AAATTGAACG GTAAAACGTT GCAAAACGAA
1501 CCGGAGCCGG ATTTTGATGA AGGCGGTATG GTTTCAGAGC CGCAGCAGTA
1551 A
```

This corresponds to the amino acid sequence <SEQ ID 1838; ORF 590.a>:

```
a590.pep
1   MKKPLISVAA ALLGVALGTP YYLGVAEES LTQQQKILQE AGFLTVESHQ
51  YERGWFTSTE TTVIRLKP EL LHNAQKYL PD NLKTVLEQPV TLVNHITHGP
101 FAGGFGTQAY IETEFKYAPE TEKVLERFFG KQVPVSLANT VYFNGSGKME
151 VSVPAFDYEE LSGIRLHWEG LTGETVYQKG FKSyrNGYDA PLFKIKLADK
201 GDAAFEKVHF DSETSDGINP LALGSSNLTL EKFSLEWKEG VDYNVKLNEL
251 VNLVTDLQIG AFINPNGSIA PSKIEVGKLA FSTKTGESGA FIDSEGQFRF
301 GTLVYGDKEY GPLDIHIAAE HLDASALTVL KRKFARISAK KMTEEQIRND
351 LIAAVKGEAS GLFTHNPVLD IKTFRFTLPS GKIDVGGKIM FKDMKKEDLN
401 QLGLMLKKTE ADIRMSIPQK MLEDLAVSQA GNIFSVNAED EAEGRASLDE
451 INETLRLMVD STVQSMAREK YLTNGDQID TAISLKNNQL KLNGKTLQNE
501 PEPDFDEGGM VSEPQQ*
```

m590/a590 97.8% identity in 462 aa overlap

```

                                     10      20      30
m590.pep                               WFTSMETTVIRLKPPELLNNARKYLPDNLKT
a590      VKAEESLTQQQKILQEAGFLTVESHQYERGWFTSTETTVIRLKPPELLHNAQKYL PDNLKT
           30      40      50      60      70      80

           40      50      60      70      80      90
m590.pep  VLEQPVTLVNHITHGPFAGGFGTQAYIETEFKYAPETEKVLERFFGKQVPASLAN TVYFN
a590      VLEQPVTLVNHITHGPFAGGFGTQAYIETEFKYAPETEKVLERFFGKQVPVSLAN TVYFN
           90     100     110     120     130     140

           100     110     120     130     140     150
m590.pep  GSGKMEVSVPAFDYEEELSGIXLHWEXLTGETVYQKGFKSYRNGYDAPLFKIKLADKGDAA
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928

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|||||
a590      GSGKMEVSVPAFDYEELSGIRLHWEGLTGETVYQKGFKSYRNGYDAPLFKIKLADKGDAA
          150      160      170      180      190      200

          160      170      180      190      200      210
m590.pep  FEKVHFDSETSDGINPLALGSSNLTLEKFSLEWKEGV DYNVKNELVNLVTDLQIGAFIN
          |||||
a590      FEKVHFDSETSDGINPLALGSSNLTLEKFSLEWKEGV DYNVKNELVNLVTDLQIGAFIN
          210      220      230      240      250      260

          220      230      240      250      260      270
m590.pep  PNGSIAPSKIEVGKLAFFSTKTGESGAFINSEGGQFRFDTLVYGDEKYGPLDIHIAAEHLDA
          |||||
a590      PNGSIAPSKIEVGKLAFFSTKTGESGAFIDSEGGQFRFGTLVYGDEKYGPLDIHIAAEHLDA
          270      280      290      300      310      320

          280      290      300      310      320      330
m590.pep  SALTVLKRKFAQISAKKMTTEEQIRNDLIAAVKGEASGLFTNPNVLDIKTFRFTLPSGKID
          |||||
a590      SALTVLKRKFARISAKKMTTEEQIRNDLIAAVKGEASGLFTNPNVLDIKTFRFTLPSGKID
          330      340      350      360      370      380

          340      350      360      370      380      390
m590.pep  VGGKIMFKDMKKEDLNQLGLMLKKTEADIRMSIPQKMLEDLAVSQAGNIFSVNAEDEAEG
          |||||
a590      VGGKIMFKDMKKEDLNQLGLMLKKTEADIRMSIPQKMLEDLAVSQAGNIFSVNAEDEAEG
          390      400      410      420      430      440

          400      410      420      430      440      450
m590.pep  RASLDDINETLRLMVDSTVQSMAREKYLTNGDQIDTAISLKNQKLKNGKTLQNEPEPD
          |||||
a590      RASLDDINETLRLMVDSTVQSMAREKYLTNGDQIDTAISLKNQKLKNGKTLQNEPEPD
          450      460      470      480      490      500

          460
m590.pep  FDEGGMVSEPPQX
          |||||
a590      FDEGGMVSEPPQX
          510

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1839>:

m590-1.seq

```

1  ATGAAAAAAC CTTTGATTTC GGTGCGGCA GCATTGCTCG GCGTTGCTTT
51  GGGCACGCCT TATTATTGG GTGTCAAAGC CGAAGAAAGC TTGACGCAGC
101 AGCAAAAAAT ATTGCAGGAA ACGGGCTTCT TGACCGTCGA ATCGCACCAA
151 TATGAGCGCG GCTGGTTTAC CTCTATGGAA ACGACGGTCA TCCGTCTGAA
201 ACCCGAGTTG CTGAATAATG CCCGAAAATA CCTGCCGAT AACCTGAAAA
251 CAGTGTGGA ACAGCCGGT ACCTGGTTA ACCATATCAC GCACGGCCCT
301 TTCGCCGCG GATTCGGCAC GCAGGCGTAC ATTGAACCG AGTTCAAATA
351 CGCGCCTGAA ACGGAAAAG TTCTGGAACG CTTTTTTGGA AAACAAGTCC
401 CGGCTTCCT TGCCAATACC GTTTATTTA ACGGCAGCGG TAAATGGAA
451 GTCACTGTC CCGCCTTCGA TTATGAAGAG CTGTCGGGCA TCAGGCTGCA
501 CTGGGAAGGC CTGACGGGAG AAACGGTTA TCAAAAAGGT TTCAAAGCT
551 ACCGGAACGG CTATGATGCC CCCTTGTTA AAATCAAGCT GGCAGACAAA
601 GGCATGCGG GTTGTGAAA AGTGCAATTG GATTCGGAAT CTCAGACGG
651 CATCAATCCG CTTGCTTTGG GCAGCAGCAA TCTGACCTTG GAAAAATTCT
701 CCCTAGAATG GAAAGAGGGT GTCGATTACA ACGTCAAGTT AAACGAAGT
751 TTCAATCTTG TTACCGATT GCAGATTGGC GCGTTTATCA ATCCCAACGG
801 CAGCATCGCA CCTTCCAAA TCGAAGTCGG CAACTGGCT TTTTCAACCA
851 AGACCGGGGA ATCAGGCGCG TTTATCAACA GTGAAGGGCA GTTCCGTTT
901 GATACACTGG GTACGGCGA TGAATAATAC GGCCCGCTGG ACATCCATAT
951 CGCTGCCGAA CACCTCGATG CTTCTGCCTT AACCGTATTG AACGCAAST
1001 TTGCACAAAT TTCCGCCAAA AAAATGACCG AGGAACAAAT CCGCAATGAT
1051 TTGATTGCCG CCGTCAAAGG AGAGGCTTCC GGACTGTTC CCAACAATCC
1101 CGTATTGGAC ATTAATACTT TCCGATTAC GCTGCCATCG GAAAAATCG
1151 ATGTGGGCGG AAAAATCATG TTTAAAGACA TGAAGAAGGA AGATTTGAAT
1201 CAATTGGGTT TGATGCTGAA GAAACCGAA GCCGACATCA GAATGAGTAT

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1251 TCCCCAAAAA ATGCTGGAAG ACTTGGCGGT CAGTCAAGCA GGCAATATTT
 1301 TCAGCGTCAA TGCCGAAGAT GAGGCGGAAG GCAGGGCAAG TCTTGACGAC
 1351 ATCAACGAGA CCTTGCCTCT GATGGTGGAC AGTACGGTTC AGAGTATGGC
 1401 AAGGGAAAAA TATCTGACTT TGAACGGCGA CCAGATTGAT ACTGCCATTT
 1451 CTCTGAAAAA CAATCAGTTG AAATTGAACG GTAAAAAGTT GCAAAACGAA
 1501 CCGGAGCCGG ATTTTGATGA AGGCGGTATG GTTTCAGAGC CGCAGCAGTA
 1551 A

This corresponds to the amino acid sequence <SEQ ID 1840; ORF 590-1>:

m590-1.pep

1 MKKPLISVAA ALLGVALGTP YYLGVKAES LTQQQKILQE TGFLTVESHO
 51 YERGWFSTME TTVIRLKP EL LNNARKYLPD NLKTVLEQPV TLVNHITHGP
 101 FAGGFCTQAY IETEFKYAPE TEKVLERFFG KQVPASLANT VYFNGSGKME
 151 VSVPAFDYEE LSGIRLHWEG LTGETVYQKG FKSyrNGYDA PLFKIKLADK
 201 GDAAFEKVHF DSETSDGINP LALGSSNLTLEKFSLEWKEG VDYNVKLNEL
 251 VNLVTDLQIG AFINPNGSIA PSKIEVGKLA FSTKTGESGA FINSEGQFRF
 301 DTLVYGDEKY GPLDIHIAAE HLDASALTVL KKKFAQISAK KMTTEEQIRND
 351 LIAAVKGEAS GLFTNNPVL D IKTFRFTLPS GKIDVGGKIM FKDMKKEDLN
 401 QLGMLKKTE ADIRMSIPQK MLEDLAVSQA GNIFSVNAED EAEGRASIDD
 451 INETLRLMVD STVQSMAREK YLTNGDQID TAISLKNQL KLNGKTLQNE
 501 PEPDFDEGGM VSEPPQ*

m590-1/g590 93.6% identity in 516 aa overlap

	10	20	30	40	50	60
m590-1.pep	MKKPLISVAAALLGVALGTPYYLGVKAESLTQQQKILQETGFLTVESHQYERGWFSTME					
g590	MKKPLISVAAALLGVALGTPYYLGVKAESLTQQQKILQETGFLTVESHQYDRGWFSTTE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m590-1.pep	TTVIRLKPPELLNNARKYLPDNLKTVLEQPVTLVNHITHGPFAGGFCTQAYIETEFKYAPE					
g590	TTVIRLKPPELLHNAQKYLDPNLKIVLEQPVTLVNHITHGPFAGGFCTQAHIETEFKYAPE					
	70	80	90	100	110	120
	130	140	150	160	170	180
m590-1.pep	TEKVLERFFGKQVPASLANTVYFNGSGKMEVSVPAFDYEE LSGIRLHWEGLTGETVYQKG					
g590	TEKVLERFFGKQVPASLANTVYFNGSGKMEVSVPAFDYEE LSGIRLHWEGLTGETVYQKG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m590-1.pep	FKSYRNGYDAPLFKIKLADKGDAAFEKVHFDSETSDGINPLALGSSNLTLEKFSLEWKEG					
g590	FKSYRNSYDAPLFKIKLADKGDAAFEKAHFDSETSDGINPLALGSSNLTLEKFSLEWKEG					
	190	200	210	220	230	240
	250	260	270	280	290	300
m590-1.pep	VDYNVKLNELVNLVTDLQIGAFINPNGSIAPSKIEVGKLA FSTKTGESGA FINSEGQFRF					
g590	VDYNVKLNELVNLVTDLQIGAFINPNGSIAPSKIEVGKLA FSTKTGESGA FIDSEGRFRF					
	250	260	270	280	290	300
	310	320	330	340	350	360
m590-1.pep	DTLVYGDEKYGPLDIHIAAEHLASALTVLKRRFAQISAKKMTTEEQIRNDLIAAVKGEAS					
g590	DTLVYGDEKYGPLDIHIAAEHLASALTVLKRRFAQISAKKMTTEEQIRNDLIAAVKGDAS					
	310	320	330	340	350	360
	370	380	390	400	410	420
m590-1.pep	GLFTNNPVL DIKTFRFTLPSGKIDVGGKINFKDMKKEDLNQLGLMLKKTEADIRMSIPQK					
g590	GLFTHDVPLNIKIFRFTLPQSGKIDVGGKINFKDMKKEDLNQLGLMLKKTEANIRMSIPQK					
	370	380	390	400	410	420
	430	440	450	460	470	480
m590-1.pep	MLEDLAVSQAGNIFSVNAEDEAEGRASLDDINETLRLMVDSTVQSMAREKYLTNGDQID					
g590	MLEDLAVSQAGNIFSVNAEDEAEARASLDDINETLRLMVDSTVQSMAREKYLTLDGNQID					
	430	440	450	460	470	480
	490	500	510			
m590-1.pep	TAISLKNQLKLNGKTLQNEPEPDFDEGGNVS-EPQOX					

930

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g590      |:||||| ||||| ||||| ||||| ||| |:|
          TVISLKNNAKLNGKTLQNEPDPDFDEGDMVSGQPHX
          490      500      510

a590/m590-1 98.3% identity in 516 aa overlap

          10      20      30      40      50      60
a590.pep   MKKPLISVAAALLGVALGTPYYLGVKAEESLTQQQKILQEAGFLTVESHQYERGNFTSTE
m590-1      MKKPLISVAAALLGVALGTPYYLGVKAEESLTQQQKILQETGFLTVESHQYERGNFTSME
          10      20      30      40      50      60

          70      80      90      100     110     120
a590.pep   TTVIRLKEPELLHNAQKYLDPNLKTVLEQPVTLVNHITHGPFAGGFGTQAYIETEFKYAPE
m590-1      TTVIRLKEPELLNARKYLPNLKTVLEQPVTLVNHITHGPFAGGFGTQAYIETEFKYAPE
          70      80      90      100     110     120

          130     140     150     160     170     180
a590.pep   TEKVLERFFGKQVPVSLANTVYFNGSGKMEVSVPAFDYEELSGIRLHWEGLTGETVYQKG
m590-1      TEKVLERFFGKQVPASLANTVYFNGSGKMEVSVPAFDYEELSGIRLHWEGLTGETVYQKG
          130     140     150     160     170     180

          190     200     210     220     230     240
a590.pep   FKSyrNGYDAPLFKIKLADKGDAAFEKVHFDSETSDGINPLALGSSNLTLEKFSLEWKEG
m590-1      FKSyrNGYDAPLFKIKLADKGDAAFEKVHFDSETSDGINPLALGSSNLTLEKFSLEWKEG
          190     200     210     220     230     240

          250     260     270     280     290     300
a590.pep   VDYNVKLNELVNLVTDLQIGAFINPNSIAPSKIEVGKLAFTSTKTGESGAFIDSEGQFRF
m590-1      VDYNVKLNELVNLVTDLQIGAFINPNSIAPSKIEVGKLAFTSTKTGESGAFINSEGQFRF
          250     260     270     280     290     300

          310     320     330     340     350     360
a590.pep   GTLVYGDEKYGPLDIHIAAEHLDAASALTVLKRFARISAKKMTTEEQIRNDLIAAVKGEAS
m590-1      DTLVYGDEKYGPLDIHIAAEHLDAASALTVLKRFARISAKKMTTEEQIRNDLIAAVKGEAS
          310     320     330     340     350     360

          370     380     390     400     410     420
a590.pep   GLFTNPNVLDIKTFRFTLPSGKIDVGGKIMFKDMKKEDLNQLGLMLKKTEADIRMSIPQK
m590-1      GLFTNPNVLDIKTFRFTLPSGKIDVGGKIMFKDMKKEDLNQLGLMLKKTEADIRMSIPQK
          370     380     390     400     410     420

          430     440     450     460     470     480
a590.pep   MLEDLAVSQAGNIFSVNAEDEAEGRASLDDINETLRLMVDSTVQSMAREKYLTNGDQID
m590-1      MLEDLAVSQAGNIFSVNAEDEAEGRASLDDINETLRLMVDSTVQSMAREKYLTNGDQID
          430     440     450     460     470     480

          490     500     510
a590.pep   TAISLKNQKLNGKTLQNEPEPDPDFDEGDMVSEPQXX
m590-1      TAISLKNQKLNGKTLQNEPEPDPDFDEGDMVSEPQXX
          490     500     510

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The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1841>:

```

g591.seq
1   TTGCAAACCC TTCTAGCTTT TATCTTCGCC ATCCTGATTT TGGTCAGCCT
51  GCACGAATTC GGACACTACA TCGTCGCCAG GTTGTGCGGC GTCAAGGTTG
101 TGCCTTTTTTC CGTCGGCTTC GGCAAACCGT TTTTCACCCG AAAGCGCGGC
151 GACACCGAAT GGTGCCTCGC CCCGATTCCG TTGGGCGGCT ACGTCAAAAT
201 GGTGATACG CGCGAAGGCG AAGTATCAGA AGCCGATTTA CCTACGCTT
251 TTGACAAACA ACACCCGCC AAGCGCATCG CCATCGTCG CGCCGGTCCG
301 CTGACCAACC TCGCActggc ggTTTGTCTG TACGGACTGa gctTttcctt
351 cggcgtaaCC GAACTGCGGC CCtatgtcgg cacagtcgaA cccgacaccg

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931

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401 ttgccgCCCG CACCGGCTTC caaagcggcg acaaAATACa atccgtcaac
451 ggcgtTtccg tCCAAGACTG GAGCAGCGCG CAAACCGAAA TCGTcctcAA
501 CCTCGAAGCC Ggcaaagtcg ccgtcggcgT TCAGACGGCA TCGGGCGCGC
551 AAACCGTCCG CACCAtcgAT GCCGCAGGCA CGCCGGAAGC CGGTAAAATC
601 GCAAAAAACC AAGGCTACAT CGGACTGATG CCCTTTAAAA TCACAACCGT
651 TGCCGGCGGC GTGGAAAAAG GCAGCCCGC CGAAAAAGCA GGCCTGAAAC
701 CGGGCGACAG GCTGACTGCC GCCGACGGCA AACCCTCGC cteaTGGCAG
751 GAATGggcaa acctgACcg cCAAAGCCG ggcAAAAAAA Tcaccctgac
801 ctacgAaCGC GUcggacaaa cccaTaccgc CGACATCCGC CccgATactg
851 TCGAAcagcc cgACCACACC CTGATCgggc gcgTCGGCCT CCGtccgcaG
901 CCGGACAGGG CGTGGGACGC GCAAATCCGC CGCAGCTACC GTCCGTCTGT
951 TGTCGCGCA TTCGGCATGG GCTGGGAAAA AACCGTTTCC CACTCGTGGA
1001 CAACCCCTCA ATTTTTCGGC AAATAATCA GCGGCAACGC CTCTGTcAGC
1051 CATATTTCG GGCCGCTGAC CATTGCCGAC ATTGCCGGAC AGTCCGCCGA
1101 ACTCGGCTTG CAAAGTTATT TGGAAATTTT AGCGTTGGTC AGCATCAGCC
1151 TCGGCGTGCT GAACCTGCTG CCCGTCCCCG TTTTGGACGG CGGGCACCTC
1201 GTGTTTTATA CTGTCGAATG GATACGCGGC AAACCTTTGG GCGAACGTGT
1251 CCAAAACATC GGTTTGCGCT TCGGGCTCGC CCTGATGATG CTGATGATGG
1301 CGGCGCCTT CTCAACGAC GTTACCGGC TGATCGGTTA G

```

This corresponds to the amino acid sequence <SEQ ID 1842; ORF 591.ng>:

g591.pep..

```

1 LQTLLAFIFA ILILVSLHEF GHYIVARLCG VKVVRFSVGF SKPFFTRKRG
51 DTEWCLAPIP LGGYVKMVDI REGEVSEADL PYAFDKQHPA KRIAIVAAGP
101 LTNLALAVLL YGLSFSFGVT ELRPYVGTV E PDTVAARTGF QSGDKIQSVN
151 GVSVDWSSA QTEIVLNLEA GKVAVGVQTA SGAQTVRTID AAGTPEAGKI
201 AKNQGYIGIM PFKITTVAGG VEKGSPEAKA GLKPGDRLTA ADGKPIASWQ
251 EWANLTRQSP GKKITLTYER AGQHTADIR PDTVEQPDHT LIGRVGLRPQ
301 PDRAWDAQIR RSYRPSVVRA FGMGWEKTVS HSWTTLKFFG KLISGNASVS
351 HISGPLTIAD IAGQSAELGL QSYLEFLALV SISLGLVNL L PVPVLDGGHL
401 VFYTVIEWIRG KPLGERVQNI GLRFLALMM LMMAAFFND VTRLIG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1843>:

m591.seq

```

1 TTGCACACCC TTCTAGCTTT TATCTTCGCC ATCCTGATTT TGGTCAGCCT
51 GCACGAGTTC GGACACTACA TCGTTGCCAG ATTGTGCGGC GTCAAAGTCG
101 TACGCTTTTC CGTCGGCTTC GGCAAACCGT TTTTCACCCG AAAGCGCGGC
151 GACACCGAAT GGTGCCTCGC CCCGATTCCG TTGGGCGGTT ACGTCAAAAT
201 GTTCGATACG CGCGAAGGCG AAGTATCAGA AGCCGATTTA CCCTACGCTT
251 TTGACAAACA ACACCCCGCC AAGCGCATCG CCATCGTCGC CGCCGGCCCA
301 CTGACCAACC TCGCACTGGC GGTTTTGCTG TACGGACTGA GCTTTTCCTT
351 CGGCGTAACC GAACTGCGCC CCTACGTCGG CACAGTCGAA CCCGACACCA
401 TTGCGCGCCG CGCCGGCTTC CAAAGCGGCG ACAAATACA ATCCGTCAAC
451 GGCACACCCG TTGCAGATTG GGGCAGCGCG CAAACCGAAA TCGTCCTCAA
501 CCTCGAAGCC GGCAAAGTCG CCGTCGCGCT TCAGACGGCA TCGGGCGCGC
551 AAACCGTCCG CACCATCGAT GCCGCAGGCA CGCCGGAAGC CGGTAAAATC
601 GCAAAAAACC AAGGCTACAT CGGACTGATG CCCTTTAAAA TCACAACCGT
651 TGCCGGCGGC GTGGAAAAAG GCAGCCCGC CGAAAAAGCA GGCCTGAAAC
701 CGGGCGACAG GCTGACTGCC GCCGACGGCA AACCCTCGC CTCATGGCAA
751 GAATGGGCAA ACCTGACCCG CCAAAGCCCC GGCAAAAAA TCACCTGAA
801 CTACGAACGC GCGGACAAA CCCATACCGC CGACATCCGC CCCGATACTG
851 TCGAACAGTC CGACCACACC CTGATCGGGC GCGTCGGCCT CCGTCCGCAG
901 CCGGACAGGG CGTGGGACGC GCAAATCCGC CGCAGCTACC GTCCGTCTGT
951 TGTCGCGCA TTCGGCATGG GCTGGGAAAA AACCGTTTCC CACTCGTGGA
1001 CAACCCCTCA ATTTTTCGGC AAATAATCA GCGGCAACGC CTCCGTCAGC
1051 CATATTTCG GGCCGCTGAC CATTGCCGAC ATTGCCGGAC AGTCCGCCGA
1101 ACTCGGCTTG CAAAGTTATT TGGAAATTTT AGCACTGGTC AGCATCAGCC
1151 TCGGCGTGCT GAACCTACTG CCCGTCCCTG TTTTGGACGG CGGGCACCTC
1201 GTGTTTTATA CTGCCGAATG GATACGCGGC AAACCTTTGG GCGAACGCGT
1251 CCAAAACATC GGTTTGCGCT TCGGGCTCGC CCTCATGATG CTGATGATGG
1301 CCGTCGCTT CTCAACGAC GTTACCGGC TGCTCGGTTA G

```

This corresponds to the amino acid sequence <SEQ ID 1844; ORF 591>:

m591.pep..

```

1  LHTLLAFIFA ILILVSLHEF GHYIVARLCG VKVVRFSVGF GKPFFFTRKRK
51 DTEWCLAPIP LGGYVKMVD T REGEVSEADL PYAFDKQHPA KRIAIVAAGP
101 LTNLALAVLL YGLSFSFGVT ELRPYVG TVE PDTIAARAGF QSGDKIQSVN
151 GTPVADWGS A QTEIVLNLEA GXVAVGVQTA SGAQTVRTID AAGTPEAGKI
201 AKNQGYIGLM PFKITTVAGG VEKGS PAEKA GLKPGDRLTA ADGKPIASWQ
251 EWANLTROSP GKKITLNYER AGQHTADIR PDTVEQSDHT LIGRVGLRPQ
301 PDRAWDAQIR RSYRPSVVRA FGMGWEKTVS HSWTTLKFFG KLISGNASVS
351 HISGPLTIAD IAGQSAELGL QSYLEFLALV SISLGVNLL PVPVLDGGHL
401 VFYTAEWIRG KPLGERVQNI GLRFG LALMM LMMVAFFND VTRLLG*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m591 / g591 97.3% identity in 446 aa overlap

	10	20	30	40	50	60
m591.pep	LHTLLAFIFA	ILILVSLHEF	GHYIVARLCG	VKVVRFSVGF	GKPFFFTRKR	GDTEWCLAPIP
g591	LQTLAFIFA	ILILVSLHEF	GHYIVARLCG	VKVVRFSVGF	GKPFFFTRKR	GDTEWCLAPIP
	10	20	30	40	50	60
m591.pep	LGGYVKMVD	TREGEVSEAD	LPYAFDKQHP	AKRIAIVAAG	PLTNLALAVL	LYGLSFSFGVT
g591	LGGYVKMVD	TREGEVSEAD	LPYAFDKQHP	AKRIAIVAAG	PLTNLALAVL	LYGLSFSFGVT
	70	80	90	100	110	120
m591.pep	ELRPYVG TVE	PDTIAARAG	FQSGDKIQSV	NGTPVADWGS	AQTEIVLNLE	AGKVAVGVQTA
g591	ELRPYVG TVE	PDTIAARAG	FQSGDKIQSV	NGTPVADWGS	AQTEIVLNLE	AGKVAVGVQTA
	130	140	150	160	170	180
m591.pep	SGAQTVRTID	AAGTPEAGK	IAKNQGYIGL	MPFKITTVAG	GVKGS PAEKA	GLKPGDRLTA
g591	SGAQTVRTID	AAGTPEAGK	IAKNQGYIGL	MPFKITTVAG	GVKGS PAEKA	GLKPGDRLTA
	190	200	210	220	230	240
m591.pep	ADGKPIASWQ	EWANLTROSP	GKKITLNYER	AGQHTADIR	PDTVEQSDHT	LIGRVGLRPQ
g591	ADGKPIASWQ	EWANLTROSP	GKKITLNYER	AGQHTADIR	PDTVEQSDHT	LIGRVGLRPQ
	250	260	270	280	290	300
m591.pep	PDRAWDAQIR	RSYRPSVVRA	FGMGWEKTVS	HSWTTLKFFG	KLISGNASVS	HISGPLTIAD
g591	PDRAWDAQIR	RSYRPSVVRA	FGMGWEKTVS	HSWTTLKFFG	KLISGNASVS	HISGPLTIAD
	310	320	330	340	350	360
m591.pep	IAGQSAELGL	QSYLEFLALV	SISLGVNLLP	VVPVLDGGHL	VFYTAEWIRG	KPLGERVQNI
g591	IAGQSAELGL	QSYLEFLALV	SISLGVNLLP	VVPVLDGGHL	VFYTAEWIRG	KPLGERVQNI
	370	380	390	400	410	420
m591.pep	GLRFG LALMM	LMMVAFFND	VTRLLGX			
g591	GLRFG LALMM	LMMVAFFND	VTRLLGX			
	430	440				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1845>:

a591.seq

a591.pep

1	LHTLLAFIFA	ILILVSLHEF	GHYIVARLCG	VKVVRFSVGF	GKPFFTTRKR
51	DTEWCLAPIG	LGGYVKMVDI	REGEVSEADL	PYAFDKQHPA	KRIAIVAASV
101	<u>LTNLALAVLL</u>	YGLSFSFGVT	ELRPYVGTVE	PDIIAARAGF	QSGDKIQSGN
151	GTPVADWGS	QTEIVNLLEA	GKVAVGQVTA	SGAQTVRTID	AAGTPEAGKI
201	AKNQGYIGLM	PFKITTVAGG	VEKGSPAIEA	GLKPGDRLTA	ADGKPIASWQ
251	EWANLTRQSP	GKKIPLTYER	AGQTHITADIR	PDIVEQPDHT	LIGRVGLRPQ
301	PDRAWDAIIR	RSYRPSVVRA	FGMGWEKTVS	HSWTHLKFEG	KLPSGNSGVS
351	HISGLPTADI	IAGQSAELGL	QSYLEFLALV	SISLGLVNLN	LIVLDGASHL
401	VFYTAEWIRG	KPLGERVONI	GLRGLALMM	LMMAVAFFND	VTRLIG*

m591.pep	10	20	30	40	50	60
	LHTLLAFIFAILILVSLHEFGHYIVARLCGVKVVRFVSFGFKPFFTRKRGDTEWCLAPIP					
a591	10	20	30	40	50	60
	LHTLLAFIFAILILVSLHEFGHYIVARLCGVKVVRFVSFGFKPFFTRKRGDTEWCLAPIP					
m591.pep	70	80	90	100	110	120
	LGGYVKMVDTREGEVSEADLPYAFDKQHPAKRIAIVAAGPLTNLALAVLLYGLSFSFGVT					
a591	70	80	90	100	110	120
	LGGYVKMVDTREGEVSEADLPYAFDKQHPAKRIAIVAAGPLTNLALAVLLYGLSFSFGVT					
m591.pep	130	140	150	160	170	180
	ELRPYVGTVEPDTIAARAGFQSGDKIQSVNGTFPADWGSQAQTEIVLNLEAGKVAVGVQTA					
a591	130	140	150	160	170	180
	ELRPYVGTVEPDTIAARAGFQSGDKIQSVNGTFPADWGSQAQTEIVLNLEAGKVAVGVQTA					
m591.pep	190	200	210	220	230	240
	SGAQTVRTIDAAGTPEAGKIAKNQGYIGLMPFKITTVAGGVEKGSPEAKAGLKPGRDLTA					
a591	190	200	210	220	230	240
	SGAQTVRTIDAAGTPEAGKIAKNQGYIGLMPFKITTVAGGVEKGSPEAKAGLKPGRDLTA					

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	250	260	270	280	290	300
m591.pep	ADGKPIASWQEWANLTRQSPGKKITLNYERAGQTHADIRPDTVEQSDHTLIGRVGLRPQ					
a591	ADGKPIASWQEWANLTRQSPGKKITLTYERAGQTHADIRPDTVEQPDHTLIGRVGLRPQ					
	250	260	270	280	290	300
	310	320	330	340	350	360
m591.pep	PDRAWDAQIRRSYRPSVVRAFGMGWEKTVSHSWTTLKFFGKLISGNASVSHISGPLTIAD					
a591	PDRAWDAQIRRSYRPSVVRAFGMGWEKTVSHSWTTLKFFGKLISGNASVSHISGPLTIAD					
	310	320	330	340	350	360
	370	380	390	400	410	420
m591.pep	IAGQSAELGLQSYLEFLALVSISLGVNLPLVPVLDGGHLVFYTAEWIRGKPLGERVQNI					
a591	IAGQSAELGLQSYLEFLALVSISLGVNLPLVPVLDGGHLVFYTAEWIRGKPLGERVQNI					
	370	380	390	400	410	420
	430	440				
m591.pep	GLRFGLALMMLMMAVAFFNOVTRLLGX					
a591	GLRFGLALMMLMMAVAFFNOVTRLLGX					
	430	44C				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1847>:

g592.seq..

```

1 atgattccgg acgtgttcgg tcagattttt tcgggcgcgt tcaaattcga
51 cgcggcagca ggcggcttac tcggcggctc gatttcgcaa acgatgatga
101 tgggcatcaa acgcggcctg tattccaaag aggcgggtat gggttccgcg
151 ccgaaccccg ccgcccgcgc cgaagtgaag caccctgttt cgcaaggtat
201 gattcaaatg ctgggcgtgt ttgtcgatac catcatcggt tgttcttgca
251 ccgccttcac catcttgatt taccaacagc cttatggcga ttgagcgggt
301 gcggcgctga cgcaggcggc gattgtcagc caagtggggc aatggggcgc
351 ggggtttcct gccgtcatcc tgtttatgtt tgccttttcc accggtatcg
401 gcaactatgc ctatgccgag tccaacgtcc aattcatcaa aagccattgg
451 ctgattaccg ccgttttccg tatgctgggt ttggcgtggg tctatttcgg
501 cgcgggtgcc aatgtgcctt tggctcggga tatggcggat atggcgatgg
551 gcatcatggc gtggatcaac ctgcgtcgca tctgtctgct ctgcgcattg
601 gcgttttatgc tgcgtgcgca ttacacgcgc aagctgaaaa tgggcaaaaga
651 ccccgagttc aaactttccg aacatccggg cctgaaacgc cgcatacaat
701 ccgatgtttg gtaa

```

This corresponds to the amino acid sequence <SEQ ID 1848; ORF 592.ng>:

g592.pep ..

```

1 MIPDVFGQIF SGAFKFDAAA GLLGGLISQ TMMGIKRL YSNEAGMGSA
51 PNAAAAAEVK HPVSQGMQIM LGVFVDTIIV CSCTAFIILI YQPYGDLGG
101 AALTQAAIVS QVGQWGAGFL AVILFMFAPS TVIGNYAYAE SNVQFIKSHW
151 LITAVFRMLV LANVYFGAVA NVPLVNDMAD MAMGIMAWIN LVAILLLSPL
201 AFMLLRDYTA KLKMGKDPEF KLSEHGLKR RIKSDVW*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1849>:

m592.seq ..

```

1 ATGATTCCGG ACGTGTTCGG TCAGATTTT TCAGGCGCGT TCAAATTCGA
51 CGCGGCAGCA GCGGCTTAC TCGGCGGTCT GATTTCGCAA ACGATGATGA
101 TGGGCATCAA ACGCGGCTG TATTCCAACG AGGCGGGTAT GGGTTCGCG
151 CCGAACCCCG CCGCGCCGC CGAAGTGAAA CACCCTGTTT CGCAAGGTAT
201 GATTCAAATG CTGGGCGTGT TTGTCGATAC CATCATCGTT TGTCTTGCA
251 CCGCCTTCAT CATCTTGATT TACCAACAGC CTTACGGCGA TTTGAGCCGT
301 GCGGCGCTGA CGCAGGCGGC GATTGTCAGC CAAGTGGGCG AATGGGCGC
351 GGGCTTCCTC GCGTCATCC TGTATTATGT TGCCTTTTCC ACCGTTATCG
401 GCAACTATGC CTATGCCGAG TCCAAGTCC AATTTCATCA AAGCCATTGG
451 CTGATTACCG CCGTTTTCGG TATGCTGGTT TTGGCGTCGG TCTATTTCGG
501 CGCGGTTGCC AATGTGCCIT TGGTCTGGGA TATGGCGGAT ATGGCGATGG
551 GCATTATGGC GTGGATCAAC CTTGTGCCA TCCTGCTGCT CTCGCCCTTG

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935

601 GCGTTTATGC TGCTGCGCGA TTACACCGCC AAGCTGAAAA TGGGCAAAGA
 651 CCCCAGAGTTC AAACCTTCCG AACATCCGGG CCTGAAACGC CGTATCAAAT
 701 CCGACGTTTG GTAA

This corresponds to the amino acid sequence <SEQ ID 1850; ORF 592>:

m592.pep ..
 1 MIPDVFGQIF SGAFKFDAAA GLLGGLISQ TMMGIKRG LYSNEAGMGSA
 51 PNAAAAAAEVK HPVSQGM IQM LGVFVDTIIV CSCTAFIILI YQQPYGDL SG
 101 AALTQAAI VS QVGQWGAGFL AVILEMF AFS TVIGNYAYAR SNVQFIKSHW
 151 LITAVFRMLV LAWVYFGAVA NVPLVWDMAD MAMGIMAWIN LVAILLLSPL
 201 AFMLLRDYTA KLKMGKDPEF KLSEHPGLKR RIKSDVW*

m592 / g592 100.0% identity in 237 aa overlap

	10	20	30	40	50	60
m592.pep	MIPDVFGQIFSGAFKFDAAAGLLGGLISQTMMGIKRG LYSNEAGMGSAFNAAAAAAEVK					
g592	MIPDVFGQIFSGAFKFDAAAGLLGGLISQTMMGIKRG LYSNEAGMGSAFNAAAAAAEVK					
	10	20	30	40	50	60
	70	80	90	100	110	120
m592.pep	HPVSQGM IQM LGVFVDTIIVCSCTAFIILIYQQPYGDL SGAALTQAAI VSQVGQWGAGFL					
g592	HPVSQGM IQM LGVFVDTIIVCSCTAFIILIYQQPYGDL SGAALTQAAI VSQVGQWGAGFL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m592.pep	AVILEMF AFS TVIGNYAYAESNVQFIKSHWLITAVFRMLV LAWVYFGAVANVPLVWDMAD					
g592	AVILEMF AFS TVIGNYAYAESNVQFIKSHWLITAVFRMLV LAWVYFGAVANVPLVWDMAD					
	130	140	150	160	170	180
	190	200	210	220	230	
m592.pep	MAMGIMAWINLVAILLLSPLAFMLLRDYTA KLKMGKDPEF KLSEHPGLKRRIKSDVW*					
g592	MAMGIMAWINLVAILLLSPLAFMLLRDYTA KLKMGKDPEF KLSEHPGLKRRIKSDVW*					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1851>:

a592.seq
 1 ATGATTCGGG ACGTGTTCCG TCAGATTTTT TCGGGCGCGT TCAAATTCGA
 51 CGCGGCAGCA GCGGCTTAC TCGGCGGTCT GATTTCGCAA ACGATGATGA
 101 TGGGCATCAA ACGCGCCTG TATTCCAACG AGGCGGGTAT GGGTTCGCGC
 151 CCGAACGCCG CCGCCGCCGC CGAAGTGAAA CACCCTGTTT CGCAAGGTAT
 201 GATTCAAATG CTGGGCGTGT TTGTCGATAC CATCATCGTT TGTCTCTGCA
 251 CCGCCTTCAT CATCTTGATT TACCAACAGC CTTACGGCGA TTTGAGCGGT
 301 CCGGCGCTGA CGCAGGCGGC GATTGTCAGC CAACTGGGGC AATGGGGCGC
 351 GGGCTTCCTC GCCGTCATCC TGTTTATGTT TGCCTTTTCC ACCGTTATCG
 401 GCAACTATGC CTATGCCGAG TCCACGCTCC AATTCATCAA AAGCCATTGG
 451 CTGATTACCG CCGTTTTCGG TATGCTGGTT TTGGCGTGGG TCTATTTCCG
 501 CGCGGTTGCC AATGTGCCTT TGGTCTGGGA TATGGCGGAT ATGGCGATGG
 551 GCATTATGGC GTGGATCAAC CTTGTCGCCA TCCTGCTGCT CTCGCCCTTG
 601 GCGTTTATGC TGCTGCGCGA TTACACCGCC AAGCTGAAAA TGGGCAAAGA
 651 CCCCAGAGTTC AAACCTTCCG AACATCCGGG CCTGAAACGC CGTATCAAAT
 701 CCGACGTTTG GTAA

This corresponds to the amino acid sequence <SEQ ID 1852; ORF 592.a>:

a592.pep
 1 MIPDVFGQIF SGAFKFDAAA GLLGGLISQ TMMGIKRG LYSNEAGMGSA
 51 PNAAAAAAEVK HPVSQGM IQM LGVFVDTIIV CSCTAFIILI YQQPYGDL SG
 101 AALTQAAI VS QVGQWGAGFL AVILEMF AFS TVIGNYAYAE SNVQFIKSHW
 151 LITAVFRMLV LAWVYFGAVA NVPLVWDMAD MAMGIMAWIN LVAILLLSPL
 201 AFMLLRDYTA KLKMGKDPEF KLSEHPGLKR RIKSDVW*

m592/a592 100.0% identity in 237 aa overlap

936

	10	20	30	40	50	60
m592.pep	MI PDVFGQIFSGAFKFDAAAGLLGGLISQTMIMGIRGLYSNEAGMGSAPNAAAAAEVK					
a592	MI PDVFGQIFSGAFKFDAAAGLLGGLISQTMIMGIRGLYSNEAGMGSAPNAAAAAEVK					
	10	20	30	40	50	60
	70	80	90	100	110	120
m592.pep	HPVSQGMIOQLGVFVDTIIVCSCTAFIILIYQQPYGDLGAALTQAAIVSQVGQWGAGFL					
a592	HPVSQGMIOQLGVFVDTIIVCSCTAFIILIYQQPYGDLGAALTQAAIVSQVGQWGAGFL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m592.pep	AVILFMFAFSTVIGNYAYAESNVQFIKSHWLITAVFRMLVLAWVYFGAVANVPLVWDMAD					
a592	AVILFMFAFSTVIGNYAYAESNVQFIKSHWLITAVFRMLVLAWVYFGAVANVPLVWDMAD					
	130	140	150	160	170	180
	190	200	210	220	230	
m592.pep	MAMGIMAWINLVAILLLSPLAFMLLRDYTAKLMGKDPEFKLSEHPGLKRRIKSDVWX					
a592	MAMGIMAWINLVAILLLSPLAFMLLRDYTAKLMGKDPEFKLSEHPGLKRRIKSDVWX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1853>:

g593.seq..

```

1  atgcttgaac tgaacggact ctgcaaatgc ttcggcgcca aaacggctcgc
51  cgacaacatc tgcctgactg tcgggcgcgg caaaatactc gccgtactgg
101  ggcggtcggg ctgcggcaaa tccaccctgc tgaatatgat tgcgggcacg
151  gtccggccgg acggcgcgga aattcggctg aacggggaaa acattacctg
201  tatccgcccc gaaaaacgcc gtatctcgct gatgtttcaa gattacgcgc
251  tgtttcccca tatgagtgcg ctggaaaata cggcattcgg tttgaaaatg
301  caaaaaatgc cgaaagccga agccgaacgc ctgccttgtg cggcacttgc
351  cgaagtcggg ctggaaaacg aggcgcaccg caagcctgaa aaactttccg
401  gaggcgagaa gcaacggttg gcaactggcg gcgctttggt tgtccgccct
451  tccctgctgt tgctggatga atcgttttcc agtttggaac cgcatttgcg
501  cgaccggctg cgccgtatga ccgccgaacg catccgcaag ggcggcatcc
551  ctgccgtttt ggtaacgcat tcgcccgaag aggcctgcac ggcggcggac
601  gaaatcgccg tcatgcacga ggggaaaatc cttcaatgcg gacgcccga
651  aaccttgatt caaacgcctg ccggcggtga ggtcgcccggt cggatggggc
701  tgcccaatac cgacgatgac cgccatattc cgcaaaatgc cgtgtgcttg
751  gacaatcatg gaacggaatg ccgtctgctg tccctcgctc gcctgcccga
801  ctgctcccg ctttcgcccg tccatcccga acacggcgag ctgaccttaa
851  acctgactgt cggacaacat acggacggta tttccggaaa cggtaacggc
901  cgcatccgcg tcgatgaagg gcgtatcgct cgtttccgat ga

```

This corresponds to the amino acid sequence <SEQ ID 1854; ORF 593.ng>:

g593.pep..

```

1  MLELNLCKC FGGKTVADNI CLTVGRGKIL AVLGRSGCGK STLLNMIAGI
51  VRPDGGEIRL NGENITCMPP EKRRISLMFQ DYALFPHMSA LENTAFGLKM
101  QKMPKAEAEER LALSALAEVG LENEHRKPE KLSGGEKQRL ALARALVVRP
151  SLLLLDESFS SLDTHLRDRL RRMTAERIRK GGIPAVLVTH SPEEACTAAD
201  EIAVMHEGKI LQCGTPETLI QTPAGVQVAR LMGLPNTDDD RHIPQNAVCL
251  DNHGTECRLL SLVRLPDSLRL LSAVHPEHGE LTLNLTVGQH TDGISGNQTV
301  RIRVDEGRIV RFR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1855>:

m593.seq

```

1  ATGCTTGAAC TGAACGGACT CTGCAAACGC TTCGGCAATA AAACCGTCGC
51  CGACAACATC TGCCTGACTG TCGGGCGCGG CAAAATACTC GCCGTTTGG
101  GCGGTCGGG CTGCGGAAAA TCCACCCTGC TGAATATAAT TGCGGGGATT
151  GTCCGGCCGG ACGGCGGGGA AATATGGCTG AACGGAGAAA ACATTACCCG

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201 TATGCCGCCC GAAAAACGCC GTATCTCGCT GATGTTTCAA GATTACGCGC
251 TGTTTCCCCA TATGAGTGCG CTGGAAAATG CGGCATTTCG TTTGAAAATG
301 CAAAAAATGC CGAAAGCCGA AGCCGAACGC CTCGCCATGG CGGCACTTGC
351 CGAAGTCGGA CTGGAACACG AGGCGCACCG CAAGCCTGAA AACTTTCCG
401 GAGGCGAGAA GCAACGGCTG GCGTTGGCGC GCGCTTTGGT TGTCCGCCCT
451 TCCCTGCTGC TGTGGACGA ATCGTTTTC AGTTTGGACA CGCATTTCG
501 CGGCACGCTG CGCCGTATGA CTGCCGAACG TATCCGAAAC GGCGGCATCC
551 CTGCCGTTTT GGTAAACGCAT TCGCCGAAG AAGCCTGTAC GACGGCAGAC
601 GAAATCGCCG TGATGCATAA AGGGAGGATT CTACAATACG GTACGCCCGA
651 AACATTGGTC AAAACACCAT CCTGCGTGCA GGTGCGCCGA CTGATGGGTT
701 TGCCCAATAC CGACGATAAC CGCCATATTC CGCAACATGC GGTGCGTTTC
751 GACCAAGACG GCATGGAGTG CCGCGTATTA TCCCGTACCT GTTGGCCCGA
801 ATCGTTCAGC CTGTCCGTCC TCCATCCGGA ACACGGCATC CTGTGGCTGA
851 ACCTCGATAT GCGGCACGCC GGGGCGGTAT CGGGCAAGGA TACGGTACGC
901 ATCCATATCG AAGAACGGGA AATCGTCCGC TTCCGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1856; ORF 593>:

```

m593.pep ..
  1 MLELNLCKR FGNKTVADNI CLTVGRGKIL AVLGRSGCGK STILLNIIAGI
 51 VRPDGGEIWL NGENITRMPP EKRRISLMFQ DYALFPHMSA LENAAGFLKM
101 QKMPKAEAEER LAMAALAEVG LENEHRKPE KLSGGEKQRL ALARALVVRP
151 SLLLLDESFS SLDTHLRGTL RRMTAERIRN GGIPAVLVTH SPEEACTTAD
201 EIAVMHKGRI LQYGTPELTV KTPSCVQVAR LMGLPNTDDN RHIPQHVRP
251 DQDGMCECVL SRTCLPESES LSVLHPEHGI LWLNLMRHA GAVSGKDTVR
301 IHIEEREIVR FR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m593 / g593 83.4% identity in 313 aa overlap

	10	20	30	40	50	60
m593.pep	MLELNLCKRFGNKT	VADNICLTVGRGKIL	AVLGRSGCGKSTLLNII	AGIVR	PDGGEIWL	
g593	MLELNLCKCFGGKT	VADNICLTVGRGKIL	AVLGRSGCGKSTLLNMI	AGIVR	PDGGEIWL	
	10	20	30	40	50	60
	70	80	90	100	110	120
m593.pep	NGENITRMPPEKRR	ISLMFQDYALFPHMSA	LENAAGFLKM	QKMPKAEAEER	LAMAALAEVG	
g593	NGENITCMPPEKRR	ISLMFQDYALFPHMSA	LENTAFGLKM	QKMPKAEAEER	LALSALAEVG	
	70	80	90	100	110	120
	130	140	150	160	170	180
m593.pep	LENEHRKPEKLSGGEK	QRLALARALVVRPS	LLLLDESFS	SLDTHLRGTL	RRMTAERIRN	
g593	LENEHRKPEKLSGGEK	QRLALARALVVRPS	LLLLDESFS	SLDTHLRDRL	RRMTAERIRK	
	130	140	150	160	170	180
	190	200	210	220	230	240
m593.pep	GGIPAVLVTHSPEEACT	ADEIAVMHKGRI	LQYGTPELTV	KTPSCVQVAR	LMGLPNTDDN	
g593	GGIPAVLVTHSPEEACT	ADEIAVMHEGKIL	QCGTPETLIQ	TPAGVQVAR	LMGLPNTDDD	
	190	200	210	220	230	240

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	250	260	270	280	290	299
m593.pep	RHIPQHAVRFDQDGMCECRVLSRTCLPESFSLSVLHPEHGILWLNLDLMD-RHAGAVSGKDTV					
	: : : : : : : : : : : :					
g593	RHIPQNAVCLDNHGTECRLLSLVRLPDSLRLSAVHPEHGELTNLTVGQHTDGISGNGTV					
	250	260	270	280	290	300
	300	310				
m593.pep	RIHIEEREIVRFRX					
	: : :					
g593	RIRVDEGRIVRFRX					
	310					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1857>:

a593.seq

1	ATGCTTGAAC	TGAACGGACT	CTGCAAACGC	TTCGGCGGCA	AAACGGTTGC
51	CGACGATATC	TGCTGACTG	TCGGGCGCGG	CAAAATACTC	GCCGTTTGG
101	GGCGGTCGGG	CTGCGGCAAA	TCCACCCTGC	TGAATATGAT	TGCGGGCATC
151	GTCCGGCCGG	ACGGCGGGGA	AATATGGCTG	AATGGGGAAA	ACATTACCCG
201	TATGCCGCC	GAAAAACGCC	GTATTTTCGT	GATGTTTCAA	GATTACGCGC
251	TGTTTCCCA	TATGAGTGCA	CTGGAATG	CGGCATTCCG	TTTGAAAATG
301	CAAAAAATGC	CGAAAGCCGA	AGCCGAAAGC	CTCGCCATGG	CGGCACTTGC
351	CGAAGTCGGA	CTGGAACG	AGGCGCACCG	CAAGCCTGAN	AAACTTTCCG
401	GAGGCGAAAA	GCAACGGTTG	GCACTGGCGC	GCGCTTTGGT	TGTCCGCCCT
451	TCCCTGCTGC	TGTTGGACGA	ATCGTTTTC	AGTTTGGACA	CGCATTGCG
501	CGACCGGCTG	CGCGCATGA	CTGCCGAACG	TATCCGCAAG	GGCGGCATCC
551	CTGCCGTTTT	GGTAACGCAT	TCGCCGGAAG	AGGCCTGCAC	GGCGGCAGAC
601	GAAATCGCCG	TCATGCACGA	GGGGAATC	CTTCAATGCG	GTACGCCCGA
651	AACCTTGGTT	CAAACGCCTG	CCGGCGTGCA	GGTCGCCCAT	CTGATGGGGC
701	TGCCCCAATAC	CGACGATGAC	CGCCATATTC	CGCAACATGC	GGTGCGTTTC
751	GACCAAGACG	GCATGGAGTG	CCGCGTATTA	TCCCGTACCT	GTTTGCCCGA
801	ATCGTTCAGC	CTGTCCGTCC	TCCATCCGGA	ACACGGCATC	CTGTGGCTGA
851	ACCTCGATAT	GCCGCACGCC	GGTGAAATAT	CGGGAAACGA	TACGGTACGC
901	ATCCATATCG	AAGACAGGGA	AATCGTCCGC	TTCCGCTGA	

This corresponds to the amino acid sequence <SEQ ID 1858; ORF 593.a>:

a593.pep

1	MLELNLCKR	FGGKTVADDI	CLTVGRGKIL	AVLGRSGCGK	STLLNMIAGI
51	VRPDGGEIWL	NGENITRMPP	EKRRIQLMFQ	DYALFPHMSA	LENAAFLKLM
101	QKMPKAEAES	LAMAALAEVG	LENEAHRKPX	KLSSGGEKQRL	ALARALVVRP
151	SLLLDESFS	SLDTHLRDRL	RRMTAERIRK	GGIPAVLVTH	SPEEACTAAD
201	EIAVMHEGKI	LQCGTPETLV	QTPAGVQVAH	LMGLENTDDD	RHIPQHAVRF
251	DQDGMCECVL	SRTCLPESFS	LSVLHPEHGI	LWLNLDMPHA	GEISGNDTVR
301	IHIEDREIVR	FR*			

m593/a593 92.9% identity in 312 aa overlap

	10	20	30	40	50	60
m593.pep	MLELNLCKRFGNKTVDNICLTVGRGKILAVLGRSGCGKSTLLNIIAGIVRPDGGEIWL					
	: : : : : : : : : : : : :					
a593	MLELNLCKRFGGKTVADDICLTVGRGKILAVLGRSGCGKSTLLNMIAGIVRPDGGEIWL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m593.pep	NGENITRMPPKRRISLMFQDYALFPHMSALENAAFGLKMQKMPKAEERLAMAALAEVG					
	: : : : : : : : : : : : :					
a593	NGENITRMPPKRRISLMFQDYALFPHMSALENAAFGLKMQKMPKAEESLAMAALAEVG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m593.pep	LENEAHRKPXKLSSGGEKQRLALARALVVRPSLLLDESFSLLDTHLRCTLRMTAERIRN					
	: : : : : : : : : : : : :					
a593	LENEAHRKPXKLSSGGEKQRLALARALVVRPSLLLDESFSLLDTHLRDRLRRMTAERIRK					
	130	140	150	160	170	180
	190	200	210	220	230	240
m593.pep	GGIPAVLVTHSPEEACTTADEIAVMHKGRILQYGTPTLVKTPSCVQVARLMGLEPNTDDN					

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|||||:|||||:|:| | |||||:|: | |||:|||||:
a593  GGIPAVLVTHSPEEACTAADEIAVMHEGKILQCGTPETLVQTPAGVQVAHLMGLPNTDD
      190      200      210      220      230      240

      250      260      270      280      290      300
m593.pep RHIPQHAVRFDQDGMECRVLSRTCLPESFSLSVLHPEHGILWLNLDMRHAGAVSGKDTVR
|||||:|||||:|:| | |||||:|: | |||:|||||:
a593  RHIPQHAVRFDQDGMECRVLSRTCLPESFSLSVLHPEHGILWLNLDMPHAGEISGNDTVR
      250      260      270      280      290      300

      310
m593.pep IHIEEREIVRFRX
|||||:|||||:|:| |
a593  IHIEDREIVRFRX
      310

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1859>:

g594.seq..

```

1  atgggtgcag ataccgatgg cgacaaggat gttcggctta atcgaacggg
51  tctcgttttt agcatactcc ggctgctgtt ccgcatcgga attgggatcg
101 gtaagttcgc cgttcaggcc tttcaggctt ttaagctgct gatctgtacg
151 gttgagcacc caaatcggtt tgccttgcca ctcgccggtc agcagctgac
201 ccgcttcgat tttactgaca tccacctcga cggcagcacc ggaggccttg
251 gctttttccg aagggaaaaa actggccaca aacggcgttg ccacacccaa
301 tgctgccact ccgccgcgc cgcaggtcgc aagtgtcagg aaacggcggc
351 ggccgttggt gatttcttga ttatccatta ttcagtcgtc ctaatatattt
401 gggaatgccg agccattaaa cattgcaatt ttaccagtt tgcagtgata
451 ctcaaagcat tatttaaaat aaggtaa

```

This corresponds to the amino acid sequence <SEQ ID 1860; ORF 594.ng>:

g594.pep

```

1  MGADTDGDKD VRLNRTGLVF SILRLLFRIG IGIGKFAVQA FQVFKLLICT
51  VEHPNRFALP LGGQQLTRFD FTDIHLDGST GGLGFFREK TGHKRRCHTQ
101 CCHSARAAGR KCQETAAVV DFLIIHYSVV LIFWECRAIK HCNFTQFAVI
151 LKALFKIR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1861>:

m594.seq

```

1  ATGGGTGCAG ATACCGATGG CGACAAGGAT GTTCGGCTTA ATCGAACGGG
51  TCTCGTTTTT AGCATACTCC GGCTGCTGTT CCGCATCGGA ATTGGGATCG
101 GTAAGTTTCGC CGTTCAGGCC TTTcaggctt TTAAGCTGCT GATCTGTACG
151 GTTGAGCACC CAAATCGGTT TGCCTTGCCA CTCGGCGGTC AGCAGCTGAC
201 CCGCTTCGAT TTTACTGACA TCCACCTCGA CGGCAGCACC GCGCGCCTTG
251 GCTTTTTCG AAGGGAaaaa ACTGGCCACA AACGGCGTTG CCACACCCAA
301 TGCTGCCACT CCGCCCGCGC CGCAGGTGCG GAGTGTcagg AAACGGCGGC
351 GGCCGTGTTT GATTCTTGA TTATCCATTA TTCAGTCGTC CTAATATTTT
401 GGGAATACCG AGCCATTAAA CGTTGCAATT TTACCCAGTT TGCAGTGATA
451 CTCAAAGCAT TATTAAAAAT AAGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1862; ORF 594>:

m594.pep

```

1  MGADTDGDKD VRLNRTGLVF SILRLLFRIG IGIGKFAVQA FQVFKLLICT
51  VEHPNRFALP LGGQQLTRFD FTDIHLDGST GGLGFFREK TGHKRRCHTQ
101 CCHSARAAGR ECQETAAVV DFLIIHYSVV LIFWEYRAIK RCNFTQFAVI
151 LKALFKIR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m594 / g594 98.1% identity in 158 aa overlap

940

	10	20	30	40	50	60
m594.pep	MGADTDGDKDVRLNRTGLVFSILRLLFRIGIGIGKFAVQAFQVFKLLICTVEHPNRFALP					
g594	MGADTDGDKDVRLNRTGLVFSILRLLFRIGIGIGKFAVQAFQVFKLLICTVEHPNRFALP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m594.pep	LGGQQLTRFDFTDIHLDGSTGGLGFFRREKTGHKRRCHTQCCHSARAAGRECQETAAAVV					
g594	LGGQQLTRFDFTDIHLDGSTGGLGFFRREKTGHKRRCHTQCCHSARAAGRECQETAAAVV					
	70	80	90	100	110	120
	130	140	150	159		
m594.pep	DFLIHYSVVLIFWEYRAIKRCNFTQFAVILKALFKIRX					
g594	DFLIHYSVVLIFWEYRAIKRCNFTQFAVILKALFKIRX					
	130	140	150			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1863>:

```

a594.seq
1  ATGGGTGCAG ATACCGATGG CGACAAGGAT GTTCGGCTTA ATCGAACGGG
51  TCTCGTTTTT AGCATACTCC GGCTGCTGTT CCGCATCGGA ATTGGGATCG
101 GTAAGTTCGC CGTTCAGGCC TTTCAGGTCT TTAAGCTGCT GATCTGTACG
151 GTTGAGCACC CAAATCGGTT TGCCTTGCCA CTCGGCGGTC AGCAACTGAC
201 CCGCTTCGAT TTTACTGACA TCCACCTCGA CGGCAGCACC GGCGGCCTTG
251 GCTTTTCCG AAGGGAAAAA ACTGGCCACA AACGGCGTTG CCACACCCAA
301 TGTGCCACT CCGCCGCGC CGCAGGTCGC GAGTGTGAGG AAACGGCGGC
351 GGCGGTTGTT GATTCTTGA TTATCCATTA TTCAGTCGTC CTAATATTTT
401 GGGAAATACG AGCCATTAAA CGTTGCAATT TTACCCAGTT TGCAGTGATA
451 CTCAAAGCAT TATTAAAAAT AAGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1864; ORF 594.a>:

```

a594.pep
1  MGADTDGDKD VRLNRTGLVF SILRLLFRIG IGIGKFAVQA FQVFKLLICT
51  VEHPNRFALP LGGQQLTRFD FTDIHLDGST GGLGFFRREK TGHKRRCHTQ
101 CCHSARAAGR ECQETAAAVV DFLIHYSVSV LIFWEYRAIK RCNFTQFAVI
151 LKALFKIR*

```

m594/a594 100.0% identity in 158 aa overlap

	10	20	30	40	50	60
m594.pep	MGADTDGDKDVRLNRTGLVFSILRLLFRIGIGIGKFAVQAFQVFKLLICTVEHPNRFALP					
a594	MGADTDGDKDVRLNRTGLVFSILRLLFRIGIGIGKFAVQAFQVFKLLICTVEHPNRFALP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m594.pep	LGGQQLTRFDFTDIHLDGSTGGLGFFRREKTGHKRRCHTQCCHSARAAGRECQETAAAVV					
a594	LGGQQLTRFDFTDIHLDGSTGGLGFFRREKTGHKRRCHTQCCHSARAAGRECQETAAAVV					
	70	80	90	100	110	120
	130	140	150	159		
m594.pep	DFLIHYSVVLIFWEYRAIKRCNFTQFAVILKALFKIRX					
a594	DFLIHYSVVLIFWEYRAIKRCNFTQFAVILKALFKIRX					
	130	140	150			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1865>:

```

g595.seq..
1  atgagaaaat tcaatttgac cgcattgtcc gtgatgcttg ccttgggttt
51  gaccgcgtgc cagccgccgg aggcggagaa agccgcgccg gccgcgtccg
101 gtgagacca atccgccaac gaaggcgggt cggtcggtat cgccgtcaac

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```
151 gacaatgcct gcgaaccgat gaatctgacc gtgccgagcg gacaggttgt
201 gttcaatatt aaaaaacaaca gcggccgcaa gctcgaatgg gaaatcctga
251 agggcgtgat ggtggtggac gaacgcgaaa atatcgcccc cgggctttcc
301 gacaaaatga accgtaacct gctgccgggc gaatacgaaa tgacctgcgg
351 ccttttgacc aatccgcgcg gcaagctggt ggtagccgac agcggcttta
401 aagacaccgc caacgaagcg gatttgaaaa aactgccccca accgctcgcc
451 gactataaag cctacgttca aggcgaggtt aaagagctgg cggcgaaaac
501 caaaaccttt accgaagccg tcaaagcagg cgacattgaa aaggcgaaat
551 ccctgtttgc cgccaccgcg gtccattacg aacgcacgca accgattgcc
601 gagcttttca gcgaactcga ccccgtcac gatgcgtgtg aagacgactt
651 caaagacggg gcgaaagatg ccgggtttac cggttccac cgtatcgaa
701 acgccctttg ggtggaaaaa gacgtatccg gcgtgaagga aaccgcggcc
751 aaactgatga ccgatgtcga agccctgcaa aaagaaatcg acgcattggc
801 gttccctccg ggcaaagtgg tcggcggcgc gtccgaactg attgaagaag
851 cggcgggcag taaaatcagc ggcaagaag accgttacag ccacaccgat
901 ttgagcgact tccaagctaa tcgggacgga tctaaaaaaa tcgtcgattt
951 gttccgtccg ttgattgagg ccaaaaacaa agccttggtg gaaaaaacgg
1001 ataccaactt caaacaggtc aacgaaatc tggcgaaata ccgcaccaa
```

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1051 gacgggttttg aaacctacga caagctgagc gaagccgacc gcaaagcatt
 1101 acaggtcctcct attaacgcgc ttgccgaaga ccttgcccaa cttcgcgga
 1151 tactcggctt gaaataa

This corresponds to the amino acid sequence <SEQ ID 1866; ORF 595.ng>:

g595.pep ..
 1 MRKFNLALS VMLALGLTAC QPPEAEKAAP AASGETQSAN EGGSVGIADV
 51 DNACEPMNLT VPSGQVVFNI KNNSGRKLEW EILKGVMVVD ERENIAPGLS
 101 DKMNRNLLPG EYEMTCGLLT NPRGKLVVAD SGFKDTANEA DLEKLPQPLA
 151 DYKAYVQGEV KELAATKTF TEAVKAGDIE KAKSLFAATR VHYERIEPIA
 201 ELFSELDPIV DATEDDFKDG AKDAGFTGFH RIEHALWVEK DVSGVKETAA
 251 KLMTDVEALQ KEIDALAFPP GKVVGGASEL IEEAAGSKIS GEEDRYSHTD
 301 LSDFQANADG SKKIVDLFRP LIEAKNKALL EKTDTNFKQV NEILAKYRTK
 351 DGFETYDKLS EADRKALQAP INALAEDLAQ LRILGLK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1867>:

m595.seq
 1 ATGAGAAAAT TCAATTTGAC CGCATTGTCC GTGATGCTTG CTTAGGTTT
 51 GACCGCGTGC CAGCCGCCGG AGCGGAGAAA AGCTGCGCCG GCAGCGTCCG
 101 GTGAGGCGCA AACCGCCAAC GAGGGCGGTT CGGTCACTAT CGCCGTCAAC
 151 GACAAATGCCT GCGAACCGAT GGAACGTACC GTGCCGAGCG GACAGGTTGT
 201 GTTCAATATT AAAACAACA GCGGCCGCAA GCTCGAATGG GAAATCCTGA
 251 AAGCGGTGAT GGTGGTGGAC GAGCGCGAAA ACATCGCCCC CGGACTTCC
 301 GATAAAATGA CCGTCACCCT GTTGCCGGGC GAATACGAAA TGAATTCGG
 351 TCTTTTGACC AATCCGCGCG GCAAGCTGGT GGTAACCGAC AGCGGCTTTA
 401 AAGACACCGC CAACGAAGCG GATTGGGAAA AACTGTCCCA ACCGCTCGCC
 451 GACTATAAAG CCTACGTTCA AGCGGAGGTT AAAGAGCTGG TGGCGAAAC
 501 CAAAACCTTT ACCGAAGCCG TCAAAGCAGG CGACATTGAA AAGGCGAAAT
 551 CCCTTTTGGC CGACACCGCG GTCCATTACG AACGCATCGA ACCGATTGCC
 601 GAGCTTTTCA GCGAACTCGA CCCCCTCATC GATGCGCGTG AAGACGACTT
 651 CAAAGACGGC GCGAAAGATG CCGGATTAC CGGCTTTCAC CGTATCGAAT
 701 ACGCCCTTTG GGTGGAAGAA GACGTGTCCG CGGTGAAGGA AATTGACGCG
 751 AAACCTGATG CCGATGTCGA AGCCCTGCAA AAAGAAATCG ACGCATTGGC
 801 GTTTCCTCCG GGCAAGGTGG TCGCGGCGCG GTCCGAACG ATTGAAGAAG
 851 TGGCGGCGAG TAAATCAGC GGCGAAGAAG ACCGGTACAG CCACACCGAT
 901 TTGAGCGACT TCAAAGCCAA TGTGGACGGA TCTAAAAAAA TCGTCGATTT
 951 TTCCGTCCG CTGATCGAGG CCAAAAACAA AGCCTTGTG GAAAAAACCG
 1001 ATACCAACTT CAAACAGGTC AACGAAATTC TGGCGAAATA CCGGACTAAA
 1051 GACGGTTTTG AAACCTACGA CAAGCTGGGC GAAGCCGACC GCAAAGCGTT
 1101 ACAGGCCTCT ATTAACGCGC TTGCCGAAGA CCTTGCCCAA CTTCCGCGCA
 1151 TACTCGGCTT GAAATAA

This corresponds to the amino acid sequence <SEQ ID 1868; ORF 595>:

m595.pep
 1 MRKFNLALS VMLALGLTAC QPPEAEKAAP AASGEAQTAN EGGSVSIAVN
 51 DNACEPMELT VPSGQVVFNI KNNSGRKLEW EILKGVMVVD ERENIAPGLS
 101 DKMTVTLLPG EYEMTCGLLT NPRGKLVVTD SGFKDTANEA DLEKLSQPLA
 151 DYKAYVQGEV KELVAKTKTF TEAVKAGDIE KAKSLFADTR VHYERIEPIA
 201 ELFSELDPIV DAREDDFKDG AKDAGFTGFH RIEYALWVEK DVSGVKEIAA
 251 KLMTDVEALQ KEIDALAFPP GKVVGGASEL IEEVAGSKIS GEEDRYSHTD
 301 LSDFQANVDG SKKIVDLFRP LIEAKNKALL EKTDTNFKQV NEILAKYRTK
 351 DGFETYDKLG EADRKALQAS INALAEDLAQ LRILGLK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m595 / g595 95.4% identity in 388 aa overlap

	10	20	30	40	50	60
m595.pep	MRKFNLALS	VMLALGLTAC	QPPEAEKAAP	AASGEAQTAN	EGGSVSIAVN	DNACEPMELT
g595	MRKFNLALS	VMLALGLTAC	QPPEAEKAAP	AASGETQSAN	EGGSVGIADV	DNACEPMNLT
	10	20	30	40	50	60
	70	80	90	100	110	120

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m595.pep  VPSGQVVFNINNNSGRKLEWEILKGMVVDERENIAPGLSDKMTVTLLPGEYEMTCGLLT
          ||||||||||||||||||||||||||||||||||||||||: |||||||||||
g595      VPSGQVVFNINNNSGRKLEWEILKGMVVDERENIAPGLSDKMNRLNLLPGEYEMTCGLLT
          70      80      90      100     110     120

          130     140     150     160     170     180
m595.pep  NPRGKLVVTD SGFKDTANEADLEKLSQPLADYKAYVQGEVKELVAKTKTFTEAVKAGDIE
          |||||||: |||||||||||||||||||||||||||||||||||: |||||||
g595      NPRGKLVVADSGFKDTANEADLEKLQPLADYKAYVQGEVKELAAKTKTFTEAVKAGDIE
          130     140     150     160     170     180

          190     200     210     220     230     240
m595.pep  KAKSLFADTRVHYERIEPIAE L FSELD PVIDAREDDFKDGAKDAGFTGFHRIEYALWVEK
          ||||||| ||||||||||||||||||||||||||||||||||| |||||||
g595      KAKSLFAATRVHYERIEPIAE L FSELD PVIDACEDDFKDGAKDAGFTGFHRIEHALWVEK
          190     200     210     220     230     240

          250     260     270     280     290     300
m595.pep  DVSGVKEIAAKLMTDVEALQKEIDALAFPPGKVVGGA SELIEEVAGSKISGEEDRYSHTD
          ||||||| |||||||||||||||||||||||||||||||||||: |||||||
g595      DVSGVKETA AKLMTDVEALQKEIDALAFPPGKVVGGA SELIEEAAAGSKISGEEDRYSHTD
          250     260     270     280     290     300

          310     320     330     340     350     360
m595.pep  LSDFQANVDGSKKIVDLFRPLIEAKNKALLEKTD TNFKQVNEILAKYRTKDGFTYDKLG
          |||||||: ||||||||||||||||||||||||||||||||||| |||||||
g595      LSDFQANADGSKKIVDLFRPLIEAKNKALLEKTD TNFKQVNEILAKYRTKDGFTYDKLS
          310     320     330     340     350     360

          370     380     389
m595.pep  EADRKALQASINALAEDLAQLRGI LGLKX
          ||||||| |||||||||||||||||||
g595      EADRKALQAPINALAEDLAQLRGI LGLKX
          370     380

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1869>:

```

a595.seq
1  ATGAGAAAAT TCAATTGAC CGCATTGTCC GTGATGCTTG CCTTAGGTTT
51  GACCGCGTGC CAGCCGCGCG AGGCGGAGAA AGCTGCGCCG GCAGCGTCCG
101 GTGAGGCGCA AACCGCCAAC GAGGCGGTT CGGTCAGTAT CGCCGTCAAC
151 GACAAATGCC TCGAACCGAT GGAAGTACC GTGCCGAGCG GACAGGTTGT
201 GTTCAATATT AAAACAACA GCGGCCGCAA GCTCGAATGG GAAATCCTGA
251 AAGGCGTGAT GGTGGTGGAC GAGCGCGAAA ACATCGCCCC CGGACTTTCC
301 GATAAAATGA CCGTACCCCT GTTGCCGGGC GAATACGAAA TGA CT TGCGG
351 TCCTTTGACC AATCCGCGCG GCAAGCTGGT GGTAACCGAC AGCGGCTTTA
401 AAGACACCGC CAACGAAGCG GATTGGAAA AACTGTCCCA ACCGCTCGCC
451 GACTATAAAG CCTATGTTCA AGGCGAAGTC AAAGAGCTGG TGCGGAAAAC
501 CAAAACCTTT ACCGAAGCCG TCAAAGCAGG CGACATTGAA AAGGCGAAAT
551 CCCTGTTTGC CGACACCCGC GTCCATTACG AACGCATCGA ACCGATTGCC
601 GAGCTTTTCA GCGAACTCGA CCGGTCATC GATGCGCGTG AAGACGACTT
651 CAAAGACGGC GCGAAAGATG UCGGATTTAC CGGCTTCCAC CGTATCGAAT
701 ACGCCCTTTG GGTGGAAAAA GACGTGTCCG GCGTGAAGGA AATTGCAGCG
751 AAAGTATGTA CCGATGTCGA AGCCCTGCAA AAAGAAATCG ACGCATTGGC
801 GTTTCCTCCG GGCAAGGTGG TCGGCGGCGC GTCCGAAC TGTAAGAAG
851 TGGCGGGCAG TAAATCAGC GGCGAAGAAG ACCGGTACAG CCACACCGAT
901 TTGAGCGACT TCCAAGCCAA TGTGGACGGA TCGAAAAAAA TCGTCGATTT
951 GTTCCGTCGG TTGATCGAGA CAAAAACAA AGCCTTGTG GAAAAACCG
1001 ATACCAACTT CAAACAGGTC AACGAAATTC TGGCGAAATA CCGGACTAAA
1051 GACGGTTTGT AAACCTACGA CAAGCTGGGC GAAGCCGACC GCAAAGCGTT
1101 ACAGGCCTCT ATTAACGCGC TTGCCGAAGA CCTTGCCCAA CTTCGCGGCA
1151 TACTCGGCTT GAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1870; ORF 595.a>:

```

a595.pep
1  MRKENLTALS VMLALGLTAC QPPEAEKAAP AASGEAQTN EGGSVSIAVN
51  DNACEPMELT VPSGQVVFNI KNNSGRKLEW EILKGMVVVD ERENIAPLGS

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944

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101 DKMTVTLLPG EYEMTCGLLT NPRGKLVVTD SGFKDTANEA DLEKLSQPLA
151 DYKAYVQGEV KELVAKTKTF TEAVKAGDIE KAKSLFADTR VHYERIEPIA
201 ELFSELDPVI DAREDDFKDG AKDAGFTGFH RIEYALWVEK DVSGVKEIAA
251 KLMTDVEALQ KEIDALAFPP GKVVGASEL IEEVAGSKIS GEEDRYSHTD
301 LSDFQANVDG SKKIVDLFRP LIETKNKALL EKTDTNFKQV NEILAKYRTK
351 DGFETYDKLG EADRKALQAS INALAEDLAQ LRGILGLK*

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m595/a595 99.7% identity in 388 aa overlap

m595.pep	10	20	30	40	50	60
	MRKFNLTAHSVMLALGLTACQPPEAEKAAPAASGEAQTANEGGSVSIIVNDNACEPMELT					
a595	MRKFNLTAHSVMLALGLTACQPPEAEKAAPAASGEAQTANEGGSVSIIVNDNACEPMELT					
	10	20	30	40	50	60
m595.pep	70	80	90	100	110	120
	VPSGQVVFNIKNSGRKLEWEILKGMVVDERENIAPGLSDKMTVTLLPGEYEMTCGLLT					
a595	VPSGQVVFNIKNSGRKLEWEILKGMVVDERENIAPGLSDKMTVTLLPGEYEMTCGLLT					
	70	80	90	100	110	120
m595.pep	130	140	150	160	170	180
	NPRGKLVVTD SGFKDTANEA DLEKLSQPLADYKAYVQGEVKELVAKTKTFTEAVKAGDIE					
a595	NPRGKLVVTD SGFKDTANEA DLEKLSQPLADYKAYVQGEVKELVAKTKTFTEAVKAGDIE					
	130	140	150	160	170	180
m595.pep	190	200	210	220	230	240
	KAKSLFADTRVHYERIEPIAE L FSELDPVIDAREDDFKDGAKDAGFTGFHRIEYALWVEK					
a595	KAKSLFADTRVHYERIEPIAE L FSELDPVIDAREDDFKDGAKDAGFTGFHRIEYALWVEK					
	190	200	210	220	230	240
m595.pep	250	260	270	280	290	300
	DVSGVKEIAAKLMTDVEALQKEIDALAFPPGKVVGASELIEEVAGSKISGEEDRYSHTD					
a595	DVSGVKEIAAKLMTDVEALQKEIDALAFPPGKVVGASELIEEVAGSKISGEEDRYSHTD					
	250	260	270	280	290	300
m595.pep	310	320	330	340	350	360
	LSDFQANVDGSKKIVDLFRPLIEAKNKALLEKTDNFKQVNEILAKYRTK DGFETYDKLG					
a595	LSDFQANVDGSKKIVDLFRPLIETKNKALLEKTDNFKQVNEILAKYRTK DGFETYDKLG					
	310	320	330	340	350	360
m595.pep	370	380	389			
	EADRKALQAS INALAEDLAQLRGILGLKX					
a595	EADRKALQAS INALAEDLAQLRGILGLKX					
	370	380				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1871>:

g596.seq. (partial).

```

1  ..atgctgctct tggacgagcc gaccaaccac ttggatgcggy aatcggtgga
51  atggctggag caattcctcg tgcgcttccc cggcacagtg gtcgcggtaa
101 cgcacgaccg ctacttcctc gacaacgccg ccgaatggat ttggaactc
151 gaccgcggac acggcattcc gtggaaggc aattactcgt cttggctgga
201 gcagaaagaa aaacgcttgg aaaacgaggc gaaatccgaa gccgcgcgcg
251 tgaaggcgat gaagcaggaa ttggaatggg tgcgccaaaa tgccaaaggc
301 gcgcaagcca agcccaaagc gcgtttggcg cgttttgaag aaatgagcaa
351 ctacgaatac caaaaacgca acgaaactca ggaatcttt atccctgttg
401 ccgagcggtt gggtaacgaa gtgattgaat ttgtgaatgt ttccaaatcg

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945

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451   ttccggcgata aagtgtctga- tgacgggtttg agcttcaaa tgccggcggg
501   cgcgattgtc ggcacatcgc gcccgaaacg cgcgggtaaa tcgacgctgt
551   tcaaaatgat tgcgggcaaa gagcagcccg attcgggcga agtgaaaatc
601   gggcaaacgg tgaaaatgag cttgattgac caaagcccg aaggtttgca
651   aaacgacaaa accgtgttcg acaacattgc cgaaggctgc gatattttgc
701   aggtcggaca gtttgaaatc cccgcccgcc aatatttggg acgcttcaac
751   tttaaaggca gcgaccaaag caaaatcgca aggcagcttt ccggcggcga
801   acgcggccgt ctgcacttgg caaaaacctt gttgggcggc ggcaatgtgt
851   tgctgctgga cgaaccgtcc aacgatctcg acgtggaac cctgcgcgcg
901   ttggaagacg cattgttga atttgccgcg agcgtgatgg tgatttcgca
951   cgaccgctgg tttctcgacc gcatagccac gcatacttg gcgtgtgaag
1001  qcgactccaa atgggtgttc ttcgacgcga actatcaaga atacgaagcc
1051  gacaagaaac gccgactcgg caaagaaggc gcgaaaccga aacgcatcaa
1101  atacaaaccg gtaacgcgtt aa

```

This corresponds to the amino acid sequence <SEQ ID 1872; ORF 596.ng>:

g596.pep (partial).

```

1   ..MLLLDEPTNH LDAESVEWLE QFLVRFPQTV VAVTHDRYFL DNAAEWILEL
51  DRGHGIPWK NYSSWLEQKE KRLNEAKSE AARVKAMRQE LEWVRQNAKG
101 RQAKPKARLA RFEEMSNEY QKRNETQEIF IPVAERLNE VIEFVNVSKS
151 FGDKVLIDGL SFKVPAGAIV GIIGPNGAGK STLFKMIAGK EQPDSGEVKI
201 GQTVKMSLID QSREGLQNDK TVFDNIAEGR DILQVGQFEI PARQYLGRFN
251 FKSDSQSKIA RQLSGGERGR LHLAKTLLGG GNVLLDDEPS NDLDVETLRA
301 LEDALLEFAG SVMVISHDRW FLDRIATHIL ACEGDSKWVF FDGNYQEYEA
351 DKRRRLGKEG AKPKRIKYKP VTR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1873>:

m596.seq..

```

1   ATGTCCCAAC AATACGTCTA TTCTATGCTG CGCGTGAGCA AGGTTGTGCG
51  GCCGCAGAAA ACCATCATT AAGATATTTT CCTTCTTTT TTCCCCGGCG
101 CGAAAAATCGG CCTGCTCGGT TTGAACGGCG CGGGCAAGTC CACCGTGCTG
151 CGGATTATGG CGGGCGTGGA TAAGGAATTT GAGGGCGAAG CCGTGCCGAT
201 GGGCGGCATC AAAATCGGCT ACCTGCCGCA AGAGCCTGAG CTTGATCCGG
251 AAAAAACCGT GCGCGAGGAA GTGGAAAGCG GTTTGGGCGA AGTGGCTGCC
301 GCGCAGAAAC GTTTGGAAGA AGTGTATGCC GAGTACGCCA ATCTGTATGC
351 GGATTTTGAC GCGTTGGCAG AAGAGCAGGG CCGCTTGGA GCGATTATTG
401 CGGCAGGTTT GTCCACGGGC GCGGTGCGG AACACGAATT GGAAATCGCC
451 GCCGACGCGC TGCGCCTGCC GGAATGGGAT GCCAAATCG ATAATTTGTC
501 CGGCGGTGAA AACGCGCGCG TTGCCTTTGT CAAACTCTTG TTGAGCAAGC
551 CCGATATGCT TTTGCTGGAC GAGCCGACCA ACCACTTGA TGCGGAATCG
601 GTCGAGTGGC TGGAGCAATT TCTCGTGCGC TTCCCCGGCA CAGTCGTTGC
651 GGTAACGCAC GACCGCTACT TCCTCGACAA CGCCGCCGAA TGGATTTTGG
701 AACTCGACCG CGGCCATGGT ATTCCGTGGA AAGGCAATTA CTCGTCTTGG
751 CTGGAGCAGA AAGAAAAACG CTTGGAAGAA GAGGCAAAAT CCGAAGCCGC
801 GGGCGTGAAG GCGATGAAGC AGGAATTGGA ATGGGTGCGC CAAAATGCCA
851 AAGGCCGCCA AGCCAAGTCC AAAGCGCGTT TGGCTCGTTT TGAAGAAATG
901 AGCAACTACG AATACCAAAA ACGCAATGAA ACGCAGGAAA TCTTTATTCC
951 CGTTGCCGAG CGTTTGGGTA ACGAAGTGAT TGAATTTGTA AATGTTTCCA
1001 AATCGTTTCG CGATAAAGTG CTGATTGACG ATTTGAGCTT CAAAGTGCCT
1051 GCGGGCGCGA TTGTGCGCAT CATCGGCCCG AACGGCGCGG GTAAATCTAC
1101 GCTGTTCAAA ATGATTTCGG GCAAAGAGCA GCCTGATTCC GGCGAGGTGA
1151 AAATCGGACA AACCGTGAAA ATGAGCTTGA TTGACCAAAG CCGCGAAGGT
1201 TTGCAAAACG ACAAACCGT GTTCGACAAC ATTGCCGAG GCCGCGACAT
1251 TTTGCAGGTT GGTCAGTTTG AAATCCCGC CCGCAATAT TTGGGCGGTT
1301 TCAACTTCAA AGGCAGCGAC CAAAGCAAAA TTGCAGGTCA ATTGTCTGGC
1351 GGCGAAGCGG GTCGTCTGCA CTTGGCAAAA ACCTTGTTGA GCGCGGGCAA
1401 TGTATTGCTG CTGGATGAAC CGTCTAACGA CCTTGACGTG GAAACCCTGC
1451 GCGCGTTGGA AGACGCATTG TTGGAATTTG CCGGCAGCGT GATGGTGATT
1501 TCGCAGGACC GTTGGTTCCT CGACCGCATC GCCACGCATA TCTTGGCGTG
1551 TGAAGGCGAC TCTAAATGGG TGTTCTTCGA CGGCAACTAT CAGGAATACG
1601 AAGCCGACAA GAAACGCCGT TTGGGCGAAG AAGGCGCGAA ACCGAAACGC
1651 ATCAAATACA AACCGTAAC GCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1874; ORF 596>:

m596.pep..

946

```

1  MSQQYVYSML RVSKVVPQK TIIKDISLSF FPGAKIGLLG LNGAGKSTVL
51  RIMAGVDKEF EGEAVPMGGI KIGYLPQEPD LDPEKTVREE VESGLGEVAA
101 AQKRLEEVYA EYANPDADF ALAEEQGRLE AIIAAGSSTG GGAEHELEIA
151 ADALRLPEWD AKIDNLSGGE KRRVALCKLL LSKPDMLLD EPTNHLDAES
201 VEWLEQFLVR FPGTVVAVTH DRYFLDNAAE WILEDRGHG IPWKGNYSW
251 LEQEKRLN EAKSEAAVRK AMKQELWVR QNAKGRQAKS KARLARFEEM
301 SNYEYQKRNE TQEIFIPVAE RLGNEVIEFV NVSKSFGDKV LIDDLSEFKVP
351 AGAIVGIIGP NGAGKSTLFK MISGKEQPDG GEVKIGQTVK MSLIDQSREG
401 LQNDKTVFDN IAEGRDILQV GQFEIPARQY LGRFNFKGSD QSKIAGQLSG
451 GERGRHLAK TLLSGGNVLL LDEPSNDLDV ETLRALEDAL LEFAGSVMVI
501 SHDRWFLDRI ATHILACEGD SKWVFFDGNV QEYADKKRR LGEEGAKPKR
551 IKYKPVTR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m596 g596 98.4% identity in 373 aa overlap

```

          160      170      180      190      200      210
m596.pep  LPWDADAKIDNLSGGEKRRVALCKLLSKPDMLLDDEPTNHLDAESVWLEQFLVRFPGTV
          |||||
g596      MLLDDEPTNHLDAESVWLEQFLVRFPGTV
                  10      20      30

          220      230      240      250      260      270
m596.pep  VAVTHDRYFLDNAAEWILELDRGHGIPWKGNYSWLEQEKRLNEAKSEAAVRKAMKQE
          |||||
g596      VAVTHDRYFLDNAAEWILELDRGHGIPWKGNYSWLEQEKRLNEAKSEAAVRKAMKQE
                  40      50      60      70      80      90

          280      290      300      310      320      330
m596.pep  LEWVRQNAKGRQAKSKARLARFEEMSNEYEQKRNETQEIFIPVAERLGNEVIEFVNVSKS
          |||||
g596      LEWVRQNAKGRQAKPKARLARFEEMSNEYEQKRNETQEIFIPVAERLGNEVIEFVNVSKS
                  100     110     120     130     140     150

          340      350      360      370      380      390
m596.pep  FGDKVLIDDLSEFKVPAGAIVGIIGPNGAGKSTLFKMISGKEQPDGSEVKIGQTVKMSLID
          |||||
g596      FGDKVLIDGLSEFKVPAGAIVGIIGPNGAGKSTLFKMIAGKEQPDGSEVKIGQTVKMSLID
                  160     170     180     190     200     210

          400      410      420      430      440      450
m596.pep  QSREGLQNDKTVFDNIAEGRDILQVGQFEIPARQYLGFRNFKGSDQSKIAGQLSGGERGR
          |||||
g596      QSREGLQNDKTVFDNIAEGRDILQVGQFEIPARQYLGFRNFKGSDQSKIARQLSGGERGR
                  220     230     240     250     260     270

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947

	460	470	480	490	500	510
m596.pep	LHLAKTLLSGGNVLLDDEPSNDLDVETLRALEDALLEFAGSVMVISHDRWFLDRIATHIL					
g596	LHLAKTLLSGGNVLLDDEPSNDLDVETLRALEDALLEFAGSVMVISHDRWFLDRIATHIL					
	280	290	300	310	320	330
	520	530	540	550	559	
m596.pep	ACEGDSKWVFFDGNVQEYADKKRRLGEEGAKPKRIKYKPVTRX					
g596	ACEGDSKWVFFDGNVQEYADKKRRLGEEGAKPKRIKYKPVTRX					
	340	350	360	370		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1875>:

```

a596.seq
1  ATGTCCCAAC AATACGTCTA TTCTATGCTG CGCGTGAGCA AGGTGTGCGC
51  GCCGCAGAAA ACCATCATT AAGATATTTC CCTTTCTTTC TTCCCCGGCG
101 CGAAAATCGG TTTGCTCGGT TTGAACGGCG CGGGCAAGTC CACCGTGCTG
151 CGGATTATGG CGGGCGTGGG TAAAGAATTT GAGGGCGAAG CCGTGCCGAT
201 GGGCGGTATT AAAATCGGCT ACCTGCCGCA AGAGCCTGAG CTTGATCCGG
251 AAAAAACCGT GCGTGAGGAA GTGGAAAGCG GTTTGGGCGA AGTGGCTGCC
301 GCGCAGAAAC GTTTGGAGGA AGTGTATGCC GAGTACGCCA ATCCCGATGC
351 GGATTTTGAC GCGTTGGCGG AAGAGCAGGG GCGTTTGGA GCGATTATTG
401 CGGCGGGTTC GTCCACGGGC GCGGTGCGG AACACGAATT GGAAATCGCT
451 GCGGACGCGC TGGCCTGCC GGAATGGGAT GCCAAAATCG ATAATTTGTC
501 CGGCGGTGAA AAACGCCGCG TCGCTTTGTG CAAACTCTTG TTGAGCAAGC
551 CCGATATGCT TTTGCTGGAC GAGCCGACCA ACCACTTGGA TCGGAATCG
601 GTCGAGTGGC TGGAGCAATT TCTCGTGCGC TTCCCCGTA CAGTCGTTGC
651 CGTAACACAC GACCGCTACT TCCTCGACAA CGCCGCCGAA TGGATTTTGG
701 AACTCGACCG CGGGCACGGT ATTCCGTGGA AAGGAAATTA CTCGTCTTGG
751 TTGGAGCAGA AAGAAAAACG TTTGAAAAAC GAGGCGAAAT CCGAAGCCGC
801 GCGCGTGAAA GCGATGAAGC AGGAATTGGA ATGGGTGCGC CAAAATGCCA
851 AAGGCGGTCA AGCCAAGTCC AAAGCGCGTT TGGCGCGTT TGAAGAAATG
901 AGCAACTATG AATACCAAAA ACGCAATGAA ACGCAGGAAA TCTTCATTCC
951 CGTCGCCGAG CGTTTGGGTA ACGAAGTGAT TGAATTTGTG AATGTTTCCA
1001 AATCGTTCCG CGACAAAGTG CTGATTGACG ATTTGAGCTT CAAAGTGCCCT
1051 GCGGCGCGCA TTGTCGGCAT CATCGGTCCG AACGGCGCGG GTAAATCGAC
1101 ACTGTTTAAA ATGATTGCGG GCAAAGAGCA GCCCGATTCC GGTGAAGTGA
1151 AAATCGGGCA AACCGTGAAA ATGAGCTTGA TTGACCAAAG CCGCGAAGGT
1201 TTGCAAAACG ACAAACCGT GTTCGACAA ACCTTGTGG GTCGCCATAT
1251 TTTACAGGTC GGGCAGTTTG AAATCCCCG CCGCCAATAT TTGGGACGCT
1301 TCAATTTCAA AGGCAGCGAC CAAAGCAAAA TCACGGGGCA GCTTTCCGGC
1351 GGCGAACGCG GACGTTTGCA CTTGGCAAAA ACCTTGTGG GCGGTGGCAA
1401 TGTGTTGCTG CTGGACGAAC CGTCCAACGA CCTCGACGTG GAAACCTGCG
1451 GCGCGTTGGA AGACGCATTG CTGGAATTG CCGGCAGCGT GATGGTGATT
1501 TCGCACGACC GCTGGTTCCT CGACCGTATT GCTACGCATA TCTTGGCTTG
1551 CGAAGGCGAC TCCAATGGG TGTCTTTGA CGGCAACTAT CAGGAATACG
1601 AAGCCGACAA GAAACGCCGA CTCGGCGAAG AAGGCACGAA ACCGAAACGC
1651 ATCAAATACA AACCGGTAAC GCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1876; ORF 596.a>:

```

a596.pep
1  MSQQYVYSML RVSKVVPQK TTIKDISLSF FPGAKIGLLG LNGAGKSTVL
51  RIMAGVDKEF EGEAVPMGGI KIGYLPQEPE LDPEKTVREE VESGLGEVAA
101 AQKRLEEVYA EYANPDADF ALAEEQGRLE AIIAAGSSTG GGAHEHELEIA
151 ADALRLPEWD AKIDNLSGGE KRRVALCKLL LSKPDMLLLD EPTNHLDAES
201 VEWLEQFLVR FPGTVVAVTH DRYFLDNAEF WIEELDRGHG IPWKGNYSWS
251 LEQKEKRLN EAKSEAARVK AMKQELEWVR QNAKGRQAKS KARLARFEEM
301 SNYEYQKRNE TQEIFIPVAE RLGNIEVIEF NVSKSFGDKV LIDDLSFKVP
351 AGAIVGIIGP NGAGKSTLFK MIAGKEQPDS GEVKIGQTVK MSLIDQSREG
401 LQNDKTVFDN IAEGRDILQV GQFEIPARQY LGRFNFKGSQ QSKITGQLSG
451 GERGRLHLAK TLLGGGNVLL LDEPSNDLDV ETLRALEDAL LEFAGSVMVI
501 SHDRWFLDRI ATHILACEGD SKWVFFDGNV QEYADKKRRR LGEEGTPKPKR
551 IKYKPVTR*

```

m596/a596 99.3% identity in 558 aa overlap

948

	10	20	30	40	50	60
m596.pep	MSQQYVYSMLRVSKVVPQKTI IKDISLSFFPGAKIGLLGLNGAGKSTVLRIMAGVDKEF					
a596	MSQQYVYSMLRVSKVVPQKTI IKDISLSFFPGAKIGLLGLNGAGKSTVLRIMAGVDKEF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m596.pep	EGEAVPMGGIKIGYLPQEPELDPEKTVREEVESGLGEVAAAQKRLEEVYAEYANPDADFD					
a596	EGEAVPMGGIKIGYLPQEPELDPEKTVREEVESGLGEVAAAQKRLEEVYAEYANPDADFD					
	70	80	90	100	110	120
	130	140	150	160	170	180
m596.pep	ALAEQGRLEAIIAAGSSTGGGAHEHELEIAADALRLPEWDAKIDNLSGGEKRRVALCKLL					
a596	ALAEQGRLEAIIAAGSSTGGGAHEHELEIAADALRLPEWDAKIDNLSGGEKRRVALCKLL					
	130	140	150	160	170	180
	190	200	210	220	230	240
m596.pep	LSKPDMLLDPEPTNHLDAESVEWLEQFLVRFPGTVVAVTHDRYFLDNAAEWILEDRGHG					
a596	LSKPDMLLDPEPTNHLDAESVEWLEQFLVRFPGTVVAVTHDRYFLDNAAEWILEDRGHG					
	190	200	210	220	230	240
	250	260	270	280	290	300
m596.pep	IPWKGNYSWLEQKEKRLNEAKSEAARVKAMKQELEWVRQNAKGRQAKSKARLARFEEM					
a596	IPWKGNYSWLEQKEKRLNEAKSEAARVKAMKQELEWVRQNAKGRQAKSKARLARFEEM					
	250	260	270	280	290	300
	310	320	330	340	350	360
m596.pep	SNYEYQKRNETQEIFIPVAERLGNIEVIEFVNVSKSFGDKVLIDDLSEFKVPAGAIVGIIGP					
a596	SNYEYQKRNETQEIFIPVAERLGNIEVIEFVNVSKSFGDKVLIDDLSEFKVPAGAIVGIIGP					
	310	320	330	340	350	360
	370	380	390	400	410	420
m596.pep	NGAGKSTLFKMIISGKEQPDSEVKIGQTVKMSLIDQSREGLQNDKTVFDNIAEGRDILQV					
a596	NGAGKSTLFKMIAGKEQPDSEVKIGQTVKMSLIDQSREGLQNDKTVFDNIAEGRDILQV					
	370	380	390	400	410	420
	430	440	450	460	470	480
m596.pep	GQFEIPARQYLGRFNFKGSDQSKIAGQLSGGERGRHLAKTLLSGGNVLLDEPSNDLDV					
a596	GQFEIPARQYLGRFNFKGSDQSKITGQLSGGERGRHLAKTLLGGGNVLLDEPSNDLDV					
	430	440	450	460	470	480
	490	500	510	520	530	540
m596.pep	ETLRALEDALLEFAGSVMVISHDRWFLDRIATHILACEGDSKWVFFDGNVQYEYADKKRR					
a596	ETLRALEDALLEFAGSVMVISHDRWFLDRIATHILACEGDSKWVFFDGNVQYEYADKKRR					
	490	500	510	520	530	540
	550	559				
m596.pep	LGEEGAKPKRIKYPVTRX					
a596	LGEEGTPKRIKYPVTRX					
	550					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1877>

g597.seq

1 ATGCTGCTTC ATGTCAGCAA TTCCCTCAAA CAGCTTCAGG AAGAGCGTAT
51 CCGCCAAGAA CGTATCCGCC AAGAGCGTAT CCGTCAGGCG CGCGGCAACC
101 TTGCTTCCGT CAACCGCAA CAGCGCGAGG CTTGGGACAA ATTCCAAAAA

949

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151 CTCAATACCG AGCTGAACCG TTTGAAAACG GAAATCGCCG CTACGAAAGC
201 GCAGATTTCG CGTTTCGTAT CGGGGAACTA TAAAAACAGC CGGCCGAATG
251 CGGTTGCCCT GTTCCTGAAA AACGCCGAAC CGGGTCAGAA AAACCGCTTT
301 TTGCGTTATA CGCGTTATGT AAACGCCTCC AATCGGGAAG TTGTCAAGGA
351 TTTGGAAAAA CAGCAGAAGG CTTTGGCGGT ACAAGAGCAG AAAATCAACA
401 ATGAGCTTGC CCGTTTGAAG AAAATTCAGG CAAACGTGCA ATCCCTGCTG
451 AAAAAACAGG GTGTAACCGA TCGCGCGGAA CAGACGGAAA GCCCGAGACA
501 GAATGCCAAA ATCTCCAAAG ATGCCGAAA ACTGCTGGAA CAGAAAGGGA
551 ACAGAGCAGCA GCTGAACAAG CTCTTGAGCA ATTTGgagaa aaaaaaagcc
601 gaacaccgCA TTcaygAtgc: ygAagcaaaA agaAATTGG CTGAaycCaa
651 actGgcggca gccgAAAAAG CCAGAAAAGA AGCGGCGCAG CAGAAGGCTG
701 AAGCGCGCAGG TCGCGAAATG TCCAACCTGA CCGCCGAAGA CAGGAACATC
751 CAAGCGCCTT CGGTTATGGG TATCGGCAGT GCCGACGgTT TCAGCCGCAT
801 GCAGGGACGT TTGAAAAAAC CGGTTGACGG TGTGCCGACC GGGCTTTTTCG
851 GGCAGAACCG GAGCGGcggc GATGTTTGA AAGGCGTgTT CTATTCCACT
901 GCGCCTGCAA CGGTTGAAAG CATTGCGCcg gGAACggtaa GCTATGCGGA
951 cgaGTTGGAC GGCTACGGCA AAGTGGTCTG GATCGATCAC GGCGAGAATC
1001 ACATCAGCAT CTATGCCGGT TTGAGCGAAA TTTCGCCCG CAAGGGTTAT
1051 AAGGTCGCGG CAGGAAGCAA AATCGGCAG AGCGGTCGCG TGCCGGACGG
1101 GGAAGAGGGG CTTTACCTGC AAATACGTGA TCGAGGTCAG GTGTTGAACC
1151 CTTCCGGGCTG GATACGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1878; ORF 597>:

```

g597.pep
1  MLLHVSNSLK QLQEEIRIQE RIRQERIROA RGNLASVNRK QREAWDKFQK
51  LNTLNLRLKT EVAATKAQIS RFVSGNYKNS RPNVALFLK NAEFGQKNRF
101 LRYTRVYNAS NREVVKDLEK QQKALAVQEQ KINNELARLK KIQANVQSLL
151 KKQGVTDAAE QTESRRQNAK ISKDARKLLE QKGNEQQLNK LLSNLEKXKA
201 EHRIQDAEAK RKLAEAKLAA AEKARKEAAG QKAEARRRAE SNLTAEDRNI
251 QAPSVMGIGS ADGFSRMQGR LKKPVDGVPT GLFGQNRSGG DVWKGVFYST
301 APATVESIAP GTVSYADELD GYGKVVVIDH GENYISIIYAG LSEISAGKGY
351 TVAAGSKIGT SGSLPDGEEG LYLOIRYRGQ VLNPSGWIR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1879>:

```

m597.seq
1  ATGCTGCTTC ATGTCAGCAA TTCCCTCAAA CAGCTTCAGG AAGAGCGTAT
51  CCGCCCAAGAG CGTATCCGTC AGGCGCGCGG CAACCTTGCT TCCGTCAACC
101 GCAAAACAGCG CGAGGCTTGG GACAAGTTCC AAAAATCAA TACCGAGCTG
151 AACCGTTTGA AAACGGAAGT CGCCGCTACG AAAGCGCAGA TTTCCCGTTT
201 CGTATCGGGG AACTATAAAA ACAGCCAGCC GAATCGCGTT GCCCTGTTCC
251 TGAAAAACGC CGAACCAGGT CAGAAAAACC GCTTTTTCG TTATACGCGT
301 TATGTAAACG CCTCCAATCG GGAAGTTGTC AAGGATTGGA AAAAAACGCA
351 GAAGGCTTTG GCGGTACAAG AGCAGAAAAT CAACAATGAG CTTGCCCGTT
401 TGAAGAAAAA TCAGGCAAAAC GTGCRATCTC TGCTGAAAAA ACAGGGGTGA
451 ACCGATGCGG CGGAACAGAC GGAAGCCGCG AGACAGAATG CCAAAATCGC
501 CAAAGATGCC CGAAAACTGC TGAACAGAAA AGGGAACGAG CAGCAGCTGA
551 ACAAGCTCTT GAGCAATTG GAGAAGAAAA AGGCCGAACA CCGCATTCAG
601 GATGCGGAAG CAAAAAGAAA ATTGGCTGAA GCCAGACTGG CGGCAGCCGA
651 AAAAGCCAGA AAAGAACGGG CGCAGCAGAA GGCTGAAGCA CGACGTGCGG
701 AAATGTCCAA CCTGACCGCC GAAGACAGGA ACATCCAAGC GCCTTCGGTT
751 ATGGGTATCG GCAGTGCCGA CGGTTTCAGC CGCATGCAAG GACGTTTGAA
801 AAAACCGGTT GACGGTGTGC CGACCGGACT TTTCCGGCAG AACCGGAGCG
851 GCGGCGATAT TTGGAAGAGC GTGTTCTATT CCACTGCACC GGCACCGGTT
901 GAAAGCATTG CGCCGGGAAC GGTAAGCTAT GCGGACGAGT TGGACGGCTA
951 CGGCAAAATG GTCGTGGTGC ATCAGGGCGA GAACTACATC AGCATCTATG
1001 CCGGTTTGAG CGAAATTTCC GTCGGCAAGG GTTATATGGT CGCGGCAGGA
1051 AGCAAAATCG GCTCGAGCGG GTCGCTGCCG GACGGGGAAG AGCGGCTTTA
1101 CCTGCAAAAT CGTTATCAAG GTCAGGTATT GAACCTTCG AGCTGGATAC
1151 GTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1880; ORF 597>:

```

m597.pep
1  MLLHVSNSLK QLQEEIRIQE RIRQARGNLA SVNRRQREAW DKFQKLNTL
51  NRLKTEVAAT KAQISRFVSG NYKNSOPNAV ALFLKNAEPG QKNRFLRYTR
101 YVNASNREVV KDLEKQKAL AVQEQKINNE LARLKKIQAN VQSLLKKQGV
151 TDAAEQTESR RQNAKIAKDA RKLLEQKGNE QQLNKLNSL EKKKAEHRIQ
201 DAEAKKKLAE ARLAAAEKAR KEAAQQAEEA RRAEMSNLTA EDRNIQAPSV
251 MGIGSADGFS RMQGRKKPV DGVPTGLFGQ NRSGGDIWKG VFYSTAPATV
301 ESIAPGTVSY ADELDTGKGV VVDHGENYI SIYAGLSEIS VGKGYMVAAG
351 SKIGSSGSLP DGEEGLYLQI RYQGQVLNPS SWIR*

```

950

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 597 shows 96.1% identity over a 389 aa overlap with a predicted ORF (ORF 597) from *N. gonorrhoeae*:

```
m597/g597 96.1% identity in 389 aa overlap

      10      20      30      40      50      60
g597.pep MLLHVSNSLKQLQEERIRQERIRQERIRQARGNLASVNRKQREAWDKFQKLNTELNRLKT
          |||||
m597      MLLHVSNSLKQLQEERIRQ-----ARGNLASVNRKQREAWDKFQKLNTELNRLKT
          10      20      30      40      50

      70      80      90     100     110     120
g597.pep EVAATKAQISRFSVSGNYKNSRPNNAVALFLKNAEPGQKNRFLRYTRYVNASNREVVKDLEK
          |||||
m597      EVAATKAQISRFSVSGNYKNSQPNNAVALFLKNAEPGQKNRFLRYTRYVNASNREVVKDLEK
          60      70      80      90     100     110

      130     140     150     160     170     180
g597.pep QOKALAVOEQKINNELARLKKIQANVQSLLKKQGVTDAAEQTESRRQNAKISKDARKLLE
          |||||
m597      COKALAVOEQKINNELARLKKIQANVQSLLKKQGVTDAAEQTESRRQNAKIAKDARKLLE
          120     130     140     150     160     170

      190     200     210     220     230     240
g597.pep QKGNFQQLNKLLSNLEKKKAHRIQDAEAKRKLAEAKLAAAEKARKEAAQQAEEARRAEM
          |||||
m597      QKGNFQQLNKLLSNLEKKKAHRIQDAEAKRKLAEAKLAAAEKARKEAAQQAEEARRAEM
          180     190     200     210     220     230

      250     260     270     280     290     300
g597.pep SNLTAEDRNIQAPSVMGIGSADGFSRMQGRLLKRPVDPVPTGLFGQNRSGGDVWKGVFYST
          |||||
m597      SNLTAEDRNIQAPSVMGIGSADGFSRMQGRLLKRPVDPVPTGLFGQNRSGGDIWKGVFYST
          240     250     260     270     280     290

      310     320     330     340     350     360
g597.pep APATVESIAPGTVSYADELDGYGKVVVIDHGENYISIIYAGLSEISAGKGYTVAAGSKI GT
          |||||
m597      APATVESIAPGTVSYADELDGYGKVVVIDHGENYISIIYAGLSEISVKGKGYMVAAGSKIGS
          300     310     320     330     340     350

      370     380     390
g597.pep SSSLPDGEEGLYLQIRYRGQVLPNSGWIRX
          |||||
m597      SSSLPDGEEGLYLQIRYRGQVLPNSGWIRX
          360     370     380
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1881>

```
a597.seq
1  ATGCTGCTTC ATGTCAGCAA TTCCCTCAAG CAGCTTCAGG AAGAGCGTAT
51  CCGCCAAGAA CGTATCCGCC AAGAGCGTAT CCGTCAGGCG CGCGGCAACC
101 TTGCTTC CGT CAACCGCAA CAGCGCGAGG CTTGGGACAA GTTCCAAAA
151 CTCAATACCG AGCTGAACCG TTTGAAAACG GAAGTCGCCG CTACGAAAGC
201 GCAGATTTC CGTTTCGTAT CGGGGAAC TA AAAACAGC CAGCCGAATG
251 CGGTGCCCT GTTCCTGAAA AACGCCGAAC CGGTCAGAA AAACCGCTT
301 TTGCGTTATA CGCGTTATGT AAACGCCCTCC AATCGGGAAG TTGTCAGGA
351 TTTGGAAAAA CAGCAGAAGG CTTTGGCGGT ACAAGAGCAG AAAATCAACA
401 ATGAGCTTGC CCGTTTGAAG AAAATTCAGG CAAACGTGCA ATCCCTGCTG
451 AAAAAACAGG GTGTAACCGA TCGGCGCGAA CAGACGGAAA GCCGCAGACA
501 GAATGCCAAA ATGCCCAAAG ATGCCCGAAA ACTGCTGGAA CAGAAAGGGA
551 ACGAGCAGCA GCTGAACAAG CTCTTGAGCA ATTGGAGAA GAAAAAGGCC
601 GAACACCGCA TTCAGGATGC GGAAGCAAAA AAAAAATTGG CTGAAGCCAG
651 ACTGGCGGCA CGCGAAAAAG CCAGAAAAAG AGCGGCGCAG CAGAAGGCTG
701 AAGCAGCAGC TCGGGAATG TCCAACCTGA CCGCCGAAGA CAGGAACATC
751 CAAGCGCCTT CGTTATGGG TATCGGCAGT GCCGACGGT TCAGCCGCAT
801 GCAGGACGT TTGAAAAAAC CGGTGACGG TGTGCCGACC GGACTTTTCG
851 GGCAGACCG GAGCGCGGC GATGTTTGA AAGCGGTGTT CTATTCCACT
901 GCACCGCAA CGGTTGAAAG CATTCGCCG GGAACGGTAA GCTATGCGGA
```

951

```

951 CGAGTTGGAC GGCTACGGCA AAGTGGTCGT GGTGATCAC GCGGAGAACT
1001 ACATCAGCAT CTATGCCGGT TTGAGCGAAA TTTCCGTCGG CAAGGGTTAT
1051 ATGTCGCGG CAGGAAGCAA AATCGGCTCG AGCGGGTCGC TGCCGGACGG
1101 GGAAGAGGGG CTTTACCTGC AAATACGTTA TCAAGGTCAG GTATTGAACC
1151 CTTGAGCTG GATACGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1882; ORF 597.a>:

```

a597.pep
1  MLLHVSNSLK QLQEERIRQE RIRQERIRQA RGNLASVNRK QREAWDKFQK
51  LNTELNRLKT EVAATKAQIS RFVSGNYKNS QPNAVALFLK NAEFGQKNRF
101 LRYTRYVNAS NREVVKDLEK QQKALAVQEQ KINNELARLK KIQANVQSL
151 KKQGVTDAAE QTESRRQNAK IAKDARKLLE QKGNEQQLNK LLSNLEKKKA
201 EHRIQDAEAK RKLAEARLAA AEKARKEAAQ QKAEARRAEM SNLTAEDRNI
251 QAPSVMGIGS ADGFSRMQGR LKKPVDGVPT GLFGQNRSGG DVWKGVFYST
301 APATVESIAP GTVSYADELD GYGKVVVDH GENYISIIYAG LSEISVGKGY
351 MVAAGSKIGS SGSLPDGEEG LYLQIRYQGQ VLPSSWIR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 597 shows 98.5% identity over a 389 aa overlap with a predicted ORF (ORF 597) from *N. meningitidis*

m597/a597 98.5% identity in 389 aa overlap

	10	20	30	40	50	60
a597.pep	MLLHVSNSLKQLQEERIRQERIRQARGNLASVNRKQREAWDKFQKLNTELNRLKT					
m597	MLLHVSNSLKQLQEERIRQERIRQ-----ARGNLASVNRKQREAWDKFQKLNTELNRLKT					
	10	20	30	40	50	
	70	80	90	100	110	120
a597.pep	EVAATKAQISRFVSGNYKNSQPNAVALFLKNAEFGQKNRFLRYTRYVNASNREVVKDLEK					
m597	EVAATKAQISRFVSGNYKNSQPNAVALFLKNAEFGQKNRFLRYTRYVNASNREVVKDLEK					
	60	70	80	90	100	110
	130	140	150	160	170	180
a597.pep	QQKALAVQEQKINNELARLKKIQANVQSLKKQGVTDAAEQTESRRQNAKIAKDARKLLE					
m597	QQKALAVQEQKINNELARLKKIQANVQSLKKQGVTDAAEQTESRRQNAKIAKDARKLLE					
	120	130	140	150	160	170
	190	200	210	220	230	240
a597.pep	QKGNEQQLNKLLSNLEKKKAEHRIQDAEAKRKLAEARLAAAEKARKEAAQKAEARRAEM					
m597	QKGNEQQLNKLLSNLEKKKAEHRIQDAEAKRKLAEARLAAAEKARKEAAQKAEARRAEM					
	180	190	200	210	220	230
	250	260	270	280	290	300
a597.pep	SNLTAEDRNIQAPSVMGIGSADGFSRMQGRLLKKPVDGVPTGLFGQNRSGGDVWKGVFYST					
m597	SNLTAEDRNIQAPSVMGIGSADGFSRMQGRLLKKPVDGVPTGLFGQNRSGGDIWKGVFYST					
	240	250	260	270	280	290
	310	320	330	340	350	360
a597.pep	APATVESIAPGTVSYADELDGYGKVVVDHGENYISIIYAGLSEISVGKGYMVAAGSKIGS					
m597	APATVESIAPGTVSYADELDGYGKVVVDHGENYISIIYAGLSEISVGKGYMVAAGSKIGS					
	300	310	320	330	340	350
	370	380	390			
a597.pep	SGSLPDGEEGLYLQIRYQGQVLPSSWIRX					
m597	SGSLPDGEEGLYLQIRYQGQVLPSSWIRX					
	360	370	380			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1883>:

```
g601.seq
1  ATGTTCCCAA CCGCAATTT GGTCGACGAA ATTGATGTGC CGAATATAGG
51  TCGTCTGAAA GCCACGCTCA TCAACGCGGG CATTCCGACC GTTTTCCTGA
101 ACGCCGCCGA CTTGGGCTAC ACGGCAAAG AGTTGCAGGA CGACATCAAC
151 AACGATGCCG CCGCGCTGGA AAAATTTGAA ACCATCCGCG CATATGGCGC
201 GCTGAAAATG GGTGTGATCA GCGACGTATC CGAAGCCGCC GCCCGCGCGC
251 GCACGCCGAA ACCCGCCTTC GTCGCGCCCG CCGCCGATTA CACCGCCTCC
301 AGCGGCAAAA CCGTAAACGC CGCCGACATC GATTTGCCGG TACGCGCCCT
351 GAGCATGGGC AAATGCAACC ACGCTATGAT GGGCATCGCC TCGGTGCCCA
401 TCGCCGCCGC CGTGCTCGGT ACGCTGGTCA ACCTTGCCGC AGGCGGCGGA
451 ACGCGTAAAG AAGTGCCTT CCGGCATCCG TCAGGTACGC TCGGTGTCGG
501 TGCTGCCGCG GAATGTCAGG ACGGACAATG GACGCCGCGc aaagcggta
551 tgaGCCGCAG CGCACgctg attatggaaa gttgGGTGCg cgttcccgat
601 gattGTTTTT GA
```

This corresponds to the amino acid sequence <SEQ ID 1884; ORF 601.ng>:

```
g601.pep
1  MFPTGNLVDE IDVPNIGRLK ATLINAGIPT VFLNAADLGY TGKELQDDIN
51  NDAAALEKFE TIRAYGALKM GLISDVSEAA ARARTPKPAF VAPAADYTAS
101 SGKTVNAADI DLPVRALSMG KLHHAMMGIA SVAIAAAVLG TLVNLAAGGG
151 TRKEVRFGHP SGTLRVGAAA ECQDQGWTA KAVMSRSARV IMESWVRVPD
201 DCF*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1885>:

```
m601.seq
1  ATGTTCCCAA CCGCAATTT GGTCGATGAA ATTGATGTGC CGAATATAGG
51  CCGTTTGAAA GCCACGCTCA TCAACGCGGG CATTCCGACC GTTTTCCTGA
101 ATGCCGCCGA CTTGGGCTAC ACAGGCAAAG AGTTGCAAGA CGACATCAAC
151 AACGATGCCG CGGCTTTGGA AAAATTCGAG AAAATCCGCG CTTACGGTGC
201 GCTGAAAATG GGTCTGATCA GCGACGTATC CGAAGCTGCC GCTCGCGCGC
251 ACACGCCGAA AGTCGCCTTC GTCGCGCCCG CCGCCGATTA CACCGCCTCC
301 AGTGGCAAAA CCGTGAACGC CGCCGACATC GATTGCTGG TACGCGCCCT
351 GAGCATGGGC AAATGCAACC ACGCGATGAT GGGTACCGCC TCTGTGCCA
401 TTGCGACCGC CGCCGCCGTA CCGGTACGC TGGTCAACCT TGCCGCAGGC
451 GGCGGAACGC GTAAAGAAAGT GCGCTTCGGG CATCCTCCG GCACATTGCG
501 CGTCGGTGCA GCCGCCGAAT GTCAGGACGG ACAATGGACG GCCACCAAAG
551 CGGTCAATGAG CCGTAGCGCA CGCGTGATGA TGAAGGTTG GGTACGGGTG
601 CCTGAGGATT GTTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1886; ORF 601>:

```
m601.pep
1  MFPTGNLVDE IDVPNIGRLK ATLINAGIPT VFLNAADLGY TGKELQDDIN
51  NDAAALEKFE KIRAYGALKM GLISDVSEAA ARAHTPKVAF VAPAADYTAS
101 SGKTVNAADI DLLVRALSMG KLHHAMMGTA SVAIATAAAV PGTLVNLAAG
151 GGTRKEVRFH HPSGTLRVGA AAECQDQWT ATKAVMSRSA RVMMEGWVRV
201 PEDCF*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 601 shows 94.1% identity over a 205 aa overlap with a predicted ORF (ORF 601.ng) from *N. gonorrhoeae*:

m601/g601

	10	20	30	40	50	60
m601.pep	MFPTGNLVDEIDVPNIGRLKATLINAGIPTVFLNAADLGYTGKELQDDINNDAAALEKFE					
g601	MFPTGNLVDEIDVPNIGRLKATLINAGIPTVFLNAADLGYTGKELQDDINNDAAALEKFE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m601.pep	KIRAYGALKMGLISDVSEAAARAHTPKVAFVAPAADYTASSGKTVNAADIDLLVRALSMG					

953

```

|||||
g601      TIRAYGALKMGLISDVSEAAARATPKPAFVAPAADYTASSGKTVNAADIDLVRALSMG
              70      80      90      100     110     120

              130     140     150     160     170     180
m601.pep  KLHHAMMGTA SVAIATAAAVPGTLVNLAAGGGTRKEVRFHPSGTLRVGAAAECDGQWT
|||||
g601      KLHHAMMGIA SVAI--AAAVLGTLVNLAAGGGTRKEVRFHPSGTLRVGAAAECDGQWT
              130     140     150     160     170

              190     200
m601.pep  ATKAVMSRSARVMMEGWVRVPEDCFX
|||
g601      AAKAVMSRSARVIMESWVRVPDDCFX
              180     190     200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1887>:

```

a601.seq
1  ATGTTCCCAA CCGGCAAITT GGTGATGAA ATTGATGTGC CGAATATAGG
51  CCGTTTGAAA GCCACGCTCA TCAACGCGGG CATTCCGACC GTTTTCCTGA
101 ATGCCGCCGA CTTGGGCTAC ACGGGCAAAG AGTTGCAAGA CGACATCAAC
151 AACGATGCCG CAGCTTTGGA AAAATTCGAG AAAATCCGCG CTTACGGTGC
201 GCTGAAAATG GGTCTGATCA GCGACGTATC CGAAGCTGCC GCCCGCGCGC
251 ACACGCCGAA AGTCGCCTTC GTCGCGCCCG CCGCCGATTA CACCGCCTCC
301 AGTGGCAAAA CCGTGAATGC CGCCGACATC GATTTGCTGG TACGCGCCCT
351 GAGCATGGGC AAATTGCACC ACGCGATGAT GGGTACCGCC TCTGTTGCCA
401 TTGCGACCGC CGCCGCCGTG CCCGGTACGC TGGTCAACCT TGCCGCAGGC
451 GCGGGAACGC GTAAAGAAGT GCGCTTCGGG CATCCTTCCG GCACATTGCG
501 CGTCGGTGCA GCCGCCGAAT GTCAGGACGG ACAATGGACG GCCACCAAAG
551 CGGTTATGAG CCGCAGCGCA CGCGTGATGA TGGAAGGTTG GGTCAAGGTG
601 CCGGAAGATT GTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1888; ORF 601.a>:

```

a601.pep
1  MFPTGNLVDE IDVPNIGRLK ATLINAGIPT VFLNAADLGY TGKELQDDIN
51  NCAAALEKFE KIRAYGALKM GLISDVSEAA ARAHTPKVAF VAPAADYTAS
101 SGKTVNAADI DLLVRALSMG KLHHAMMGTA SVAIATAAAV PGTLVNLAAG
151 GSTRKEVRFH HPSGTLRVGA AAECQDGQWT ATKAVMSRSA RVMMEGWVRV
201 PEDCF*

```

m601/a601 100.0% identity in 205 aa overlap

```

              10      20      30      40      50      60
m601.pep  MFPTGNLVDEIDVPNIGRLKATLINAGIPTVFLNAADLGYTGKELQDDINNDAALEKFE
|||||
a601      MFPTGNLVDEIDVPNIGRLKATLINAGIPTVFLNAADLGYTGKELQDDINNDAALEKFE
              10      20      30      40      50      60

              70      80      90      100     110     120
m601.pep  KIRAYGALKMGLISDVSEAAARAHTPKVAFVAPAADYTASSGKTVNAADIDLLVRALSMG
|||||
a601      KIRAYGALKMGLISDVSEAAARAHTPKVAFVAPAADYTASSGKTVNAADIDLLVRALSMG
              70      80      90      100     110     120

              130     140     150     160     170     180
m601.pep  KLHHAMMGTA SVAIATAAAVPGTLVNLAAGGGTRKEVRFHPSGTLRVGAAAECDGQWT
|||||
a601      KLHHAMMGTA SVAIATAAAVPGTLVNLAAGGGTRKEVRFHPSGTLRVGAAAECDGQWT
              130     140     150     160     170     180

              190     200
m601.pep  ATKAVMSRSARVMMEGWVRVPEDCFX
|||||
a601      ATKAVMSRSARVMMEGWVRVPEDCFX
              190     200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1889>:

```
g602.seq
1  ATGTTGCTCC ATCAATGCGA CAAAGCGCGA CATATGCGTC CCTTTCTGCT
51  CGGCGGGCAG ATAAACCGTC ATCGTCAGGC GAGCAACCGT GGATTGTGTT
101 CCTTCGGCGG TTTTCAGGGT AATCGGGAAG CGCAGGTCTT TAATGCCGAC
151 CTGATTGATC GGCAGGTTGC GCAAATCTCT GCTGGATTGC ACGTCTGCAA
201 TGGCGTTCAT GCGTTGTTT TCCTTAATAT TCAGATAATT ATTGAGATGT
251 GTGTATTGTA TGGCAGGcag atgccgtctg aAAAAacgct gtcggCCGCC
301 TGCCTGCAAA Tgcgagatta TATCACTTGC TTTtggcgcg TGCATTGA
```

This corresponds to the amino acid sequence <SEQ ID 1890; ORF 602.ng>:

```
g602.pep
1  MLLHQCDKAR HMRPFLGGQ INRHRQASNR GLCSFGGFQG NREAQVFNAD
51  LIDRQIAQIS AGLHVCNGVH ALFVLNIQII IEMCVLYGRQ MPSEKTLsAA
101 CLQMRDYITC FWRlh*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1891>:

```
m602.seq
1  ATGTTGCTCC ATCAATGCGA CAAAGCGCGA CATATGCGTC CCCTTCTGCT
51  CAGCAGGCAG GTAAACCGTC ATGGTCAGAC GGGCAATGGT GGACTGGATG
101 CCTTCTGCAG TTTGCAGGGT AATCGGAAAG CGCAGGTCTT TGATACCGAC
151 CTGATTGATC GGCAGATTGC GCAAATCTCG GCTGGATTGC ACGTCTGCAA
201 TAGTGTTTCAT GAGTTGTTT TCCTTAATAT TCATGTAATT GTTGAGATGT
251 GTGCATGGTA TGGCGTTTCC GCCGGGGAAT ATACCGTCAA TCTGCAAATG
301 CGAGATTATA TCACTCGCTT TTAGCAGCTG CATTGA
```

This corresponds to the amino acid sequence <SEQ ID 1892; ORF 602>:

```
m602.pep
1  MLLHQCDKTR HMRPLLSRQ VNRHGQTGNG GLDAFCSLQG NRKAQVFDTD
51  LIDRQIAQIS AGLHVCNSVH ELFFLNHVI VEMCAWYGVS AGEYTVNLQM
101 RDYITRF*QL H*
```

m602/g602 65.2% identity in 115 aa overlap

	10	20	30	40	50	60
m602.pep	MLLHQCDKTRHMRPLLSRQVNRHGQTGNGGLDAFCSLQGNRKAQVFDTDLIDRQIAQIS					
	: : : :: : : : : : : : : : :					
g602	MLLHQCDKARHMRPFLGGQINRHRQASNRGLCSFGGFQGNREAQVFNADLIDRQVAQIS					
	10	20	30	40	50	60
	70	80	90	100	110	
m602.pep	AGLHVCNSVHELFFLNHVI VEMCAWYGVSAGEYTVN---LQMRDYITRF*QLHX					
	: : : : : : : : : : : : : :					
g602	AGLHVCNGVHALFVLNIQII IEMCVLYGRQMPSEKTLsAACLQMRDYITCFWRlhX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1893>:

```
a602.seq
1  ATGTTGCTCC ATCAATGCGA CAAAGCGCGA CATATGCGTA CCCTTCTGCT
51  CGGCAGGCAG GTAAACCGTC ATGGTCAGAC GGGCAACTGT GGACTGGATG
101 CCTTCTGCAG TTTGCAGGGT AATCGGAAAG CGCAGGTCTT TGATACCGAC
151 CTGATTGATC GGCAGATTGC GCAAATCTCG GCTGGATTGC ACGTCTGCAA
201 TAGTGTTTCAT GAGTTGTTT TCCTTAATAT TCATGTAATT GTTGAGATGT
251 GTGCATGGTA TGGCGTTTCC ACCGGGGAAT ATACCGTCAA TCTGCAAATG
301 CGAGATTATA TCACTCGCTT TTAGCAGCTG CATTGA
```

This corresponds to the amino acid sequence <SEQ ID 1894; ORF 602.a>:

```
a602.pep
1  MLLHQCDKAR HMRTLLGRQ VNRHGQTGNC GLDAFCSLQG NRKAQVFDTD
51  LIDRQIAQIS AGLHVCNSVH ELFFLNHVI VEMCAWYGVS TGEYTVNLQM
101 RDYITRF*QL H*
```

m602/a602 95.5% identity in 111 aa overlap

955

	10	20	30	40	50	60
m602.pep	MLLHQCDKTFHMRPLLSRQVNRHGQTGNNGGLDAFCSLQGNRKAQVFDTDLIDRQIAQIS					
a602	MLLHQCDKARHMRPLLSRQVNRHGQTGNNGGLDAFCSLQGNRKAQVFDTDLIDRQIAQIS					
	10	20	30	40	50	60
	70	80	90	100	110	
m602.pep	AGLHVCNSVHELFFLNHIVIVEMCAWYGVVSAGEYTVNLQMRDYITRFQLHX					
a602	AGLHVCNSVHELFFLNHIVIVEMCAWYGVSTGEYTVNLQMRDYITRFQLHX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1895>:

g603.seq

```

1   ATGGATTCCC GCCTGCGTGG GAATGACGCT AGGAAATACG GCATACGCTT
51  TGCCCAAAGA GGCCGTCTGA AACACACTCC GCCCAACGCC CATCCTTTT
101 CAGACGGCCC CGCACCAAAA AAACAACCAC AAATAACAAG GAGAAACATC
151 ATGTCCGACC AACTCATTCT TGTCCTGAAC TGCGTCAGTT CATCGCTCAA
201 AGGCGCCGTT ATCGACCGCA AAAGCGGCAG CGTCGTCCTA AGCTGCCTCG
251 GGGAAACGCTT GACTACGCCC GAAGCCGTCA TTACCTTCAA CAAAGACGGC
301 AACAAACGCC AAGTTCCTCT GAGCGGCCGC AACTGCCACG CCGCGCGCGT
351 GGGTATGCTG TTGAACGAAC TGGAAAAACA CGGACTGCAC GACCGCATCA
401 AAGCCATCGG CCGCCGCATC GCCCAGGCGC GCGAAAAATA TCACGAGTCC
451 GTCCTCATCG ACCAAGACGT CCTTGACGAA CTGAAAGCCT GCATCCCGTT
501 CGCCCGCGTG CACAACCCCG CCAACATCAG CGGCATCCTC GCCGCGCAGG
551 AACACTTTCC CGGCCTGCCC AACGTCGGCG TGATGGACAC CTCGTTCCAC
601 CAAACCATGC CGGAGCGGGC CTACACTTAT GCCGTGCCGC GCGAATTGCG
651 CAAAAAATAC GCCTTCCGCC GCTACGGTTT CCACGGTACC GGTATGCGTT
701 ACGTCGCCCC TGAAGCCGCA CGCATCTTGG GCAAACCTct ggaaGACATC
751 CGCATGATTA TTGCCCACTT AGGCAACGGC GCATCTATTA CCGCCGTCAA
801 AAACGGCAAA TCCGTCGATA CCGGTATGGG TTTACGCGCG ATCGAAGGTT
851 TGGTAATGGG TACAGTTTGC GGCACACCG ATCCGGGCGT ATACAGCTAT
901 CCGACTTTCC ACGCAGGGAT GGATGTTGCC CAAGTTGATG AAATGCTGAA
951 CGAAAAATCA GGTTCCTCCG GTATTTCCga actTCCCAAC GACTGCCGCA
1001 CCCTCGAAAT CGCCGCCGAC GAAGGCCGCG AAGCGCGCGC CCTCGCCCTc
1051 gaAGTCATGA CCTGCCGCTT CGCCAAATAC ATCGCTTCGA TGGCTGTGGC
1101 CTGCGGCAGT GTTGACGCAC TCGTGTTTAC CGCGGTATC GGCAGAAACT
1151 CGCGTAATAT CCGTGCCAAA ACCGTTTCTT ATCTTGATT CTGGGTCTG
1201 CATATCGACA CCAAAGCCAA TATGGAAAAA CGTACGGCA ATTCCGGCAT
1251 TATCAGCCCG ACCGATTCTT CTCGGCTGT TTTGGTCGT CCGACCAATG
1301 AAGAACTGAT GATTGCCTGC GACACTGCCG AACTTGCCGG CATCTTGTAG

```

This corresponds to the amino acid sequence <SEQ ID 1896; ORF 603.ng>:

g603.pep

```

1   MDSRLRGND RYKIRFAQR GRLKHTPPNA HPFSDGPAPK KQPOTTRNI
51  MSDQLILVLN CVSSSLKGAV IDRKSGSVVL SCLGERLTTP EAVITFNKDG
101 NKRQVPLSGR NCHAGAVGML LNELEKHGLH DRIKAIGRRI AHGGEKYHES
151 VLIDQDVLDE LKACIPFAPL HNPANISGIL AAQEHFPLP NVGVMDTSFH
201 QTMPERAYTY AVPRELRKKY AFRRYGFHGT GMRYVAPEAA RILGKPLEDI
251 RMIIAHLNG ASITAVKNGK SVDTGMGFTP IEGLVMGTRC GDTDPGVYSY
301 PTFHAGMDVA QVDEMLNEKS GFPGISLPLN DCRTLEIAAD EGREGARLAL
351 EVMTCRLAKY IASMAVACGS VDALVFTGGI GENSRNIRAK TVSYLDLFLG
401 HDTKANMEK RYGNSGIISP TDSSPAVLVV PTNEELMIAC DTAEALGIL*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1897>:

m603.seq

```

1   CTGTCTCTGC GTAGGCGGGG ACGGAATAAC GATAGAAAAT GCGGCATACG
51  CTTTGCCCAA AGAGGCCGTC TGAAACACCT TGCGCCTGAT GTCTGC.CTT
101 TTTCAGACGA CCCCACTA AAAAAACAAC CACAACTAC AAGGAGAAAC
151 ATCATGTCCG ACCAACTCAT CCTCGTTCTG AACTGCGGCA GTTCATCGCT
201 CAAAGGCGCC GTTATCGACC GAmAAAGCGG CAGCGTCGTC CTAAGCTGCC
251 TCGCGCAACG cCtGACCAG CCCGAAGCCG TCATTACGTT CAACAAAGAC

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301 GGCAACAAAC GCCAAGTTCC CCTGAGCGGC CGAAATTGCC ACGCCGGCGC
351 GGTGGGTATG CTTTGAACG AACTGGAAAA ACACGGTCTG CACGACCGCA
401 TCAAAGCCAT CGGCCACCGC ATCGCCACG GCGGCGAAAA ATACAGCGAG
451 TCTGTTTGA TCGACCAGGC CGTAATGGAC GAACTCAATG CCTGCATTCC
501 GCTTGCGCCG CTGCACAACC CCGCCAACAT CAGCGGCATC CTGCGCCGAC
551 AGGAACATTT CCCCGGTCTG CCAATGTGCG GCGTGATGGA TACTTCGTTC
601 CACCAAACCA TGCCGGAGCG TGCTACACT TATGCCGTGC CGCGCGAGTT
651 GCGTAAAAAA TACGCTTTCC GCCGCTACGG TTTCCACGGC ACCAGTATGC
701 GTTACGTTGC CCTGAAGCC GCACGCATCT TGGGCAAACC TCTGGAAGAC
751 ATCCGCATGA TTATTGCCCA CTAGGCAAC GGCGCATCCA TTACCGCCAT
801 CAAAAACGGC AAATCCGTCG ATACCASTAT GGGTTTCACG CCGATCGAAG
851 GTTGTGTAAT GGGTACACGT TCGGCGGACA TCGATCCGGG CGTATACAGC
901 TATCTGACTT CCCACGCCGG GATGGATGTT GCCCAAGTGG ATGAAATGCT
951 GAACAAAAAA TCAGGTTTGC TCGGTATTTC CGAACTTTCC AACGACTGCC
1001 GCACCCCTCGA AATCGCCGCC GACGAAGGCC ACGAAGGCGC GCGCCTCGCC
1051 CTCGAAGTCA TGACCTACCG CCTCGCCAAA TACATCGCTT CGATGGCTGT
1101 GGGCTGCGGC GCGTTGACG CACTCGTGT T CACCGGCGGT A7CGGCGAAA
1151 ACTCGCGTAA TATCCGTGCC AAAACCGTTT CCTATCTTGA TTTCTTGGGT
1201 CTGCACATCG ACACCAAAGC CAATATGAA AAACGCTACG GCAATTCGGG
1251 CATTATCAGC CCGACCGATT CTCTCCGGC TGTTTTGGTT GTCCCGACCA
1301 ATGAAGAACT GATGATTGCC TGCGACACTG CCGAACTTGC CGGCATCTTG
1351 TAG

```

This corresponds to the amino acid sequence <SEQ ID 1898; ORF 603>:

m603.pep

```

1 LSSRRRGRNN DRKCGIRFAQ RGRLKHLAPD VCXFSDDPTL KKQPQTTRRN
51 IMSDQLILVL NCGSSSLKGA VIDRXSGSVV LSCGLGERLTT PEAVITFNKD
101 GNKRQVPLSG RNCHAGAVGM LLNELEKHGL HDRIKAIGHR IAHGGEKYSE
151 SVLIDQAVMD ELNACIPLAP LHNPNANISGI LAAQEHFPGL PNVGVMDTSF
201 HQTMPERAYT YAVPRELRKK YAFRRYGFHG TSMRYVAPEA ARILGKPLED
251 IRMIIAHLGN GASITAIKNG KSVDTSMGFT PIEGLVMGTR CGDIDPGVYS
301 YLTSHAGMDV AQVDEMLNKK SLLLGISELS NDCRTLEIAA DEGHEGARLA
351 LEVMTYRLAK YIASMAVCGC GVDALVFTGG IGNSRNIRA KTVSYLDFLG
401 LHIDTKANME KRYGNSGIIS PTDSSPAVLV VPTNEELMIA CDTAELAGIL
451 *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 603 shows 91.6% identity over a 450 aa overlap with a predicted ORF (ORF 603.ng) from *N. gonorrhoeae*:

m603/g603

```

          10      20      30      40      50      60
m603.pep  LSSRRRGRNDRKCGIRFAQRGRLKHLAPDVCXFSDDPTLKKQPQTTRRNIMSDQLILVL
          ::||| || |:: || ||||| ||||| ||:: ||| |:: ||||| ||||| |||||
g603      MDSRLRG-NDARKYGIRFAQRGRLKHTPPNAHPFSDGPAPKKQPQTTRRNIMSDQLILVL
          10      20      30      40      50

          70      80      90      100     110     120
m603.pep  NCGSSSLKGAVIDRXSGSVVLSCLGERLTTPEAVITFNKDGNKRVPLSGRNCHAGAVGM
          || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g603      NCVSSSLKGAVIDRKSGSVVLSCLGERLTTPEAVITFNKDGNKRVPLSGRNCHAGAVGM
          60      70      80      90      100     110

          130     140     150     160     170     180
m603.pep  LLNELEKHGLHDRIKAIGHRIAHGGEKYSESVLIDQAVMDENACIPLAPLHNPNANISGI
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g603      LLNELEKHGLHDRIKAIGHRIAHGGEKYHESVLIDQDVLDELKACIPFAPLHNPNANISGI
          120     130     140     150     160     170

          190     200     210     220     230     240
m603.pep  LAAQEHFPGLPNVGVMDTSFHTQTMPERAYTYAVPRELRKKYAFRRYGFHGTSMRYVAPEA
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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g603	LAAQEHFPGLPNVGVMDTSFHQTMPERAYTYAVPRELRKKYAFRRYGFHGTGMRYVAPEA	180	190	200	210	220	230
m603.pep	ARILGKPLEDIRMIIAHLGNGASITAIKNGKSVDTSMGFTPIEGLVMGTRCGDIDPGVYS	250	260	270	280	290	300
g603	ARILGKPLEDIRMIIAHLGNGASITAVKNGKSVDTGMGFTPIEGLVMGTRCGDIDPGVYS	240	250	260	270	280	290
m603.pep	YLTSHAGMDVAQVDEMLNKKSGLLGISLSNDCRTLEIAADEGHEGARLALEVMYTRLAK	310	320	330	340	350	360
g603	YPTFHAGMDVAQVDEMLNEKSGFPGISLPNDCRTLEIAADEGREGARLALEVMTCRLAK	300	310	320	330	340	350
m603.pep	YIASMAVCGGVDALVFTGGIGENSRNIRAKTVSYLDFLGLHIDTKANMEKRYGNSGIIS	370	380	390	400	410	420
g603	YIASMAVACGSVDALVFTGGIGENSRNIRAKTVSYLDFLGLHIDTKANMEKRYGNSGIIS	360	370	380	390	400	410
m603.pep	PTDSSPAVLVVPTNEELMIACDTAELAGILX	430	440	450			
g603	PTDSSPAVLVVPTNEELMIACDTAELAGILX	420	430	440	450		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1899>:

```

a603.seq
1  CTGTCTCTCGC GTAGGCGGGG ACGGAATAAC GATAGAAAAT GCGGCATACG
51  CTTTGCCCAA AGAGGCCGTC TGAAACACAC TCCGCCCAAC GCCCATCCTT
101 TTTCAGACGA CCCACACC. AAAAAACAAC CACAACTAC AAGGAGAAAC
151 TTTGATCTCG ACCAACTCAT TCTGTCTG AACTGCGGCA GTTCATCGCT
201 CAAAGGTGCC GTTATCGACC GCAAAGCGG CAGCGTCGTC CTAAGCTGCC
251 TCGGCGAACG CCTGACCACG CCGAAGCCG TCATTACGTT CAGCAAAGAC
301 GGCAACAAAC GCCAAGTTCC CCTGAGCGGC CGGAATGCC ACGCCGGCGC
351 GTGGGGTATG CTGTTGAACG AACTGGAAAA ACACGAACTG CACGACCGCA
401 TTCAAGCCGT CGGCCACCGC ATCGCCACG GCGGCGAAAA ATACAGCGAG
451 TCTGTTTTGA TCGACCAGGC CGTAATGGAC GAACTCAATG CCTGCATTCC
501 GCTTGCGCCG CTGCACAACC CCGCCAACAT CAGCGGCATC CTCGCCSCAC
551 AGGAACATTT CCCCGGTCTG CCAATGTG GCGTGATGGA TACTTCGTTT
601 CACCAAACCA TGCCGGAGCG TGCCTACACT TATGCCGTGC CGCGCGAGTT
651 GCGTAAAAAA TACGCTTTCC GCGCTACGG TTTCCACGGC ACCAGTATGC
701 GTTACGTTGC CCCTGAAGCC GCATGCATCT TGGGCAAAAC TCTGGAAGAC
751 ATCCGCATGA TTATTGCCCA CTIAGGCAAC GGCGCATCCA TTACCGCCAT
801 CAAAAACGGC AAATCCGTG ATACCAGTAT GGGTTTCACG CCGATCGAAG
851 GTTTGGTAAT GGTACGCGC TCGGCGGATA TCGACCCGGG CGTATACAGC
901 TATCTGACTT CACACGCCGG TTTGATGTT GCACAAGTTG ATGAAATGCT
951 GAATAAAAAA TCAGGCTTGC TCGGTATTTC CGAACTCTCC AACGACTGCC
1001 GCACCCTCGA AATCGCCGCC GACGAAGGCC ACGAAGGCGC GCGCCTCGCC
1051 CTCGAAGTTA TGACCTACCG CCTCGCCAAA TACATCGCTT CGATGGCTGT
1101 GGGCTGCGGC GCGGTGACG CACTCGTGTT CACCGCGCGT ATCGGCGAAA
1151 ACTCGCGTAA TATCCGTGCC AAAACCGTTT CCTATCTTGA TTTCTTGGGT
1201 CTGCACATCG ACACCAAGC CAATATGAA AAACGCTACG GCAATTCGGG
1251 TATTATCAGC CCGACCGATT CTCTCCGGC TGTCTTGETT GTCCCGACCA
1301 ATGAAGAACT GATGATTGCC TCGGACACTG CCGAACTTGT CGGCATCTTG
1351 TAG

```

This corresponds to the amino acid sequence <SEQ ID 1900; ORF 603.a>:

```

a603.pep
1  LSSRRRGRNN DRKCGIRFAQ RGRLLKHTPPN AHPFSDDPTX KKQPQTTRRN
51  IMSDQLILVL NCGSSSLKGA VIDRKSGSVV LSCLGERLTT PEAVITFSKD
101 GNKRQVPLSG RNCHAGAVGM LLNELEKHEL HDRIQAVGHR IAHGGEKYSE
151 SVLIDQAVMD ELNACIPLAP LFNPNANISGI LAAQEHFPGL PNVGVMDTSF

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958

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201  HQTMPERAYT YAVPRELRKK YAFRRYGFHG TSMRYVAPEA ACILGKPLED
251  IRMIIAHLGN GASITAIKNG KSVDTSMGFT PIEGLVMGTR CGDIDPGVYS
301  YLTSHAGLDV AQVDEMLNKK SGLLGISELS NDCRTLEIAA DEGHEGARIA
351  LEVMTYRLAK YIASMAVGCG GVDALVFTGG IGNSRNIRA KTVSYLDFLG
401  LHIDTKANME KRYGNSGIIS PTDSSPAVLV VPTNEELNIA CDTAELVGIL
451  *

```

m603/a603 96.7% identity in 450 aa overlap

```

          10      20      30      40      50      60
m603.pep  LSSRRRGRNDRKCGIRFAQRGLKHLAPDVCXFSDDPTLKKQPQTTRRNIMSDQLILVL
a603      LSSRRRGRNDRKCGIRFAQRGLKHTPPNAHPFSDDPTXKKQPQTTRRNIMSDQLILVL
          10      20      30      40      50      60

          70      80      90      100     110     120
m603.pep  NCGSSSLKGAVIDRXSGSVVLSCLGERLTTP EAVITFNKDGNGKRVPLSGRNCHAGAVGM
a603      NCGSSSLKGAVIDRXSGSVVLSCLGERLTTP EAVITFSKDGNGKRVPLSGRNCHAGAVGM
          70      80      90      100     110     120

          130     140     150     160     170     180
m603.pep  LLNELEKHGLHDRIKAIGHRIAHHGGEKYESVLI DQAVMDELNACIPLAPLHPANISGI
a603      LLNELEKHGLHDRIQAVGHRIAHHGGEKYESVLI DQAVMDELNACIPLAPLHPANISGI
          130     140     150     160     170     180

          190     200     210     220     230     240
m603.pep  LAAQEHFPGLPNVGVMDSFHHQTMPERAYTYAVPRELRKKYAFRRYGFHGTSMRYVAPEA
a603      LAAQEHFPGLPNVGVMDSFHHQTMPERAYTYAVPRELRKKYAFRRYGFHGTSMRYVAPEA
          190     200     210     220     230     240

          250     260     270     280     290     300
m603.pep  ARILGKPLEDIRMIIAHLGN GASITAIKNGKSVDTSMGFTPIEGLVMGTRCGDIDPGVYS
a603      ACILGKPLEDIRMIIAHLGN GASITAIKNGKSVDTSMGFTPIEGLVMGTRCGDIDPGVYS
          250     260     270     280     290     300

          310     320     330     340     350     360
m603.pep  YLTSHAGMDVAQVDEMLNKKSGLLGISELSNDCRTLEIAADEGHEGARLALEVMTYRLAK
a603      YLTSHAGLDVAQVDEMLNKKSGLLGISELSNDCRTLEIAADEGHEGARLALEVMTYRLAK
          310     320     330     340     350     360

          370     380     390     400     410     420
m603.pep  YIASMAVGCGGVDALVFTGGIGENSRNIRAKTVSYLDFLGLHIDTKANMEKRYGNSGIIS
a603      YIASMAVGCGGVDALVFTGGIGENSRNIRAKTVSYLDFLGLHIDTKANMEKRYGNSGIIS
          370     380     390     400     410     420

          430     440     450
m603.pep  PTDSSPAVLVVPTNEELMIACDTAELAGILX
a603      PTDSSPAVLVVPTNEELMIACDTAELVGILX
          430     440     450

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1901>:

g604.seq

```

1  ATGCCCGAAG CGCACTTCTT TACGCGTTCC GCCGCCTGCG GCAAGGTGGA
51  CCAGCGTACC GAGCACGGCG GCGGCGATGG CGACCGAGGC GATGCCCATC
101 ATAGCGTGGT GCAGTTTGCC CATGCTCAGG GCGCGTACCG GCAAATCGAT
151 GTCGCGCGCG TTTACGGTTT TGCGCTGGA GCGGTGTAA TCGGCGGCGG
201 GCGCGACGAA GCGGGTTTC GCGTGCGCG GCGGGCGGC GGCTTCGGAT

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959

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251  ACGTCGCTGA TCAAACCCAT TTTCAGCGCG CCATATGCGC GGATGGTTTC
301  AAATTTTTC AGCGCGGCGG CATCGTTGTT GATGTCGTCC TGCAACTCTT
351  TGCCCGTGTA GCCCAAGTCG GCGGCGTTCA GGAAAACGGT CGGAATGCCC
401  GCGTTGATGA GCGTGGCTTT CAGACGACCT ATATTCGGCA CATCAATTTT
451  CTCGACCAAA TTGCCGGTTG GGAACATACT GCCTTcgcCG TCGGCTGGAT
501  CTAA

```

This corresponds to the amino acid sequence <SEQ ID 1902; ORF 604.ng>:

g604.pep

```

1  MPEAHFFTRS AACGKVDQRT EHGGDGDGRG DAHHSVVQFA HAQGAYRQID
51  VGGVYGFAAG GGVIGGGRDE GGFRRARAGG GFGYVADQTH FORAICADGF
101 KFFQRGIVV DVVLQLFARV AQVGVQENG RNARVDERGF QTTYIRHINF
151 VDQIAGWEHT AFAVGWI*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1903>:

m604.seq

```

1  ATCCCGAAG CGCACTTCTT TACGCGTTCC GCCGCTGCG GCAAGGTTGA
51  CCAGCGTACC GGGTACGGCG GCGGCGGTCG CAATGGCAAC AGAGGCGGTA
101 CCCATCATCG CGTGGTGCA GTTGCCATG CTCAGGGCGC GTACCAGCAA
151 ATCGATGTCG GCGGCGTTCA CGGTTTGGC ACTGGAGGCG GTGTAATCGG
201 CGGCGGGCGC GACGAAGGCG ACTTTCGGCG TGTGCGCGCG AGCGGCAGCT
251 TCGGATACGT CGCTGATCAG ACCCATTTTC AGCGCACCGT AAGCGCGGAT
301 TTTCTCGAAT TTTTCAAAG CCGCGGCATC GTTGTGTGATG TCGTCTTGCA
351 ACTCTTTGCC TGTGTAGCCC AAGTCGGCGG CATTCAAGAA AACGGTCGGA
401 ATGCCCGCGT TGATGAGCGT GGCTTTCAA CGGCCTATAT TCGGCACATC
451 AATTTCATCG ACCAAATTGC CGGTTGGGAA CATACTGCCT TCGCCGTCGG
501 CTGGATC

```

This corresponds to the amino acid sequence <SEQ ID 1904; ORF 604>:

m604.pep

```

1  MPEAHFFTRS AACGKVDQRT GYGGGGRNGN RGGTHHRVVQ FAHAQGAYQQ
51  IDVGGVHGFA TGGGVIGGGR DEGDFFRVRA SGSFGYVADQ THFORTVSAD
101 FLEFFQSRGI VVDVVLQLFA CVAQVGGIQE NGRNARVDER GFQTAYIRHI
151 NFIDQIAGWE HTAFVGWI

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 604 shows 83.4% identity over a 169 aa overlap with a predicted ORF (ORF 604.ng)

from *N. gonorrhoeae*:

m604/g604

	10	20	30	40	50	60
m604.pep	MPEAHFFTRS AACGKVDQRTGYGGGGRNGNRGGTHHRVVQFAHAQGAYQQIDVGGVHGFA					
g604	MPEAHFFTRS AACGKVDQRTBHGGG--DGDGRDAHHSVVQFAHAQGAYRQIDVGGVYGFA					
	10	20	30	40	50	
	70	80	90	100	110	120
m604.pep	TGGGVIGGGRDEGDFFRVRASGSFGYVADQTHFORTVSADFLEFFQSRGIVVDVVLQLFA					
g604	AGGGVIGGGRDEGGFRRARAGGFGYVADQTHFORAICADGFKFFQRGIVVDVVLQLFA					
	60	70	80	90	100	110
	130	140	150	160	169	
m604.pep	CVAQVGGIQENGRNARVDERGFQTAYIRHINFIDQIAGWEHTAFVGWI					
g604	RVAQVGGVQENGRNARVDERGFQTTYIRHINFVDQIAGWEHTAFVGWIX					
	120	130	140	150	160	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1905>:

a604.seq

```

1  ATCCCGAAG CGCACTTCTT TACGCGTTCC GCCGCTGCG GCAAGGTTGA
51  CCAGCGTACC GGGCACGGCG GCGGCGGTCG CAATGGCAAC AGAGGCGGTA
101 CCCATCATCG CGTGGTGCAA TTGCCCCATG CTCAGGGCGC GTACCAGCAA
151 ATCGATGTCG GCGGCATTCA CGGTTTGGC ACTGGAGGCG GTGTAATCGG

```


960

```

201 CGGCGGGCGC GACGAAGGCG ACTTTCGGCG TGTGCGCGCG GCGGGCAGCT
251 TCGGATACGT CGCTGATCAG ACCCATTTTC AGCGCACCGT AAGCGCGGAT
301 TTTCTCGAAT TTTTCCAAAG CTGCGGCATC GTTGTGTGATG TCGTCTTGCA
351 ACTCTTTGCC CGTGTAGCCC AAGTCGGCGG CATTCAAGAA AACGGTCGGA
401 ATGCCCCGCGT TGATGAGCGT GSCCTTCAAA CGGCCTATAT TCGGCACATC
451 AATTTCATCG ACCAAATTGC CAGTTGGGAA CATACTGCCT TCGCCGTCGG
501 CTGGATCAAG AAATTCGATT TGTACTTCGG CTGCCGGGAA CGTTACGCCG
551 TCGAGCTCAA AATCGCCTGT TTCCAAACT GCGCCGTTTT GCATCGGTAC
601 ATGGGCAATA ATGGTTTTCG CGATGTTTTT CTGCCAGATT TTGACTGTGC
651 AGATGCCGTC TGA

```

This corresponds to the amino acid sequence <SEQ ID 1906; ORF 604.a>:

```

a604.pep
1  MPEAHFFTRS AACGKVDQRT GHGGGGRNGN RGGTHHRVVQ FAHAQGAYQQ
51  IDVGGIHGFA TGGGVIGGGR DEGDFRRVRA GGSFGYVADQ THFQRTVSAD
101 FLEFFQSCGI VVDVVLQLEA RVAQVGGIQE NGRNARVDER GFQTAYIRHI
151 NFIDQIAGWE HTAFVGVWIK KFDLYFGCRE RYAVELKIAC FQNCVHLHRY
201 MGNGFADVF LPDFDCADAV *

```

m604/a604 97.0% identity in 169 aa overlap

	10	20	30	40	50	60
m604.pep	MPEAHFFTRS AACGKVDQRTGYGGGGRNGNRGGTHHRVVQFAHAQGAYQQIDVGGVHGFA					
a604	MPEAHFFTRS AACGKVDQRTGHGGGGRNGNRGGTHHRVVQFAHAQGAYQQIDVGGIHGFA					
	10	20	30	40	50	60
m604.pep	TGGGVIGGGRDEGDFRRVRASGSFGYVADQTHFQRTVSADFLFFQSRGIVVDVVLQLEA					
a604	TGGGVIGGGRDEGDFRRVRAGGSFGYVADQTHFQRTVSADFLFFQSCGIVVDVVLQLEA					
	70	80	90	100	110	120
m604.pep	CVAQVGGIQENGRNARVDERGFQTAYIRHINFIDQIAGWEHTAFVGVWIK					
a604	RVAQVGGIQENGRNARVDERGFQTAYIRHINFIDQIAGWEHTAFVGVWIKKFDLYFGCRE					
	130	140	150	160	169	
m604.pep	CVAQVGGIQENGRNARVDERGFQTAYIRHINFIDQIAGWEHTAFVGVWIK					
a604	RVAQVGGIQENGRNARVDERGFQTAYIRHINFIDQIAGWEHTAFVGVWIKKFDLYFGCRE					
	130	140	150	160	170	180
a604	RYAVELKIACFQNCVHLHRYMGNGFADVFLPDFDCADAVX					
	190	200	210	220		

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1907>:

```

g605.seq
1  ATGATGACCG AAATGCAACA ACGCGCCCAA CTGCACCGCC AAATTGGA
51  AATCGCCGAC GAAGTACGCG GCGCGGTGGA TGGCTGGGAC TTTAAACAAT
101 ACGTTCTCGG CACACTTTTC TACCGCTTTA TCAGCGAAAA CTTACCGGAC
151 TATATGCAGG CCGGCGACAG CAGCATTGAT TACGCGGCTa tGCCGGACAG
201 CATCATCAGC CCCGAAATCA AAGACGATgc cgtcaaagtc aaAGGCTATT
251 TCATCtaccC cgGCCAGCTT TTTTgcaata ttgccgcga agCCATCAA
301 AACGAAGAGC TCAACACCAA GCTGAAAGaa atCTTTACCG CGATTGAAAG
351 CTCCGCCTCC GGCTAcccgT CCGAACAAAG CATCAAAGGC TTGTTTGACG
401 ACTTCgACAC CACCAGCAGC CGGCTCGGCA GCACCGTTGC CGACAAAAAC
451 AAACGCCTTG CCGCCGTCCT TAAAGGCGTG GCGGAACTCG ATTTCCGCAA
501 TTTTGAAGAC CACCGCATCG ACCTTTTCGG TGATGCCTAC GAATACCTGA
551 TTTCCAACTA CGCcgcaAC GCAGGCAAAAT CCGGCGGCGA ATTTTTCACC
601 CCGCAAAGCG TCTCCAAGCT GATTGCGCGG CTGGCGGTGC ACGGGCAGGA
651 GAAAGTCAAC AAAATCTACG ACCCCGCTG CGGCTCGGGC AGCCTGCTCT
701 TGCAGGCGAA AAAACAGTTT GACGAACACA TCATCGAAGA AGGCTTCTTC
751 GGGCAGGAAA TCAACCACAC CACCTACAAC CTCGCCGCA TGAATATGTT
801 TCTGCACAAC GTCAATTACA ACAAAATCCA CATCGAATTG GGCACACGC
851 TGACCAACCC CAAACTCAAA GACAGCAAAC CCTTTGATGC CGTCGTCTCC
901 AATCCGCCCT ATTCCATCGA CTGGATAGGC AGCGACGACC CCACCTtgaT

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961

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951 CAACGACGAC CGCTTTGCCC CCGCAGGCGT ACTCGCACCG AAATCCAAAG
1001 CCGATTTTGC CTTTCATCCTG CACGCACTGA ACTACCTTTC CGGCAGAGGC
1051 CGCGCCGCTA TCGTCTCATT CCCCGGCATT TTCTATCGCG GCGGCGCAGA
1101 GCAGAAAATC CGCCAATATC TGGTGGAGGG CAACTATGTG GAAACCGTGA
1151 TTGCCCTTGC GCCCAATCTC TTTTACGGCA CCTGCATCGC CGTCAATATC
1201 CTGGTTTTGT CCAAACACAA AGACAATACC GACATCCAAT TCATCGACGC
1251 AAGCGGCTTC TTTAAAAAAG AAACCAACAA CAACGTCTTA ACCGAAGAAC
1301 ACATTGCCGA AATCGTCAAA CTCTTCGCCG ACAAAGCCGA TGTGCCGCAT
1351 ATCGCCCAAA ACGCCGCCCA GCAAACCGTC AAAGACAACG GCTACAACCT
1401 CGCGTCAGC AGCTATGTCG AAGCCGAAGA CACCCGCGAG GTCATCGACA
1451 TCAGCAGCT CAACGCCGAA ATCAGCGAAA CCgtcgCcaa AATCGAACGG
1501 CTGCGGCGTG AAATTGACGA AGTGATTGCA GAGATTGAAA CCTAG

```

This corresponds to the amino acid sequence <SEQ ID 1908; ORF 605.ng>:

g605.pep

```

1 MMTEMQORAQ LHRQIWKIAD EVRGAVDGDW FKQYVLGTLF YRFISENFTD
51 YMQAGDSSID YAAMPDSIIT PEIKDDAVKV KGYFIYPGQL FCNIAAEAHQ
101 NEELNNTKLKE IFTAISSAS GYPSEQGIKG LFDDFDTTSS RLGSTVADKN
151 KRLAAVLKGV AELDFGNFED HRIDLFGDAY EYLISNYAAN AGKSGGEFFT
201 PQSVSKLIAR LAVHGOEKVN KIYDPACGSG SLLIQAQKQF DEHIEEGFF
251 GQENHHTTYN LARMNMFLHN VYNKFIHEL GDTLTNPCLK DSKPFDVAVS
301 NPPYSIDWIG SDDPTLINDD RFAPAGVLAP KSKADFAPIL HALNYLSGRG
351 RAALVSFPGI FYRGGAEOKI RQYLVEGNYV ETVIALAPNL FYGTCIAVNI
401 LVLKHKHNT DIQFIDASGF FKKETNNNL TEEHIAEIVK LFADKADVPH
451 IAQNAAQQTV KNGYNLAVS SYVEAEDTRE VIDIRQLNAE ISETVAKIER
501 LRREIDEVIA EIET*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1909>:

m605.seq

```

1 ATGATGACCG AAATGCAACA ACGCGCCCAA CTGCACCGCC AAATTGGAA
51 AATTGCCGAC GAAGTACGCG GCGCGGTGGA TGGCTGGGAC TTAAACAAT
101 ACGTTCTCGG CACACTTTTC TACCGCTTTA TCAGCGAAAA CTTCACCGAC
151 TATATGCAGG CAGGCGACAG CAGTATTGAT TACGCGGCTA TGCCGGACAG
201 CATCATCACC CCCGAAATCA AAGACGATGC CGTCAAAGTT AAAGGCTATT
251 TCATCTACCG CGGCAGCTT TTTGCAATA TTGCCGCCGA AGCCCATCAA
301 AACGAAGAGC TCAACACCAA GCTGAAAGAA ATTTTACCG CGATTGAAAG
351 CTCCGCCTCC GGCTATCCGT CCGAACAGGA CATCAAAGGC CTGTTTGACG
401 ACTTCGACAC CACCAGCAGC CGGCTCGGCA GCACTGTGTC CGACAAGAAC
451 AAACGCCTTG CCGCCGTCCT CAAAGCGGTG GCGGAACCTG ATTTCCGCAA
501 TTTTGAAGAC CACCACATCG ACCTTTTCGG CGATGCCTAC GAATACCTGA
551 TTTCCAACCTA CGGTGCCAAC GCAGGCAAT CCGGCGGCGA ATTTTTCACC
601 CCGCAAAGCG TATCCAAGCT GATTGCGCGG CTGGCGGTGC ACGGACAGGA
651 GAAAGTCAAC AAAATCTACG ACCAGCTTG CGGCTCGGCG AGTCTGCTCT
701 TGCAAGCGAA AAAACAGTTT GACGAGCACA TCATCGAAGA AGGCTTCTTC
751 GGGCAGGAAA TCAACCACAC CACCTACAAC CTCGCCCGCA TGAACATGTT
801 CCTGCACAAC GTCAATTACA ACCAATTCCA CATCGAATTG GGCGACACAC
851 TGACCAACCC AAAGCTCAAA GACAGCAAAC CCTTTGATGC CATCGTTTCC
901 AATCCGCCTT ATTCCATCAA CTGGATAGGC AGCGACGACC CCACCTTAAT
951 CAACGACGAC CGCTTTGCCC CCGCAGGCGT ACTTGCCCCG AAATCCAAAG
1001 CCGATTTTGC CTTTCATCCTG CACGCACTGA ACTACCTTTC CGGCAGAGGC
1051 CGCGCCGCCA TCGTCTCATT CCCCGGCATT TTCTATCGCG GCGGCGCAGA
1101 ACAGAAAATC CGCCAATATC TGGTGGAGGG CAACTACGTG GAAACCGTGA
1151 TTGCCCTTGC GCCCAATCTC TTTTACGGCA CCGGCATCGC CGTCAATATC
1201 CTGGTTTTGT CCAAACACAA AGACAATACC GACATCCAAT TCATCGACGC
1251 AAGCGGCTTC TTTAAAAAAG AAACCAACAA CAACGTCTTA ATCGAAGAAC
1301 ACATTGCTGA AATCGTCAAA CTCTTCGCCG ATAAAGCCGA TGTGCCGCAT
1351 ATCGCCCAAA ACGCTGCCCA GCAAACCGTC AAAGACAACG GCTACAACCT
1401 CGCGTCAGC AGCTATGTCG AAGCCGAAGA CACACGCGAA ATTATCGACA
1451 TCAAACAGCT CAACGCCGAA ATCGGCGAAA CCGTCGCCAA AATCGAACGG
1501 CTGCGGCGTG AAATTGACGA AGTGATTGCA GAGATTGAAG CATGA

```

This corresponds to the amino acid sequence <SEQ ID 1910; ORF 605>:

m605.pep

```

1 MMTEMQORAQ LHRQIWKIAD EVRGAVDGDW FKQYVLGTLF YRFISENFTD
51 YMQAGDSSID YAAMPDSIIT PEIKDDAVKV KGYFIYPGQL FCNIAAEAHQ

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962

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101 NEELNTKLKE IFTAIESSAS GYPSEQDIKG LFDDFDTTSS RLGSTVADKN
151 KRLA AVLKGV AELDFGNFEN HHIDLFGDAY EYLISNYAAN AGKSGGEFFT
201 PQSVSKLIAR LAVHGQEKVN KIYDPACGSG SLLLQAKKQF DEHIEEGFF
251 GQEIHNHTYN LARMNMFLHN VNYNQFHIEL GDTLTNPKLK DSKPFDIVS
301 NPPYSINWIG SDDPTLINDD RFAPAGVLAP KSKADFAFIL HALNYLSGRG
351 RAAIVSFPGI FYRGGAEQKI RQYLVEGNYV ETVIALAPNL FYGTGIAVNI
401 LVLSKHKDNT DIQFIDASGF FKKETNNNVL IEEHIAEIVK LFADKADVP
451 IAQNAAQOTV KDNGYNLAVS SYVEAEDTRE IIDIKQLNAE IGETVAKIER
501 LRREIDEVIA EIEA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 605 shows 97.9% identity over a 513 aa overlap with a predicted ORF (ORF 605.ng) from *N. gonorrhoeae*:

m605/g605

	10	20	30	40	50	60
m605.pep	MMTEMQRAQLHRQIWKIADEVRGAVDGFQYVLGTLFYRFISENFTDYMQAGDSSID					
g605	MMTEMQRAQLHRQIWKIADEVRGAVDGFQYVLGTLFYRFISENFTDYMQAGDSSID					
	10	20	30	40	50	60
	70	80	90	100	110	120
m605.pep	YAAMPDSIITPEIKDDAVKVKGYFIYPGQLFCNIAEAHQNEELNTKLKEIFTAIESSAS					
g605	YAAMPDSIITPEIKDDAVKVKGYFIYPGQLFCNIAEAHQNEELNTKLKEIFTAIESSAS					
	70	80	90	100	110	120
	130	140	150	160	170	180
m605.pep	GYPSEQDIKGLFDDFDTTSSRLGSTVADKNKRLA AVLKGV AELDFGNFENHHIDLFGDAY					
g605	GYPSEQGIKGLFDDFDTTSSRLGSTVADKNKRLA AVLKGV AELDFGNFEDHRIDLFGDAY					
	130	140	150	160	170	180
	190	200	210	220	230	240
m605.pep	EYLISNYAANAGKSGGEFFT PQSVSKLIAR LAVHGQEKVNKI YDPACGSGSLLLQAKKQF					
g605	EYLISNYAANAGKSGGEFFT PQSVSKLIAR LAVHGQEKVNKI YDPACGSGSLLLQAKKQF					
	190	200	210	220	230	240
	250	260	270	280	290	300
m605.pep	DEHIEEGFFGQEIHNHTYNLARMNMFLHN VNYNQFHIELGDTLTNPKLKDSKPFDIVS					
g605	DEHIEEGFFGQEIHNHTYNLARMNMFLHN VNYNKFHIELGDTLTNPKLKDSKPFDAVVS					
	250	260	270	280	290	300
	310	320	330	340	350	360
m605.pep	NPPYSINWIGSDDPTLINDDRFAPAGVLAPKSKADFAFILHALNYLSGRGRAAIVSFPGI					
g605	NPPYSIDWIGSDDPTLINDDRFAPAGVLAPKSKADFAFILHALNYLSGRGRAAIVSFPGI					
	310	320	330	340	350	360
	370	380	390	400	410	420
m605.pep	FYRGGAEQKIRQYLVEGNYVETVIALAPNLFYGTGIAVNILVLSKHKDNTDIQFIDASGF					
g605	FYRGGAEQKIRQYLVEGNYVETVIALAPNLFYGTGIAVNILVLSKHKDNTDIQFIDASGF					
	370	380	390	400	410	420
	430	440	450	460	470	480
m605.pep	FKKETNNNVLIEEHIAEIVKLFADKADVP HIAQNAAQOTVKDNGYNLAVSSYVEAEDTRE					
g605	FKKETNNNVLTEEHIAEIVKLFADKADVP HIAQNAAQOTVKDNGYNLAVSSYVEAEDTRE					

```

      430      440      450      460      470      480
      490      500      510
m605.pep  I I D I K Q L N A E I G E T V A K I E R L R R E I D E V I A E I E A X
          : | | : | | | | : | | | | | | | | | | | | | | | :
g605      V I D I R Q L N A E I S E T V A K I E R L R R E I D E V I A E I E T X
          490      500      510

```

a605.seq

This corresponds to the amino acid sequence <SEQ ID 1912; ORF 605.a>:

a605.pcp

1	MMTEIQQRAQ	LHRQIWKIAD	EVRGAVDGWD	FKQYVLGTLF	YRFISENFTD
51	YMQAGDSSID	YAAMPDSIIT	PEIKDDAVKV	KGYFIYPGQL	FCNIAAEAHQ
101	NEELNNTLKE	IFTAIESSAS	GYPSEQDIKG	LFDDFDTTSS	RLGSTVADKN
151	KRLAAVLKGV	AELDFGSFED	HHIDLFEGDA	EYLSISNYAN	AKSGSGEFTT
201	PQSVSKLIAR	LAVHGQEKVN	KIYDPACGSG	SLLQAKKQF	DEHIEEGFF
251	GQENHTHTYN	LARMNMFNLN	VNYNKFHIEL	GDTLTNPKLK	DSKPFDAVVS
301	PPPSYINWIG	SGDPTLINDH	RFAPAGVLAP	KSKDAFALF	HALNYSLSRG
351	RAATVSFPGI	FYRGGAEQKI	QRYLVEGNYV	ETVALAPNL	FYGTGIAVNI
401	LVLSKHKDNT	DIQFIDAGGF	FKKETNNNVL	TEEHIAEIVK	LFADKADVPH
451	IAQNAAQQTV	KDNGYNLAVS	SYVEPEDTRE	IIDKQLNAE	ISETVAKIER
501	LRREIDEVIA	EIEA*			

m605/a605 98.1% identity in 514 aa overlap

	10	20	30	40	50	60
m605.pep	MMTEMQQR	ALHRQIW	KIADEV	RGAVDG	WDFKQY	VLGTLFYR
	:					
a605	MMTEIQQR	ALHRQIW	KIADEV	RGAVDG	WDFKQY	VLGTLFYR
	:					
	10	20	30	40	50	60
	70	80	90	100	110	120
m605.pep	YAAMPDS	ITPEIKD	DAVKVK	GYFIYP	GGQLFC	NIAAEAHQ
						NEELNTKL
						KEIFTA
						IESSAS

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a605						
	YAAMPDSIITPEIKDDAVKVKGYFIYPGQLFCNIAAEAHQNEELNTKLKEIFTAIESSAS					
	70	80	90	100	110	120
m605.pep		130	140	150	160	170
	GYPSEQDIKGLFDDFDTTSSRLGSTVADKNKRLAAVLKGVAEIDFGNFENHHIDLFGDAY					
a605						
	GYPSEQDIKGLFDDFDTTSSRLGSTVADKNKRLAAVLKGVAEIDFGSFEDHHIDLFGDAY					
	130	140	150	160	170	180
m605.pep		190	200	210	220	230
	EYLISNYAANAGKSGGEFFTPQSVSKLIARLAVHGOEKVNKIYDPACGSGSLLLQAKKQF					
a605						
	EYLISNYAANAGKSGGEFFTPQSVSKLIARLAVHGOEKVNKIYDPACGSGSLLLQAKKQF					
	190	200	210	220	230	240
m605.pep		250	260	270	280	290
	DEHIIEEGFFGQEIINHNTYNLARMNMFHNNVYNQFHIELGDTLTNPCLKD SKPFDAIVS					
a605						
	DEHIIEEGFFGQEIINHNTYNLARMNMFHNNVYNKFHIELGDTLTNPCLKD SKPFDAVVS					
	250	260	270	280	290	300
m605.pep		310	320	330	340	350
	NPPYSINWIGSDDPTLINDDRFAPAGVLAPKSKADF AFILHALNYLSGRGRAAIVSFPGI					
a605						
	NPPYSINWIGSDDPTLINDDRFAPAGVLAPKSKADF AFILHALNYLSGRGRAAIVSFPGI					
	310	320	330	340	350	360
m605.pep		370	380	390	400	410
	FYRGGAEQKIRQYLV EGNVYETVIALAPNLFYGTGIAVNILVLSKHKDNTDIQFIDASGF					
a605						
	FYRGGAEQKIRQYLV EGNVYETVIALAPNLFYGTGIAVNILVLSKHKDNTDIQFIDAGGF					
	370	380	390	400	410	420
m605.pep		430	440	450	460	470
	FKKETNNNVLEE HIAEIVKLFADKADVPHIAQNAAQCTVKDNGYNLAVSSYVEAEDTRE					
a605						
	FKKETNNNVLEE HIAEIVKLFADKADVPHIAQNAAQCTVKDNGYNLAVSSYVEPEDTRE					
	430	440	450	460	470	480
m605.pep		490	500	510		
	IIDIKQLNAEIGETVAKIERLRREIDEVIAEIEAX					
a605						
	IIDIKQLNAEIS ETVAKIERLRREIDEVIAEIEAX					
	490	500	510			

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1913>:

g606.seq

```

1  ATGTCCAAAT TTATCGCCAA ACAATCGGTC GGTGCGGAAG TCATCGACAC
51  GCCGcgCACC GAAGAAGAAG CCTGGCTTCT GAACACTGTC GAAGCCCAAg
101 cgcGGCAATG GAATCTGAAA ACGCCAGAAG TCGCCATCTA CCACTCCCC
151 GAACCCAATG CCTTTGCCAC GGGCGCATCG AGAAACAGCT CCCTGATCGC
201 CGTCAGCacc ggtttgctcg accaTatgaC GCGGACgaa gtggaagcgc
251 tgTTGCGCA CGAAATGGCG CACGTCGCGA ACGGCGACAT GGTACGCTG
301 ACGCTGAtc AAGGCGTGGT CAATACCTTT GTCGTGTTCC TGTGCGCAT
351 TATTGCCAAC CTGATTGCC CAAACAACGA CGGCAGCCAG TCCAGGGAA
401 CTTATTCTCT AGTCAGCATG GTATTCCAA TCCTGTTCGG CTCCTTGCC
451 AGCCTGATTG TCATGTGGTT CAGCCGCCAA CGCGAATACC GCGCCGAcgc
501 gggCGcgCA AAACCTGGTC GCGCACCgAA AATGATTTCC GCCTGCAAA
551 GGCTTAAAGG CAACCCGGTC GATTTGCCCG AAGAAATGAA CGCAATGGGC
601 ATCGCCGAG ATACGCGCA CTCCTGCTC AGCACCACC CTCGCTGGA
651 CAACCGAATC GCCCGCCTCA AATCGCTTTA A

```

This corresponds to the amino acid sequence <SEQ ID 1914; ORF606.ng>:

g606.pep

```

1  MSKFIKQSV GAEVIDTPRT EEEAWLLNTV EAQARQWNLK TPEVAIYHSP
51  EPNAFATGAS RNSSLIAVST GLLDHMTRE VEAVLAHEMA HVGNGDMVTL
101 TLIQGVVNTF VVFLSRIIAN LIARNNDGSQ SQGTYFLVSM VFQILFGFLA
151 SLIVMWFSRQ REYRADAGAA KLVGAPKMIS ALQRLKGNPV DLPEEMNAMG
201 IAGDTRDSL SL STHPSLDNRI ARLKS*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1915>:

m606.seq

```

1  ATGTCCAAAT TTATCGCCAA ACAATCGGTC GCGCGGAAG TTATCGACAC
51  GCGCGCACC GAAGAAGAAG CCTGGCTTTT GAACACTGTC GAAGCCCAAG
101 CGCGGCAATG GAACCTGAAA ACGCCCGAAG TCGCCATCTA CCACTCCCCC
151 GAACCCAAATG CCTTTGCCAC GGGCGCATCG AGAAACAGCT CCCTGATCGC
201 CGTCAGCACC GGTTTGCTCG ACCATATGAC GCGTGACGAA GTGGAAGCCG
251 TATTGGCGCA CGAAATGGCA CACGTCGGCA ACGGCGATAT GGTTACGCTG
301 ACGCTGATTC AAGGCGTGGT CAATACCTTT GTCGTGTTC TGTCGCGCAT
351 TATTGCCAAC CTGATTGCCC GAAACAACGA CGGCAGCCAG TCCCAGGGAA
401 CTTATTTCTT GGTGAGCATG GTATTCCAAA TCCTGTTCCG CTTCTTGCC
451 AGCTTAATTG TCATGTGGTT CAGCCGACAA CGCGAATACC GCGCCGATGC
501 GGGCGCGGCA AAACGTTGTC GCGCGCCGAA AATGATTTC GCCCTGCAA
551 GGCTCAAAGG CAACCCGCTC GATTGCCCC AAGAAATGAA CGCAATGGGC
601 ATCGCCGGAG ATACGCGCGA CTCCCTGCTC AGCACCCACC CTTCGCTGGA
651 CAACCGTATC GCCCGCTCA AATCGCTTAA A

```

This corresponds to the amino acid sequence <SEQ ID 1916; ORF 606>:

m606.pep

```

1  MSKFIKQSV GAEVIDTPRT EEEAWLLNTV EAQARQWNLK TPEVAIYHSP
51  EPNAFATGAS RNSSLIAVST GLLDHMTRE VEAVLAHEMA HVGNGDMVTL
101 TLIQGVVNTF VVFLSRIIAN LIARNNDGSQ SQGTYFLVSM VFQILFGFLA
151 SLIVMWFSRQ REYRADAGAA KLVGAPKMIS ALQRLKGNPV DLPEEMNAMG
201 IAGDTRDSL SL STHPSLDNRI ARLKS*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 606 shows 100.0% identity over a 225 aa overlap with a predicted ORF (ORF 606.ng) from *N. gonorrhoeae*:

m606/g606

	10	20	30	40	50	60
m606.pep	MSKFIKQSVGAEVIDTPRTEEEAWLLNTVEAQARQWNLKTPEVAIYHSPEPNAFATGAS					
g606	MSKFIKQSVGAEVIDTPRTEEEAWLLNTVEAQARQWNLKTPEVAIYHSPEPNAFATGAS					
	10	20	30	40	50	60
m606.pep	RNSSLIAVSTGLLDHMTREVEAVLAHEMAHVGNGDMVTLTLIQGVVNTFVVFLSRIIAN					
g606	RNSSLIAVSTGLLDHMTREVEAVLAHEMAHVGNGDMVTLTLIQGVVNTFVVFLSRIIAN					
	70	80	90	100	110	120
m606.pep	LIARNNDGSQSOGTYFLVSMVFQILFGFLASLIVMWFSRQREYRADAGAAKLVGAPKMIS					
g606	LIARNNDGSQSOGTYFLVSMVFQILFGFLASLIVMWFSRQREYRADAGAAKLVGAPKMIS					
	130	140	150	160	170	180
m606.pep	ALQRLKGNPVDLPEEMNAMGIAGDTRDSLSTHPSLDNRIARLKSIX					
g606	ALQRLKGNPVDLPEEMNAMGIAGDTRDSLSTHPSLDNRIARLKSIX					
	190	200	210	220		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1917>:

a606.seq

966

```
1 ATGTCCAAAT TCATCGCCAA ACAATCGGTC GCGCGGAAG TTATCGACAC
51 GCGCGCACC GAAGAAGAAG CCTGGCTTTT GAACACTETC GAAGCCCAAG
101 CCGCGCAATG GAACCTGAAA ACGCCCGAAG TCGCCATCTA CCACTCCCCC
151 GAACCCAATG CCTTTGCCAC GGGCGCATCG AGAAACAGCT CCCTGATCGC
201 CGTCAGCACC GGTTCGCTCG ACCATATGAC GCGTGACGAA GTGGAAGCCG
251 TATTGGCGCA CGAAATGGCA CACGTCGGCA ACGGCGATAT GGTACGCTG
301 ACGCTGATTC AAGGCGTGGT CAATACCTTT GTCGTGTTC TGTCGCGCAT
351 TATTGCCAAC CTGATTGCCC GAAACAACGA CGGCAGCCAG TCCCAGGGAA
401 CTTATTTCTT GGTGAGCATG GTATTCCAAA TCCTGTTCGG CTTCTTGCC
451 AGCTTAATTG TCATGTGGTT CAGCCGACAA CGCGAATACC GCGCCGACGC
501 GCGCGCGGCA AAACCTGGTC GCGCGCGGAA AATGATTTC GCCCTGCAA
551 GGCTTAAAGG CAACCCGGTC GATTGCCCC AAGAAATGAA CGCAATGGGC
601 ATCGCCGAG ATACGCGCA CTCCCTGCTC AGCACCCACC CTTGCTGGA
651 CAACCGAATC GCCCGCCTCA AATCGCTTTA A
```

This corresponds to the amino acid sequence <SEQ ID 1918; ORF 606.a>:

```
a606.pep
1 MSKFIKQSV GAEVIDTPRT EEEAWLLNTV EAQARQWNLK TPEVAIYHSP
51 EPNAFATGAS RNSSLIAVST GLLDHMTRE VEAFLAHEMA HVGNGDMVTL
101 TLIQGVNFTF VVFLSRIAN LIARNNDGSQ SQGTFLVSM VFQILFGFLA
151 SLIVMWFSRQ REYRADAGAA KLVGAPKMIS ALQRLKGNPV DLPEEMNAMG
201 IAGDTRDSSL STHPSLDNRI ARLKSL*
```

m606/a606 100.0% identity in 226 aa overlap

m606.pep	10	20	30	40	50	60
a606	10	20	30	40	50	60
m606.pep	70	80	90	100	110	120
a606	70	80	90	100	110	120
m606.pep	130	140	150	160	170	180
a606	130	140	150	160	170	180
m606.pep	190	200	210	220		
a606	190	200	210	220		

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1919>:

```
g607.seq
1 ATGCTGCTCG accTcgacCG CTTCCTTt tccGTCTTCC TGAAAGAAAT
51 CCGCTGCTG ACCGCCCTTG CCTGCCCAT GCTGTTGGCG CAGGTCGCGC
101 AGGTGGGCAT CCGTTTCGTC GATACCGTGA TGGCGGGCGG TCGGGCAAG
151 GAAGATTGGC CGGCGGTGGC TTTGGGCAGC AGCGCGTTTG CCACGGTTTA
201 TATTACCTTT ATGGGCATTA TGGCGGCGCT GAACCCGATG ATTGCCCAGC
251 TTTACGGCGC GGGTAAACCC GgtgAAGCAG GCGAAACGGG CGGCGAGGGG
301 ATTTGGTTTC GGCTGATTTT GGGGATTTTC GGCATGATT TGATGTGGGC
351 GCGGATTACG CCGTCCGCA ACTGGCTGAC TTGAGCGAT TATGTGGAAG
401 gcacAAtggc gcAGTATATG CTGTTACCA GCTTGGCGAT GCCGGCGCA
451 ATGGTACACC GCGACTGCA CGCTACGCT TCCAGCCTGA ACCGCCGCG
501 CCTGATTATG TTGTCAGCT TTGCGCGCTT TGTGTTGAAC GTGCCGCTGA
551 ACTATATTTT CGTTACGGC AAATTCGGTA TGCCCGCTTT GGGTGGCGCA
```

967

```

601 GGTTCGCGCG TGGCGACAAT GCGGGTGTTC TGGTTCAGCG CGCTGGCATT
651 GTGGATTTAT ATCGCCAAGG AAAAATTCTT CCGCCCGTTC GGAATGACAG
701 CGAAATTCGg caaACCGGat tGGgcGGTGT TCAAACAGAT TtGGAAAATC
751 gGcgcgCCCA TCGGGCTGTC TTATTTTTTG GAAGccaGcg cGTTTTCGTT
801 TATCGTGTTC TTGATTGCGC CTtccggCGA GGATTATGTG GCGGCGCAGC
851 AGGTCGGCAT CAGTTTGTTC GGGATTCTCT ATATGATTCC GCAAAGCGTC
901 GGCTCGGCAG GGACGGTGGC CATCGGCTTT TCGCTTGGGC GGCGCGAATT
951 TTCGCGGGCG CGTTATATTT CAGGAGTGTC GCTGGTGTTC GGCTGGGTGC
1001 TCGCCGTGAT TACCGTGCTT TCCTTGGTAT TATTCCGTTT GCCGCTGGCA
1051 AGCATGTACA ACGATGaTCC GGCAGTTTAA AGCATCGCCT CCACCGTCTT
1101 GCTGTTCCGC GGCTGTtcc aACCGGCAGA CTTCACCCAA TGTATCGCGT
1151 CCTATGCCCT GCGCGGTAC AAAGTCACCA AGGTGCCGAT GTTCATCCAC
1201 GCCGCCGCTT TCTGGGGCTG CGGCCTGCTG CCGGGCTATC TGCTCGCCTA
1251 CGTTTTCGAT ATGGGCATTT ACGGCTTCTG GACGGCATTG ATTGCCTCGC
1301 TCACCATCGC AGCCGTCGCC TTGGTGTGGT GCTTGGAAAA ATACAGTATG
1351 GAGTTGGTCA AATCACACAA GGCCGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1920; ORF 607.ng>:

g607.pep

```

1 MLLDLDRFSF SVFLKEIRLL TALALPMLLA QVAQVGIGFV DTVMAGGAGK
51 EDLAAVALGS SAFATVYITF MGIMAALNPM IAQLYGAGKT GEAGETGRQG
101 IWFLILGIF GMILMWAAT PFRNWLTLSD YVEGTMAQYM LFTSLAMPAA
151 MVHRALHAYA SSLNRPRIM LVSFAFVLN VPLNYIFVYG KFGMPALGGA
201 GCGVATMAVF WFSALALWIY IAKEKFFRPF GLTAKFGKPD WAVFRQIWKI
251 GAPIGLSYFL EASAFSFIVF LIAPFGEDYV AAQQVGISLS GILYMIPQSV
301 GSAGTVRIGF SLGRREFSRA RYISGVSLVS GWVLAVITVL SLVLFPSPLA
351 SMYNDPAVL SIASTVLLFA GLFQPADFTQ CIASALRGY KVTKVPFMIH
401 AAFAWCGGLL PGYLLAYRFD MGIYGFWTAL IASLTIAAVA LVWCLEKYSM
451 ELVKSHKAV*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1921>:

m607.seq

```

1 ATGCTGCTCG ACCTCAACCG CTTTTCCTTT CCCGTCTTCC TGAAAGAAGT
51 CCGCCTGCTG ACCACTCTTG CCCTGCCCAT GCTGTTGGCG CAGGTCGCGC
101 AGGTGGGCAT CGGTTTTGTC GATACTGTGA TGGCGGGCGG TCGGGGCAAG
151 GAAGACTTGG CCGCGGTGGC TTTGGGCAGC AGCGCGTTTG CCACGGTTTA
201 TATTACCTTT ATGGGCATTA TGGCGGCGCT GAACCCGATG ATTGCCCAGC
251 TTTACGCGCG GGTAAAACC GACGAAGTGG GCGAAACGGG GCGGCAGGGG
301 ATTTGGTTCG GGCTGTTTT GGGCGTGTT CCGCATGGTCT TGATGTGGGC
351 GGCGATTACG CCGTTCGCA ACTGGCTGAC CTTGAGCGAT TATGTGAAG
401 GCACGATGGC GCAGTATATG TTGTTACCA GCTTGGCGAT CCGCGCGGCA
451 ATGGTACACC GCGCGCTGCA CGCCTACACT TCCAGCCTGA ACCGCCCAGC
501 CCTGATTATG TTGGTCAGCT TTGCGGCGTT TGTGTTGAAC GTGCCGCTGA
551 ACTATATTTT CGTTTACGGC AAATTCGGTA TGCCCGCTTT GGGCGGCGCA
601 GGCTGCGGAC TGGCGACGAT GCGCGTGTTC TGGTTCAGCG CGCTGGCATT
651 GTGGATTAT ATCGCCAAGG AAAATTCTT CCGCCCATTC GGAATGACGG
701 CGAAATTCGG CAAACCGGAT TGGCGGTGT TCAAACAGAT TTGGAAAATC
751 GGCGCACCCA TCGGGCTGTC TTATTTTTTG GAAGCCAGCG CGTTTTCGTT
801 TATCGTGTTC TTGATTGCGC CTTTCGCGCA GGATTATGTG GCGGCGCAGC
851 AGGTCGGCAT CAGTTTGTTC GGGATTCTCT ATATGATTCC GCAAAGCGTC
901 GGCTCGGCGG GGACGGTGGC CATCGGCTTT TCGCTTGGGC GGCGCGAATT
951 TTCGCGGGCG CGTTATATTT CCGGCGTGTC ACTGGTGTTA GGATGGATGC
1001 TCGCCGTGAT TACCGTGCTT TCCTTGGTAT TATTCCGTTT GCCGCTGGTA
1051 AGTATGTACA ACAATGATCC GCGGTTTAA AGCATCGCCG CCACCGTCTT
1101 ACTGTTGGCC GGCTTGTTC AACCGGCAGA CTTCACCCAA TGTATCGCCT
1151 CCTACGCTTT GCGCGGCTAC AAAGTTACAA AGGTGCCGAT GTTCATCCAC
1201 GCCGCCGCTT TTTGGGCTG CGGCCTGCTG CCGGGCTATC TGCTCGCCTA
1251 CGTTTCAAT ATGGGCATTT ACGGCTTCTG GACGGCATTG ATTGCCTCGC
1301 TCACCATCGC CGCCATCGCC TTGGTGTGGT GCTTGGAAAT GTGCAGTAGG
1351 GAGATGGTCA GATCGCATAA GGCCGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1922; ORF 607>:

m607.pep

```

1 MLLDLNRFSF PVFLKEVRLL TALALPMLLA QVAQVGIGFV DTVMAGGAGK
51 EDLAAVALGS SAFATVYITF MGIMAALNPM IAQLYGAGKT DEVGETGRQG

```


968

101 IWFGFLGVF GMVLMWAAIT PFRNWLTLSD YVEGTMAQYM LFTSLAMPAA
 151 MVHRLHAYT SSLNRPRILM LVSFAAFVLN VPLNYIFVYG KFGMPALGGA
 201 GCGLATMAVF WFSALALWIY IAKENFFRPF GLTAKFGKPD WAVFKQIWKI
 251 GAPIGLSYFL EASAFSFIVF LIAPFGEDYV AAQVVGISLS GILYMIPQSV
 301 GSAGTVRIGF SLGRREFSRA RYISGVSLVL GWMLAVITVL SLVLFERSPLV
 351 SMYNNDDPAVL SIAATVLLFA GLFQPADFTQ CIASYALRGY KVTKVPMFIH
 401 AAAGWGCGLL PGYLLAYRFN MGIYGFWTAL IASLTIAAIA LVWCLELCSR
 451 EMVRSHKAV*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 607 shows 94.8% identity over a 459 aa overlap with a predicted ORF (ORF 607.ng) from *N. gonorrhoeae*:

m607/g607

	10	20	30	40	50	60
m607.pep	MLLDLNRFSFPVFLKEVRLTTLALPMLLAQVAQVGIGFVDTVMAGGAGKEDLAAVALGS					
g607	MLLDLDRFSFSVFLKEIRLLTALALPMLLAQVAQVGIGFVDTVMAGGAGKEDLAAVALGS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m607.pep	SAFATVYITFMGIMAALNPMIAQLYGAGKTDEVGETGRQGIWFGFLGVFGMVLWAAIT					
g607	SAFATVYITFMGIMAALNPMIAQLYGAGKTGEAGETGRQGIWFGFLGVFGMILWAAIT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m607.pep	PFRNWLTLSDYVEGTMAQYMLFTSLAMPAAMVHRLHAYTSSLNRPRILMLVSFAAFVLN					
g607	PFRNWLTLSDYVEGTMAQYMLFTSLAMPAAMVHRLHAYASSLNRPRILMLVSFAAFVLN					
	130	140	150	160	170	180
	190	200	210	220	230	240
m607.pep	VPLNYIFVYGKFGMPALGGAGCGLATMAVFWFSALALWIYIAKENFFRPFGLTAKFGKPD					
g607	VPLNYIFVYGKFGMPALGGAGCGVATMAVFWFSALALWIYIAKEKFFRPFGLTAKFGKPD					
	190	200	210	220	230	240
	250	260	270	280	290	300
m607.pep	WAVFKQIWKIGAPIGLSYFLEASAFSFIVFLIAPFGEDYVAAQVVGISLSGILYMIPQSV					
g607	WAVFKQIWKIGAPIGLSYFLEASAFSFIVFLIAPFGEDYVAAQVVGISLSGILYMIPQSV					
	250	260	270	280	290	300
	310	320	330	340	350	360
m607.pep	GSAGTVRIGFSLGRREFSRARYISGVSLVLGWMLAVITVLSLVLFERSPLVSMYNNDDPAVL					
g607	GSAGTVRIGFSLGRREFSRARYISGVSLVSGWVLAVITVLSLVLFERSPLASMYNNDDPAVL					
	310	320	330	340	350	360
	370	380	390	400	410	420
m607.pep	SIAATVLLFAGLFQPADFTQCIASYALRGYKVTKVPMFIHAAAFWGCGLLPGYLLAYRFN					
g607	SIASVLLFAGLFQPADFTQCIASYALRGYKVTKVPMFIHAAAFWGCGLLPGYLLAYRFD					
	370	380	390	400	410	420
	430	440	450	460		
m607.pep	MGIYGFWTALIASLTIAAIALVWCLELCSREMVRSKAVX					
g607	MGIYGFWTALIASLTIAAVALVWCLEKYSMEVRSKAVX					
	430	440	450	460		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1923>:

```
a607.seq
1   ATGCTGCTCG ACCTCAACCG CTTTTCCTTT TCCGTCTTCC TGAAAGAAGT
51  CCGCCTGCTG ACCGCTCTTG CCCTGCCCAT GCTGTTGGCG CAGGTCGCGC
101 AGGTGGGCAT CGGTTTTGTC GATACCGTGA TGGCGGGCGG TGCGGGCAAG
151 GAAGACTTGG CGGCGGTGGC TTTGGGCAGC AGCGCGTTTG CCACGGTTTA
201 TATTACCTTT ATGGGCATTA TGGCGGCGCT GAACCCGATG ATTGCCCAGC
251 TTTACGGCGC GGGTAAAACC GACGAAAGTG GCGAAACGGG ACGGCAGGGG
301 ATTTGGTTTC GGCTGTTTTT GGGCGTGTTT GGCATGGTCT TGATGTGGGC
351 GGCATTACG CCCTTCCGCA ACTGGCTGAC CTTGAGCGAT TATGTGAAG
401 GCACAATGGC GCAGTATATG CTGTTACCA GCTTGGCGAT GCCGGCGGCA
451 ATGGTACACC GCGCACTGCA CGCTACGCC TCCAGCCTGA ACCGCCCGCG
501 CCGTATTATG TTGGTCAGCT TTGCGGCGTT TGTGTTGAAC GTGCCGCTGA
551 AGCTATATTT CGTTTACGGC AAATTTCGTA TGCCCGCTTT GGC CGGCGCA
601 GGCTGCGGAC TGGCGACGAT GGC GGTGTTT TGGTTCAGCG CGCTGGCATT
651 GTGGATTAT ATCGCCAAGG AAAATTTCTT CCGCCCATTC GGA CTGACGG
701 CGAAATTCGG CAAACCGGAT TGGGCGGTGT TCAAACAGAT TTGGA AAATC
751 GCGCACCA TC GGGCTGTC TTATTTTGTG GAAGCCAGCG CGTTTTCGTT
801 TATCGTGT TTGATTGCGC CTTTCGGCGA GGATTATGTG GCGGCGCAGC
851 AGGTGCGCAT CAGTTTGTG GGGATTCTCT ATATGATTCC GCAAAGCGTC
901 GGCTGCGGCG GGCAGGTGCG CATCGGCTTT TCGCTTGGGC GGC GCGAATT
951 TCGCGGGCG CGTTATATTT CGGGCGTGT ACTGGTGTCA GGATGGATGC
1001 TCGCCGTGAT TACCGTGCTT TCCTTGGTAT TATTCCGTTT GCCGCTGGTA
1051 AGTATGTACA ACAATGATCC GCGGTTTTTA AGCATCGCCG CCACCGTCTT
1101 ACTGTTCCGC GGCTTGTTCC AACCGGCAGA CTTACCCCAA TGTATCGCCT
1151 CCTACGCCTT GCGCGGCTAC AAAGTTACAA AGGTGCCGAT GTTCATCCAC
1201 GCCGCGCCT TTTGGGCGTG CGGTCTGCTG CCGGGCTACC TGCTCGCCTA
1251 CCGTTTCGAT ATGGGCATTT ACGCCTTCTG GACGGCATTG ATTGCCTCGC
1301 TCACCATCGC CGCCATCGCC TTGGTGTGGT GCTTGAATT GTGCAGTAGG
1351 GAGATGGTCA GATCGCATAA GGCTGTCTGA
```

This corresponds to the amino acid sequence <SEQ ID 1924; ORF 607.a>:

```
a607.pep
1   MLLDLNRF SF SVFLKEVRLL TALALPMLLA QVAQVGIGFV DTVMAGGAGK
51  EDLAAVALGS SAFATVYITF MGIMAALNPM IAQLYGAGKT DEVGETGRQG
101 IWFGFLGVF GMVLMWAAIT PERNWLTLS D YVEGTMAQYM LFTSLAMPAA
151 MVHRLHAYA SSLNRPR LIM LVSF AAFVLN VPLNYIFVYG KFGMPALGGA
201 GCGLATMAVF WFSALALWIY IAKENFERPF GLTAKFGKPD WAVFQIWKI
251 GAPIGLSYFL EASAFS FIVF LIAPFGEDYV AAQVGISLS GILYMI PQSV
301 GSAGTVRIGF SLGRREFSRA RYISGVSLVS GWMLAVITVL SLVLF RSP LV
351 SMYNNDPAVL SIAATVLLFA GLFQPADFTQ CIASYALRGY KVTKVPMFIH
401 AA AFWGCGLL PGYLLAYRFD MGIYGFWTAL IASLTIAAIA LVWCLELC SR
451 EMVRSHKAV*
```

m607/a607 98.9% identity in 459 aa overlap

	10	20	30	40	50	60
m607.pep	MLLDLNRFSPVFLKEVRLLTTALALPMLLAQVAQVGIGFVDTV MAGGAGKEDLAAVALGS					
a607	MLLDLNRFSPVFLKEVRLLTALALPMLLAQVAQVGIGFVDTV MAGGAGKEDLAAVALGS					
	10	20	30	40	50	60
m607.pep	70	80	90	100	110	120
a607	70	80	90	100	110	120
m607.pep	SAFATVYITFMGIMAALNPMIAQLYGAGKTDEVGETGRQGIWFGFLGVFGMVLMWAAIT					
a607	SAFATVYITFMGIMAALNPMIAQLYGAGKTDEVGETGRQGIWFGFLGVFGMVLMWAAIT					
	130	140	150	160	170	180
m607.pep	PERNWLTLS DYVEGTMAQYMLFTSLAMPAA MVHRLHAYTSSLNRPR LIMLVSF AAFVLN					
a607	PERNWLTLS DYVEGTMAQYMLFTSLAMPAA MVHRLHAYTSSLNRPR LIMLVSF AAFVLN					
	190	200	210	220	230	240

970

```

m607.pep  VPLNYIFVYGKFGMPALGGAGCGLATMAVFWFSALALWIYIAKENFFRPFGLTAKFGKPD
a607      VPLNYIFVYGKFGMPALGGAGCGLATMAVFWFSALALWIYIAKENFFRPFGLTAKFGKPD
           190      200      210      220      230      240

           250      260      270      280      290      300
m607.pep  WAVFKQIWKIGAPIGLSYFLEASAFSFIVFLIAPFGEDYVAAQQVGISLSGILYMIPQSV
a607      WAVFKQIWKIGAPIGLSYFLEASAFSFIVFLIAPFGEDYVAAQQVGISLSGILYMIPQSV
           250      260      270      280      290      300

           310      320      330      340      350      360
m607.pep  GSAGTVRIGFSLGRREFSRARYISGVSLVLGWMMLAVITVLSLVLFRSPLVSMYNNDAVL
a607      GSAGTVRIGFSLGRREFSRARYISGVSLVSGWMMLAVITVLSLVLFRSPLVSMYNNDAVL
           310      320      330      340      350      360

           370      380      390      400      410      420
m607.pep  SIAATVLLFAGLFQPADFTQCIASALRGYKVTKVPMFIHAAAFWGCGLLPGYLLAYRFN
a607      SIAATVLLFAGLFQPADFTQCIASALRGYKVTKVPMFIHAAAFWGCGLLPGYLLAYRFD
           370      380      390      400      410      420

           430      440      450      460
m607.pep  MGIYGFWTALIASLTIAAIALVWCLELCSREMVRSHKAVX
a607      MGIYGFWTALIASLTIAAIALVWCLELCSREMVRSHKAVX
           430      440      450      460

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1925>:

g608.seq

```

1  ATGTCGCCCC TCCTCCCAT CATCAACCGC CTGATTCTGC AAAGCCCGGA
51  CAGCCGCTCG GAACTTACCT CCTTTGCAGG CAAAACACTG ACCCTGAACA
101 TTGCCGGGCT GAACTGGCG GGACGCATCA CAGAAGACGG TTTGCTCTCG
151 GCGGGAACG GCTTTGCAGA CACCGAAATT ACCTTCGCA ACAGCGCGAT
201 ACGGAAAATC CTCCAAGGCG GCGAACCCGG GGCTGGCGAC ATCAGGCTCG
251 AAGGCGACCT CATCTCGGC ATCGCGGTAC TGTCCCTGCT CGGCAGCCTG
301 CGTTCCCGCG CATCGGacgA ATTGGCACGG ATTTTCGGCA CGCAGGCAGg
351 catcggcagc CGTGCCACCG ACATCGGACA CGGCatCaaa CAAATCGGCA
401 GGAACATCGC OGAACAAATC GGCGGATTTT CCCGCGAACC CGAGTCcgCa
451 aacaccggca acgaagccct tgccgactgc ctCGACGAAA TAAGCAGACT
501 GCGCGACGGC GTGGAACGCC TCAACGAACG CCTCGACAGG CTCGAACGCG
551 ACATTGGAT AGACTAA

```

This corresponds to the amino acid sequence <SEQ ID 1926; ORF 608.ng>:

g608.pep

```

1  MSALLPIINR LILQSPDSRS ELTSFAGKTL TLNIAGLKLA GRITEDGLLS
51  AGNGFADTEI TFRNSAIRKI LQGEPGAGD IRLEGDLILG IAVLSLLGSL
101 RSRASDELAR IFGTQAGIGS RATDIGHGIK QIGRNIAEQI GGFSREPESA
151 NTGNEALADC LDEISRLRDG VERLNERLDR LERDIWID*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1927>:

m608.seq

```

1  ATGTCGCCCC TCCTCCCAT CATCAACCGC CTGATTCTGC AAAGCCCGGA
51  CAGCCGCTCG GAACTTGGCG CCTTTGCAGG CAAAACACTG ACCCTGAACA
101 TTGCCGGGCT GAACTGGCG GGACGCATCA CGGAAGACGG TTTGCTCTCG
151 GCGGGAACG GCTTTGCAGA CACCGAAATT ACCTTCGCA ACAGCGCGGT
201 ACAGAAAATC CTCCAAGGAG GCGAACCCGG GGCGGGCGAC ATCGGGCTCG
251 AAGGCGACCT CATCTCGGC ATCGCGGTAC TGTCCCTGCT CGGCAGCCTG
301 CGTTCCCGCG CATCGGACGA ATTGGCACGG ATTTTCGGCA CGCAGGCAGA
351 CATCGGCAGC CGTGCCGCGG ACATCGGACA CGGCATCAAA CAAATCGGCA
401 GGAACATCGC CGAACAAATC GGCGGATTTT CCCGCGAATC CGAGTCCGCA
451 AACATCGGCA ACGAAGCCCT TGCCGACTGC CTCGACGAAA TAAGCAGACT

```

971

501 GCGCGACGGC GTGGAACGCC TCAACGAACG CCTCGACCGG CTCGAACGCG
551 ACATTGGAT AGACTAA

This corresponds to the amino acid sequence <SEQ ID 1928; ORF 608>:

m608.pep

1 MSALLPIINR LILQSPDSRS ELAAFAGKTL TLNIAGLKLA GRITEDGLLS
51 AGNGFADTEI TFRNSAVQKI LQGGEFGAGD IGLEGDILG IAVLSLLGSL
101 RSRASDELAR IFGTQADIGS RAADIGHGIK QIGRNIAEQI GGFSRESESA
151 NIGNEALADC LDEISRLRDG VERLNERLDR LERDIWID*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 608 shows 95.2% identity over a 188 aa overlap with a predicted ORF (ORF 608.ng) from *N. gonorrhoeae*:

m608/g608

	10	20	30	40	50	60
m608.pep	MSALLPIINRLILQSPDSRSELAAFAGKTLTLNIAGLKLAGRITEDGLLSAGNGFADTEI					
	::					
g608	MSALLPIINRLILQSPDSRSELTSEAGKTLTLNIAGLKLAGRITEDGLLSAGNGFADTEI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m608.pep	TFRNSAVQKILQGGEFGAGDIGLEDLILGIAVLSLLGSLRSRASDELARIFGTQADIGS					
	::					
g608	TFRNSAIRKILQGGEFGAGDIRLEDLILGIAVLSLLGSLRSRASDELARIFGTQAGIGS					
	70	80	90	100	110	120
	130	140	150	160	170	180
m608.pep	RAADIGHGIKQIGRNIAEQIGGFSRESESANIGNEALADCLDEISRLRDGVERLNERLDR					
	:					
g608	RATDIGHGIKQIGRNIAEQIGGFSREPESANTGNEALADCLDEISRLRDGVERLNERLDR					
	130	140	150	160	170	180
	189					
m608.pep	LERDIWIDX					
g608	LERDIWIDX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1929>:

a608.seq

1 ATGTCCGCCC TCCTCCCAT CATCAACCGC CTGATTCTGC AAAGCCCGGA
51 CAGCCGCTCG GAACTTGCCG CCTTCGCAGG CAAACACTG ACCCTGAACA
101 TTGCCGGGTT GAACTGGCG GGACGCATCA CGGAAGACGG TTTGCTCTCG
151 GCGGGAACG GCTTTGCAGA CACCGAAATC ACCTCCGCA ACAGCGCGGT
201 ACAGAAAATC CTCCAAGGCG GCGAACCCGG GCGGGCGGAC ATCGGGCTCG
251 AAGGCGACCT CATCTCGGC ATCGCGGTAC TGTCCCTGCT CGGCAGCCTG
301 CGTTCCTCGC CATCGGACGA ATTGGCACGG ATTTTCGGCA CGCAGGCAGA
351 CATCGGCAGC CGTGCCGCGG ACATCGGACA CGGCATCAAA CAAATCGGCA
401 GGAACATCGC CGAACAAATC GGCAGATTTT CCCGCGAACC CGAGTCCGCA
451 AACATCGGCA ACGAAGCCCT TGCCGACTGC CTCGACGAAA TAAGCAGACT
501 GCGCGACGGC GTGGAACGCC TCAACGAACG CCTCGACCGG CTCGAACGCG
551 ACATTGGAT AGACTAA

This corresponds to the amino acid sequence <SEQ ID 1930; ORF 608.a>:

a608.pep

1 MSALLPIINR LILQSPDSRS ELAAFAGKTL TLNIAGLKLA GRITEDGLLS
51 AGNGFADTEI TFRNSAVQKI LQGGEFGAGD IGLEGDILG IAVLSLLGSL
101 RSRASDELAR IFGTQADIGS RAADIGHGIK QIGRNIAEQI GRFSREPESA
151 NIGNEALADC LDEISRLRDG VERLNERLDR LERDIWID*

m608/a608 98.9% identity in 188 aa overlap

10 20 30 40 50 60

```
g609.seq
1  ATG GTT TGT G ATAGACTCGA AATCTCGCT CTCGACGACG AAACCTTTGA
5  TGC GTT TGT C GGC AAT CAG C GAAGTAGCGA CATCGCGCAC CATATCTTCC
101 ACG AAT TTC G GGT TTT CGT A GGCTTTTTCG GTAACGTATT TTTCATCGGG
151 GCG TTT GAG C AGCCGATAGA GTTGGCAGCT CGCCTCGCTT TCCACAATAT
201 CGATAACTTC C GCTATACCG ACTTCGCGAT CGGAAGTCAG GCTGACGGTA
251 ACG TCGCAAC GCTGATTATG CGCGCCATAT TGGGAAATTT CTTTGAACA
301 CGGCGAAGC GAGTTTACGG GAATCATGAC CTTTCATATG TGGCCGTATG
351 CCCCGCTCTT T GATTTCACC GTGAGGCTAG CATCATACG CAGTaa
```

g609.pap

1	MVVDRLLEILA	LDDETLDAFV	GNQRSSDIAH	EIFHEFRVYV	GLFGNVFFIG
51	AFEQAVELAA	RLRFHIIDNF	LDTDFGGSAQ	ADGNVRTLIM	RAILGNFFGT
101	RAKRGYGNHD	LHTVAVCPVF	HETREADIII	Q*	

```
m609.seq
1  ATGGTTGTGG  ATAGACTCGA  AATTCTCGCT  CTCGACGACG  AAACCTCTTGA
5  TGCGTTTGTC  GGC AATCAGC  GAAGTAGCGA  CATCGCGCAC  CATATCTTCC
101 ACGAATTTCG  GGT TTTCTGA  GGC TTTTTCG  GTAACGTATT  TTT CATCGGG
151 GCGT TTAGAG  AGGCCG TAGA  GTGGCAGCT  CGCCTCGCCG  TCCCAATAAT
201 CGATGACTTC  CTC GATACCG  ACT TCGCAGT  CGGCAGT CAG  GCTGACGGTA
251 ACGT GCGAAC  GCTGGT TGTG  CGCGCCGTAT  TGGGAAATTT  CTTTGGAAAC
301 CCGCGCAAGC  GAGGTTACGG  GAATCATGAC  CTTCTACTGT  TGCCCGTATG
351 CCGCGCTGTT  TATT TCGCCG  GTAGCAGACA  CATCATAATC  CAGTAA
```

m609.pep

1	MVVDRLLEILA	LDDETLDAFV	GNQRSSDIAH	HIFHIEFRVFV	GFFGNVFFIG
51	AFEQAVELAA	RLRLHIIDDF	LDTDFGIGSG	ADGNVRTLVV	RAVLGNFFGT
101	RAKRGYGNHD	LHTVAVCPVF	DFARETDIII	Q*	

	10	20	30	40	50	60
m609.pep	MVVDRLLEILALDDETLDAFVGNQRSSDIAHHIFHEFRVVFVGGFNGVFFIGAFEQAVELAA					
	:	:	:	:	:	:
g609	MVVDRLLEILALDDETLDAFVGNQRSSDIAHHIFHEFRVVFVGLFGNVFFIGAFEQAVELAA					
	:	:	:	:	:	:
	10	20	30	40	50	60
	70	80	90	100	110	120
m609.pep	RLRLHIIDDFLDTDFGIGSQADGNVRTLVVRVLGNFFGTRAKRGYGNHDLHTVAVCVFV					
	:	:	:	:	:	:

```
a609.seq
  1  ATGGTTGTGG ATAGACTCGA AATTCTCGCT CTCGACGACG AAACCTCTGA
51  TGCAGTTTGC GGCAATCAGC GAAGTAGCCG CATCGCGCAG CATATCTTCC
101 ACGAATTTTCG GGTTTTCGTA GGCCTTTTCG GTAACGTATT TTTCATCTGG
151 GCGTTTGAGC AGGCCGTAGA GTTGGCAGCT CGCGTGCGCC TCCACATAAT
201 CGATGACTTC CTCGATACCG ACTTCGGCAT CGGCAGTCAG GCTGACGGTA
251 ACGTGCGAAC GCTGGTTTETG CGGCCCATAT TGGGAAATTT CTTTGGRAAC
301 CGGGCAAAGC GAGGTTACGG GAATCATGCA CTTCATACTG TGGCCGTATG
351 CACCGTCTTT CATTTCGCCC GTAGGGCTGA CATCATAATC CAGTAA
```

```
a609.pep
  1  MVVDRLEILA LDDETLDFAV GNQRSSDIAH HIFHEFRV FV GFFGNVFFIG
51  AFEQAVELAA RLRLHIICDF LDTDFGIGSQ ADGNVRTLVV RAILGNFFGT
101 RAKRGYGNAD LHTVAVCTVF HFAREADIII O*
```

		10	20	30	40	50	60
m609.pep		MVVDRL	EILALD	DETLD	AFVGNQ	RSSDIA	HHFHEF
a609		MVVDRL	EILALD	DETLD	AFVGNQ	RSSDIA	HHFHEF
		10	20	30	40	50	60
		70	80	90	100	110	120
m609.pep		RLRLHI	IDDFLD	TDFGIG	SQADGN	VRTL	LVVRAV
a609		RLRLHI	IDDFLD	TDFGIG	SQADGN	VRTL	LVVRAV
		70	80	90	100	110	120
		130					
m609.pep		DFARET	DIIIQX				
		:					
a609		HFAREA	DIIIQX				
		130					

g610.seq

```
1 ATGATTGGAG GGCTTATGCA ATTTCTTAC CGCAATGTTC CGGCTTCGC3
51 TATGCGCCGT ATGCGCAGGG ATGATTTTTC ACGCGCGCTG ATGCGCGAGC
101 ATATGCTGAC CGCGGATGAT TTGATTTATC CGTGTTCTGT ATTGGAGGG3
151 CGCGCGCGCG AGGAGGATGT CGCTTCTATG CCGGGCGGTGA AGCGTCAGAG
201 TTTGGACAGG TCGCTGTTTA GCGCGGAAGA GCGGGTGAAG CTCGGATTTC
251 CGATGTTGGC ACTCTTTCCC GTGGTTACGG CAARACAAAC CGGGCGTGCG
301 CAGGAGCGCT ACAATCCCCA AGGACTCGTG CCGTCAACTG tccgagcctT
351 GCGCGAGAGG TttcCgaac tggggattat gacggatgtc tccgtcgatT
401 ctatacgggt gcaacGGTCA GACGGCATGA CGGACgaaaa cggttaCTGT
451 ATGAatgatG aacCCGTAGA AGTCTTGGTG AAACAGGCTT TATGTCATGC
501 AGAGGCGGGC ACGCAGGTCG TTGCTCCTTC CGATATGATG GACGGCGGTA
551 TCGGCGCCAT CCGCGAGGCT TTGGAGGATG CCGGACATAT CCATACGGCG
601 ATTATGCGAT ATTCCGCCAA ATATGCTTCT GCAATTCFAC GACTTTCCCG
651 TGATGCGGTA GGCAGTTCGG GCAATT7TGG AAAGGCAGAT AAAAAGACCT
701 ATACATTGGA TCCTGCAAAAT ACCGATGAGG CGCTGCATGA AGTGCGCGTA
751 CATATTACAG AAGGTGCGGA TTTGGTATG GTGAAGCCCG GTTGGCGCTA
```

974

```

801 TTTGGACGTT GTCCGCCGCG TGAAGGACGA GTTCGGCGTA CCGACTTAIG
851 CCTATCAGGT TTCGGGCGAA TATGCGATGT TGCAGGCGGC GGTGCGCAAC
901 GGCTGGCTGG ACGGCGGCAA AGTGGTTTGT GAAAGCCTGC TGGCATTCAA
951 ACGTGC GGGT GCGGACGGGA TTTTGACCTA TTACGCCATT GAGGCGGCAA
1001 AGATGCTGAA GCGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1938; ORF 610.ng>:

```

g610.pep
1  MIGGLMQFPY RNVPASRMRR MRRDDFSRRL MREHMLTADD LIYPVFVLEG
51  AAREEDVPSM PGVKRQSLDR LLFTAEEAVK LGIPMLALFP VVTANKTGRA
101 QEAYNPEGLV PSTVRALRER FPELGIMTDV ALDPYTVHQD DGLTDENGYV
151 MNDETVEVLV KOALCHAEAG TQVVAPSDMM DGRIGAIREA LEDAGHIHTR
201 IMAYSAKYAS AFYGPFRDAV GSSGNLKGAD KKTQMDPAN TDEALHEVAL
251 DIQEGADMVM VKPGLPYLDV VRRVKDEFGV PTYAYQVSCE YAMLOAAVAN
301 GWLDGGKVVL ESLLAFKRAG ADGILTYIAI EAAKMLKR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1939>:

```

m610.seq
1  ATGATTGGAG GGCTTATGCA GTTTCCTTAC CGCAATGTTC CGGCTTCGCG
51  TATCGCCCGT ATGCGCAGGG ACGATTTTTC ACGCCGCTG ATGCGCGAAC
101 ACACGCTGAC CGCCGATGAT TTGATTTATC CGGTGTTTCT ATTGGAGGGG
151 TCGGCGCGCG AGGAGGATGT GCCTTCTATG CCGGGGTGTA AGCGTCAAAG
201 TTTGGACAGG CTGCTGTTTA CGGCGGAAGA GCGGTAAGC CTCGGTATTC
251 CGATGTTGGC ACTGTTCCCC GTGGTTACGG CAACACAAAC CGAGCGTGCG
301 CAGGAGGCGT ACAATCCCGA AGGACTCGTG CCGTCAACTG TCCGCGCCTT
351 GCGCGAGAGG TTTCCCGAAC TGGGCATTAT GACGGATGTC GCGCTCGATC
401 CTTATACGGT TCACGGTCAG GACGGGCTGA CCGACGAAA CCGTTATGTG
451 ATGAACGATG AAACCGTAGA GGTTTTGGTC AAGCAGGCTT TGTGCCACGC
501 TGAAGCGGGC GCGCAGGTGG TTGCCCTTTC CGATATGATG GACGGGCGTA
551 TCGGTGCGAT TCGCGAGGCG TTGGAGGATG CCGGGCATAT CCATACGCGG
601 ATTATGGCGT ATTCCGCCAA ATATGCTTCT GCATTTTACG GCCCTTTCCG
651 TGATGCGGTA GGCAGTTCGG GCAATTTGGG CAAGGCAGAT AAAAGACCT
701 ACCAGATGGA TCCGGCAAAT ACCGATGAGG CGTGCACGA AGTGGCGTTG
751 GACATTACAG AAGGTGCGGA TATGTAATG GTCAGCCCG GTTTGCCGTA
801 TTTGGACGTT GTCCGCCGCG TAAAGGACGA GTTCGGTGTG CCGACTTATG
851 CCTATCAGGT TTCGGGAGAA TACGCGATGT TCGAGGAGC GATTGCGAAC
901 GGCTGGCTGG ACGGCGGCAA AGTGGTTTGT GAAAGCCTGC TGGCATTCAA
951 ACGTGC GGGT GCGGACGGGA TTTTGACCTA TTACGCTATT GAGGCGGCAA
1001 AGATGTTGAA GCGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1940; ORF 610>:

```

m610.pep
1  MIGGLMQFPY RNVPASRMRR MRRDDFSRRL MREHMLTADD LIYPVFVLEG
51  SAREEDVPSM PGVKRQSLDR LLFTAEEAVK LGIPMLALFP VVTANKTERA
101 QEAYNPEGLV PSTVRALRER FPELGIMTDV ALDPYTVHQD DGLTDENGYV
151 MNDETVEVLV KOALCHAEAG AOVVAPSDMM DGRIGAIREA LEDAGHIHTR
201 IMAYSAKYAS AFYGPFRDAV GSSGNLKGAD KKTQMDPAN TDEALHEVAL
251 DIQEGADMVM VKPGLPYLDV VRRVKDEFGV PTYAYQVSCE YAMLOAAIAN
301 GWLDGGKVVL ESLLAFKRAG ADGILTYIAI EAAKMLKR*

```

m610/g610 98.5% identity in 338 aa overlap

	10	20	30	40	50	60
m610.pep	MIGGLMQFPYRNVPASRMRRMRRDDFSRRLMREHMLTADDLIYPVFVLEGSAREEDVPSM					
g610	MIGGLMQFPYRNVPASRMRRMRRDDFSRRLMREHMLTADDLIYPVFVLEGAAREEDVPSM					
	10	20	30	40	50	60
	70	80	90	100	110	120
m610.pep	PGVKRQSLDRLLFTAEEAVKLGIPMLALFPVVTANKTERAQEAYNPEGLVPSTVRALRER					
g610	PGVKRQSLDRLLFTAEEAVKLGIPMLALFPVVTANKTGRAQEAYNPEGLVPSTVRALRER					
	70	80	90	100	110	120
	130	140	150	160	170	180
m610.pep	FPELGIMTDVALDPYTVHGDGLTDENGYVMNDETVEVLVKOALCHAEAGAQQVAPSDMM					
g610	FPELGIMTDVALDPYTVHGDGLTDENGYVMNDETVEVLVKOALCHAEAGTQVVAPSDMM					
	130	140	150	160	170	180
	190	200	210	220	230	240
m610.pep	DGRIGAIREALEDAGHIHTRIMAYSAKYSAFYGPFRDAVGSSGNLGRADKKTQMDPAN					

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```

g610      CGRIGAIREALDAGHIHTRIMAYSAKYASAFYGPFRDAVGSSGNLGKADKKTYQMDPAN
           190      200      210      220      230      240

           250      260      270      280      290      300
m610.pep  TDEALHEVALDIQEGADMVMVKPGLPYLDVVRVKDEFVPTYAYQVSGEYAMLQAAIAN
           |||||
g610      TDEALHEVALDIQEGADMVMVKPGLPYLDVVRVKDEFVPTYAYQVSGEYAMLQAAVAN
           250      260      270      280      290      300

           310      320      330      339
m610.pep  GWLDGKVVLESLLAFKRAGADGILTYAIEAAKMLKRX
           |||||
g610      GWLDGKVVLESLLAFKRAGADGILTYAIEAAKMLKRX
           310      320      330

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1941>:

```

a610.seq
1   ATGATTGGAG  GGCTTATGCA  GTTTCCTTAC  CGCAATGTTT  CGGCTTCGCG
51  TATGCCCGGT  ATGCCGAGGG  ACGATTTTTC  ACGCCGCTG  ATGCCGAGC
101 ATACGCTGAC  TGCCGATGAT  TTGATTATC  CGGTGTTCT  ATTGGAGGGG
151 TCGGCGCGCG  AGGAGGATGT  GCCTTCTATG  CCGGCGTGA  AGCGTCAGAG
201 TTTGGACAGG  CTGCTGTTTA  CGGCGGAAGA  GGCGGTAAAG  CTCGGTATTC
251 CGATGTTGGC  ACTGTTCCCC  GTGGTTACGG  CAAACAAAAC  CGAGCGTGGC
301 CAGGAGGCGT  ACAATCCCGA  AGGACTCGTG  CCGTCAACTG  TCCGCGCCTT
351 GCGCGAGAGG  TTTCCCGAAC  TGGGCATTAT  GACGGATGTC  GCGCTCGATC
401 CTTATACGGT  GCACGGTCAG  GACGGGCTGA  CGGACGAAAA  CGGTTATGTG
451 ATGAACGATG  AAACCGTAGA  GGTTTTGGTC  AAGCAGGCTT  TGTGTCATGC
501 AGAGGCAGGC  GCACAGGTCG  TTGCTCCTTC  CGATATGATG  GATGGGCGTA
551 TCGGTGCGAT  TCGCGAGGCG  TTGGAGGATG  CCGGCGATAT  CCATACGCGG
601 ATTATGGCGT  ATTCGCCCAA  ATATGCTTCT  GCATTTTACG  GCCCTTCCG
651 TGATGCGGTA  GGCAGTTCGG  GCAATTTGGG  CAAGGCAGAT  AAAAGACCT
701 ACCAGATGGA  TCCGGCAAAT  ACCGATGAGG  CGTTGCACGA  ACTGGCGTTG
751 GACATTCAAG  AAGGTGCGGA  TATGGTGATG  GTCAAGCCCG  GTTTGCCGTA
801 TTTGGACGTT  GTCCGCCGCG  TGAAGGACGA  GTTCGGCGTG  CCGACTTATG
851 CCTATCAGGT  TTCCGGAGAA  TACGCGATGC  TGCAGGCGCG  GGTGCCAAC
901 GGCTGGCTGG  ACGGCGGCAA  AGTGGTTTTG  GAAAGCCTGC  TGGCATTCAA
951 ACGTGCGGGT  GCGGATGGGA  TTTTGACCTA  TTACGCCATT  GAGGCGGCAA
1001 AGATGCTGAA  GCGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1942; ORF 610.a>:

```

a610.pep
1   MIGGLMQFPY  RNVSASRMRR  MRRDDFSRRL  MREHTLTADD  LIYPVFVLEG
51  SAREEDVPSM  PGVKRQSLDR  LLFTAEEAVK  LGIPMLALFP  VVTANKTERA
101 QEAYNPEGLV  PSTVRALRER  FPELGIMTDV  ALDPYTVHGQ  DGLTDENGYV
151 MNDETVEVLV  KQALCHAEAG  AQVVAPSDMM  DGRIGAIREA  LEDAGHIHTR
201 IMAYSAKYAS  AFYGPFRDAV  GSSGNLGKAD  KTTYQMDPAN  TDEALHEVAL
251 DIQEGADMVM  VKPGLPYLDV  VRRVKDEFV  PTYAYQVSSE  YAMLQAAVAN
301 GWLDGKVVVL  ESLLAFKRAG  ADGILTYYAI  EAAKMLKR*

```

m610/a610 99.4% identity in 338 aa overlap

```

           10      20      30      40      50      60
m610.pep  MIGGLMQFPYRNVPASRMRRMRRDDFSRRLMREHTLTADLIYPVFVLEGSAREEDVPSM
           |||||
a610      MIGGLMQFPYRNVSASRMRRMRRDDFSRRLMREHTLTADLIYPVFVLEGSAREEDVPSM
           10      20      30      40      50      60

           70      80      90      100     110     120
m610.pep  PGVKRQSLDRLLFTAEEAVKLGIPMLALFPVVTANKTERAQEAYNPEGLVPSTVRALRER
           |||||
a610      PGVKRQSLDRLLFTAEEAVKLGIPMLALFPVVTANKTERAQEAYNPEGLVPSTVRALRER
           70      80      90      100     110     120

           130     140     150     160     170     180

```


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```

m610.pep    FPELGIMTDVALDPYTVHGDGLTDENGYVMNDETVEVLVKQALCHAEAGAQQVAPSDMM
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
a610         FPELGIMTDVALDPYTVHGDGLTDENGYVMNDETVEVLVKQALCHAEAGAQQVAPSDMM
              130      140      150      160      170      180

              190      200      210      220      230      240
m610.pep    DGRIGAIREALEDAGHIHTRIMAYSAKYASAFYGPFRDAVGSSGNLGKADKKTYQMDPAN
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
a610         DGRIGAIREALEDAGHIHTRIMAYSAKYASAFYGPFRDAVGSSGNLGKADKKTYQMDPAN
              190      200      210      220      230      240

              250      260      270      280      290      300
m610.pep    TDEALHEVALDIQEGADMVMVVKPGLPYLDVVRVKDEFQVPTAYQVSGEYAMLQAAIAN
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
a610         TDEALHEVALDIQEGADMVMVVKPGLPYLDVVRVKDEFQVPTAYQVSGEYAMLQAAVAN
              250      260      270      280      290      300

              310      320      330      339
m610.pep    GWLDGGKVVLESLLAFKRAGADGILTYAIEAAKMLKRX
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
a610         GWLDGGKVVLESLLAFKRAGADGILTYAIEAAKMLKRX
              310      320      330

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1943>:

```

g611.seq
1  ATGCCGCTCTG AAAACGGGAT GGGAAAACGG CAGCTTGCGG GCTGCCGTTT
51  GTTCGGGAAG TTAAGCCTTG TTTTCAGGCT GCTGCCCGGA CTCTGTCGAG
101 GCGGTGTCCTG CCGGGGCAGG TGCTTCGGTT TTTTCCCGAG TCGGAGCGTG
151 CGGCGCGTTA TCTTCCGCCG CGTCCGCATT Ctcgcgcagg ttgtGGCtgt
201 tatectTGGG CGGGCTGggt tgtttgcccg ccataaTTtc cagtacctgA
251 TcgcgGTCta tggtttcCCa ttCcatcagg gctttgcaca TCGTTTCCAT
301 cttgTCGCGG TTTTcatcga ggaTTTGTa ggcaacCTGA TACTgctcgt
351 ccaaaAtccg Gcggatttcc gcgtcgAtgt cctgctgggt tTTCTCGGAA
401 ATGTTTTCGG AACGGgttac gctGCGCCCC AAGAAGACTT CGCCTTCGTT
451 TTCCGCATAA ACCATCACGC CCATTTTgTc gTCATgcCG TAGCGCGTTA
501 CCATTTTCGGC TGCCATTGg GTTGCGCGTT CAAAGTCGTT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1944; ORF 611.ng>:

```

g611.pep
1  MPSENGMKR QLAGCRLFGK LSLVFRLLPG LCRGGVCRGR CFGFFPSRSV
51  RRVIFRRVRI LAQVVAVILG RAGLFARHNF QYLIAYVGFP FHQGFARHFF
101 LVAVFIEDFV GNLLLLVQNP ADFRVDVLLG FLGNVLRGTY AAPQEDFAFV
151 FRINHHAHFV AHAVARYHFA CHLGCAFKVV *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1945>:

```

m611.seq
1  ATGCCGCTCTG AAAACGGGAT GGGAAAACGG CAGCTTGCGG GCTGCCGTTT
51  GTTCGGGAAG TTAAGCCTTG TTTTCAGGCT GCTGCTCGGA CTCTGTCGAA
101 GCGGTGTCCTG CCGGGGCAGG TGCTTCGGTT TCTTCCCGAG TCGGAGCGTG
151 CGGCGCGTTA TCTTCCGCCG CGTCCGCATT CTCGCGCAGG TTGTGGCTGT
201 AATCTTTGGG CGGGCTGGGT TGTTGCCCCG CCATGATTTC CAGTACCTGA
251 TCGCGGTCTGA TGGTTTCCCA TTCCATCAGG GCTTTGCACA TCGTTTCCAT
301 CTTGTGCGCG TTTTCATCGA GGATTTTGTa GGCAACCTGA TATTGCTCGT
351 CCAAAATCCG GCGGATTTCG GCGTCGATGT CCGTCTGGGT TTTCTCGGAA
401 ATGTTTTCGG AACGGGTtAC GCTGCGTCCC AAGAAGACTT CGCCTTCGTT
451 TTCCGCATAA ACCATCACGC CCATTTTgTc GTCATGCGG TAGCGCGTTA
501 CCATTTTCGGC CGCCATTGg GTTGCGCGTT CAAAGTCGTT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1946; ORF 611>:

```

m611.pep
1  MPSENGMKR QLAGCRLFGK LSLVFRLLLG LCRSGVCRGR CFGFFPSRSV
51  KRVIKRRVRI LAQVVAVIFG RAGLFARHDF QYLIADVGFQ FHQGFARHFF
101 LVAVFIEDFV GNLLLLVQNP ADFRVDVLLG FLGNVLRGTY AASQEDFAFV
151 FRINHHAHFV AHAVARYHFA RHLGCAFKVV *

```

m611/g611 96.1% identity in 180 aa overlap

10 20 30 40 50 60

977

```

m611.pep      NPSENGMGKRQLAGCRLFGKLSLVFRLLGLCRSGVCRGRCFGFFPSRSVRRVIFRRVRI
               |||||
g611           NPSENGMGKRQLAGCRLFGKLSLVFRLLPGLCRGGVCRGRCFGFFPSRSVRRVIFRRVRI
               10      20      30      40      50      60

               70      80      90      100     110     120
m611.pep      LAQVVAVIFGRAGLFARHDFQYLIADVGFPHQGFARHFLVAVFIEDFVGNLILLVQNP
               |||||
g611           LAQVVAVILGRAGLFARHNFQYLIADVGFPHQGFARHFLVAVFIEDFVGNLILLVQNP
               70      80      90      100     110     120

               130     140     150     160     170     180
m611.pep      ADFRVDVLLGFLGNVLRGTGYAASQEDFAFVFRINHHAFVAHAVARYHFAHRLGCAFKVV
               |||||
g611           ADFRVDVLLGFLGNVLRGTGYAAPQEDFAFVFRINHHAFVAHAVARYHFACHLGCAFKVV
               130     140     150     160     170     180

m611.pep      X
               |
g611           X

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1947>:

```

a611.seq
1  ATGCCGCTCG AAAACAGGAT GGGAAAACGG CAGCTTGCGG GCTGCCGTTT
51 GTTCGGGAAG TTAAGCCTTG TTTTCAGGCT GCTGCTCGGA CTCTGTCGAA
101 GCGGTGTCTG CCGGGGCAGG TGCTTCGGTT TCTTCCGAG TCGGAGCGTG
151 CGGCGCGTTA TCTTCCGCCG CGTCCGCATT CTCGCGCAGG TTGTGGCTGT
201 AATCTTTGGG CGGCTGGGT TGTTCGCCG CCATGATTTT CAGTACCTGA
251 TCGCGGTCGA TGGTTTCCCA TTCCATCAGG GCTTTGCACA TCGTTTCCAT
301 CTGTGTCGGG TTTTCATCGA GGATTTTGTG GGCAACCTGA TACTGCTCGT
351 CCAAAATCCG GCGGATTTCG GCATCGATGT CCTGCTGGGT TTTCTCGGAA
401 ATGTTTTGCG AACGGGTAC GTCGCTCCC AAGAAGACTT CGCCTTCGTT
451 TTCCGCATAA ACCATCACGC CCATTTGTG GCTCATGCCG TAGCGCGTTA
501 CCATTTGCGG CGCCATTGG GTTGCGCGTT CAAAGTCGTT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1948; ORF 611.a>:

```

a611.pep
1  MPSENRMGKR QLAGCRLFGK LSLVFRLLLG LCRSGVCRGR CFGFFPSRSV
51 RRVIFRRVRI LAQVVAVIFG RAGLFARHDF QYLIADVGF PHQGFARHFL
101 LVAVFIEDFV GNILLVQNP ADFRIDVLLG FLGNVLRGTG AASQEDFAFV
151 FRINHHAHFV AHAVARYHFA RHLGCAFKVV *

```

m611/a611 98.9% identity in 180 aa overlap

```

               10      20      30      40      50      60
m611.pep      MPSENGMGKRQLAGCRLFGKLSLVFRLLGLCRSGVCRGRCFGFFPSRSVRRVIFRRVRI
               |||||
a611           MPSENRMGKRQLAGCRLFGKLSLVFRLLGLCRSGVCRGRCFGFFPSRSVRRVIFRRVRI
               10      20      30      40      50      60

               70      80      90      100     110     120
m611.pep      LAQVVAVIFGRAGLFARHDFQYLIADVGFPHQGFARHFLVAVFIEDFVGNLILLVQNP
               |||||
a611           LAQVVAVIFGRAGLFARHDFQYLIADVGFPHQGFARHFLVAVFIEDFVGNLILLVQNP
               70      80      90      100     110     120

               130     140     150     160     170     180
m611.pep      ADFRVDVLLGFLGNVLRGTGYAASQEDFAFVFRINHHAFVAHAVARYHFAHRLGCAFKVV
               |||||
a611           ADFRIDVLLGFLGNVLRGTGYAASQEDFAFVFRINHHAFVAHAVARYHFAHRLGCAFKVV
               130     140     150     160     170     180

m611.pep      X

```

a611 I
 X

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1949>:

```
g612.seq
1  ATGGGctttcg gcggaatat tgcAAAAAAG CTGGCcgGgGg taGATGAAAT
51  AGCCTttgac tttgacggcA TCGTCTTTGA TTTCGGGCGT GATGATGCTG
101 TCCGGCataG CGGCGTAATC AATGCTGCTG TCGCCGGCCT GCATATAGTC
151 GGTGAAGTTT TCGCTGATAA AGCGGTAGAA AAGTGTGCCG AGAACGTATT
201 GTTTAAAGTC CCAGCCATCC ACCGCGCCGC GTACTTCGTC GGCGATTTTC
251 CAAATTGGC GGTGCAGTTG GCGCGTTGT TGCATTTCGG TCATCATCGA
301 AATCCATATA TAAAGTTAAA CAAATCAAAA TCGCCTGATA TTTTCAGACG
351 ATTTTITTTAC GGGCATTCAA ATTAA
```

This corresponds to the amino acid sequence <SEQ ID 1950; ORF 612.ng>:

```
g612.pep
1  MGFGGNIKK LAGVDEIAFD FDGIVDFEGR DDAVRHSGVI NAAVAGLHIV
51  GEVFADKAVE KCAENVLFKV PAIHRAAYFV GDFPNLAVQL GALLHFGHHR
101 NPYIKLNKSK SPDIFRRFFY GHSN*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1951>:

```
m612.seq
1  ATGGGCTTCG GCGGCAATAT TGCAAAAAAG CTGGCCGGGG TAGATGAAAT
51  AGCCTTTAAC TTTGACGGCA TCGTCTTTGA TTTCGGGCGT GATGATGCTG
101 TCCGGCATAG CGGCGTAATC AATACTGCTG TCGCCTGCCT GCATATAGTC
151 GGTGAAGTTT TCGCTGATAA AGCGGTAGAA AAGTGTGCCG AGAACGTATT
201 GTTTAAAGTC CCAGCCATCC ACCGCGCCGC GTACTTCGTC GGCAATTTTC
251 CAAATTGGC GGTGCAGTTG GCGCGTTGT TGCATTTCGG TCATCATCGA
301 AATCCATATA .AAAGTTAAA CAAATCAAAA TCGCCTGATA TTTTCAGACG
351 ATTTTITTTAC GGGCATTCAA ATTAA
```

This corresponds to the amino acid sequence <SEQ ID 1952; ORF 612>:

```
m612.pep
1  MGFGGNIKK LAGVDEIAFN FDGIVDFEGR DDAVRHSGVI NTAVACLHIV
51  GEVFADKAVE KCAENVLFKV PAIHRAAYFV GNFPNLAVQL GALLHFGHHR
101 NPYXKLNKSK SPDIFRRFFY GHSN*
```

m612/g612 96.0% identity in 124 aa overlap

	10	20	30	40	50	60
m612.pep	MGFGGNIKKLAGVDEIAFNFDGIVDFEGRDDAVRHSGVINTAVACLHIVGEVFADKAVE					
g612	MGFGGNIKKLAGVDEIAFDGIVDFEGRDDAVRHSGVINAAGLHIVGEVFADKAVE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m612.pep	KCAENVLFKVPPIHRAAYFVGNFPNLAVQLGALLHFGHHRNPYXKLNKSKSPDIFRRFFY					
g612	KCAENVLFKVPPIHRAAYFVGNFPNLAVQLGALLHFGHHRNPYIKLNKSKSPDIFRRFFY					
	70	80	90	100	110	120
m612.pep	GHSNX					
g612	GHSNX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1953>:

```
a612.seq
1  ATGGGCTTCG GCGGCAATAT TGCAAAAAAG CTGGCCGGGG TAGATGAAAT
51  AGCCTTTGAC TTTGACGGCA TCGTCTTTGA TTTCGGGCGT GATGATGCTG
101 TCCGGCATAG CGGCGTAATC AATACTGCTG TCGCCTGCCT GCATATAGTC
151 GGTAAAGTTT TCGCTGATAA AGCGGTAGAA AAGTGTGCCG AGAACGTATT
201 GTTTGAAGTC CCAGCCATCC ACCGCGCCGC GTACTTCGTC GGCAATTTTC
251 CAAATTGGC GGTGCAGTTG GCGCGTTGT TGTATTTCGG TCATCATCGA
301 AATCCATAT. AAAAGTTAAA CAAATCAAAA TCGCCTGATA TTTTCAGACG
351 ATTTTITTT.AC GGGCATTCAA ATTAA
```

979

This corresponds to the amino acid sequence <SEQ ID 1954; ORF 612.a>:

```

a612.pep
  1  MGFGGNIAKK LAGVDEIAFD FDGIVFDFGR DDAVRHSGVI NTAVACLHIV
 51  GKVFADKAVE KCAENVLFEV PAIHRAAYFV GNFPNLAVQL GALLYFGHHR
101  NPYXKLNKSK SPDIFRRFFX GHSN*

m612/a612    96.0% identity in 124 aa overlap

              10      20      30      40      50      60
m612.pep      MGFGGNIAKKLAGVDEIAFNFDGIVFDFGRDDAVRHSGVINTAVACLHIVGEVFADKAVE
              |||||:|||||:|||||:|||||:|||||:|||||
a612           MGFGGNIAKKLAGVDEIAFDGIVFDFGRDDAVRHSGVINTAVACLHIVGKVFADKAVE
              10      20      30      40      50      60

              70      80      90     100     110     120
m612.pep      KCAENVLFKVP AIHRAAYFVGNFPNLAVQLGALLHFGHHRNPYXKLNKSKSPDIFRRFFY
              |||||:|||||:|||||:|||||:|||||:|||||
a612           KCAENVLFEP AIHRAAYFVGNFPNLAVQLGALLYFGHHRNPYXKLNKSKSPDIFRRFFX
              70      80      90     100     110     120

m612.pep      GHSNX
              ||||
a612           GHSNX
  
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1955>:

```

g613.seq
  1  ATGTCGCGTT CGAGCCTGTC GAGGCGTTTCG TTGAGGCGTT CCACGCCGTC
 51  GCGCAGTCTG CTTATTTCTG CGAGGCAGTC ggcaagggtc tegtgtgcgg
101  tgtttGcgGA CTCGGGTTCG CGGGAAAATC CGCCGATTTC TTCGGCGATG
151  TTCCTGCCGA TTTgtttGat GCCGTGTCCG ATGTCGGTGG CACGgttgcc
201  gatgcCTGCC TGCGTGCCGA AAATCCGTGC CAATTcgtCC GATGCGCGGG
251  AACGCAGGCT GCCGAGCAGG GACAGTACCG CgATGCCGAG GATGAGGTCC
301  CCTTCGAGCC TGATGTCGCC AGCCCCGGGT TCGCCGCTT GGAGGATTTT
351  CCGTATCGCG CTGTTGCGGA AGGTAATTC GGTGTCTGCA AAGCCGTTTC
401  CGCCCGAGAG CAAACCGTCT TCTGTGATGC GTCCCGCCAG TTTCAGCCCG
451  GCAATGTTCA GGGTCAGTGT TTTGCCTGCA AAGGAGGTAA GTTCCGAGCG
501  GCTGTCCGGG CTTTGCAGAA TCAGGCGGTT GATGATGGGG AGGAGGGCGG
551  ACATATTTTC TGATTGGGGC GGAGAATGCC TGTGTTGCT GTTGCCGCTT
601  ATTTTACAGG CTAA
  
```

This corresponds to the amino acid sequence <SEQ ID 1956; ORF 613.ng>:

```

g613.pep
  1  MSRSSLSRRS LRRSTPSRSL LISSRQSARA SLPVFADSGS RENPPICSA
 51  FLPICLMPCP MSVARLPMPA CVPKIRANSS DARERRLPSR DSTAMPRMR
101  PSSLMSPAPG SPPWRIFRIA LLRKVISVSA KPFPAESKPS SVMRPASFSP
151  AMFRVSVLPA KEVSSERLSG LCRIRRLMMG RRADIFSDWG GECLLLLLPL
201  ILQA*
  
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1957>:

```

m613.seq
  1  ATGTCGCGTT CGAGCCGGTC GAGGCGTTTCG TTGAGGCGTT CCACGCCGTC
 51  GCGCAGTCTG CTTATTTCTG CGAGGCAGTC GGCAAGGGCT TCGTTGCCGA
101  TGTTTGCGGA CTCGGATTTC CGGGAAAATC CGCCGATTTC TTCGGCGATG
151  TTCCTGCCGA TTTGTTTGTGAT GCCGTGTCCG ATGTCGGCGG CACGCTGCC
201  GATGTCTGCC TGCGTGCCGA AAATCCGTGC CAATTCGTCC GATGCGCGGG
251  AACGCAGGCT GCCGAGCAGG GACAGTACCG CGATGCCGAG GATGAGGTCC
301  CCTTCGAGCC CGATGTCGCC CGCCCCGGGT TCGCCTCCTT GGAGGATTTT
351  CTGTACCGCG CTGTTGCGGA AGGTAATTC GGTGTCTGCA AAGCCGTTTC
401  CGCCCGAGAG CAAACCGTCT TCCGTGATGC GTCCCGCCAG TTTCAGCCCG
451  GCAATGTTCA GGGTCAGTGT TTTGCCTGCA AAGGCGCAA CTTCCGAGCG
501  GCTGTCCGGG CTTTGCAGAA TCAGGCGGTT GATGATGGGG AGGAGGGCGG
551  ACATATTTTC TGATCGGGGC GGAGAATGCC TGTGTTGCT GTTGCCGCTT
  
```

980

601 ATTTTACAGG CTTAA

This corresponds to the amino acid sequence <SEQ ID 1958; ORF 613>:

```
m613.pep
  1 MSRSSRSRRS LRRSTPSRSL LISSRQSARA SLEMFADSDS RENPPICSAM
  51 FLPICLMPCP MSAARLPMSA CVPKIRANSS DARERRLPSR DSTAMPRMRS
 101 PSSPMSPAPG SPPWRIFCTA LLRKVISVSA KPFPASKPS SYMRPASFSF
 151 AMFRVSVLPA KAASSERLSG LCRIRRLMMG RRADIFSDRG GECLLLLPL
 201 ILQA*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m613/g613 94.6% identity in 204 aa overlap

	10	20	30	40	50	60
m613.pep	MSRSSRSRRSLRRSTPSRSL	LISSRQSARASLEMFADSDS	RENPPICSAMFLPICLMPCP			
g613	MSRSSLSRRSLRRSTPSRSL	LISSRQSARASLPVFADSGS	RENPPICSAMFLPICLMPCP			
	10	20	30	40	50	60
	70	80	90	100	110	120
m613.pep	MSAARLPMSACVPKIRANSS	DARERRLPSRDSTAMPRMRS	PSSPMSPAPGSPWRIFCTA			
g613	MSVARLPMPACVPKIRANSS	DARERRLPSRDSTAMPRMRS	PSSLMSPAPGSPWRIFRIA			
	70	80	90	100	110	120

981

	130	140	150	160	170	180
m613.pep	LLRKVISVSAKPFPAESKPSSVMRPASFSPAMFRVSVLPAAKASSERLSGLCRIRRLMMG					
g613	LLRKVISVSAKPFPAESKPSSVMRPASFSPAMFRVSVLPAAKEVSSERLSGLCRIRRLMMG					
	130	140	150	160	170	180
	190	200				
m613.pep	RRADIFSDRGGECLLLLLPLILQAX					
g613	RRADIFSDWGGECLLLLLPLILQAX					
	190	200				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1959>:

```
a613.seq
1  ATGTCGCGTT  CGAGCCGCTC  GAGGCGTTCG  TTGAGGCGTT  CCACGCCGTC
51  GCGCAGTCTG  CTTATTTCTG  CGAGGCAGTC  GGCAAGGGCT  TCGTTGCCGA
101 TGTTTGGCGA  CTCGGGTTCG  CGGGAAAATC  TGCCGATTTC  TCGGCGATG
151 TTCCTGCCGA  TTTGTTTGAT  GCCGTGTCCG  ATGTCGGCGG  CACGGCTGCC
201 GATGTCTGCC  TGCSTGCCGA  AAATCCGTGC  CAATTCGTCC  GATGCGCGGG
251 AACGCAGGCT  GCCSAGCAGG  GACAGTACCG  CGATGCCGAG  GATGAGGTCG
301 CCTTCGAGCC  CGATGTCGCC  CGCCCCGGGT  TCGCCGCCTT  GGAGGATTTT
351 CTGTACCGCG  CTGTTGCCGA  AGGTGATTTC  GGTGTCTGCA  AAGCCGTTTC
401 CCGCCGAGAG  CAAACCGTCT  TCCGTGATGC  GTCCCGCCAG  TTTCAACCCG
451 GCAATGTTCA  GGGTCAGTGT  TTGCCTGCG  AAGGCGGCAA  GTTCCGAGCG
501 GCTGTCCGGG  CTTTGAGAAA  TCAGGCGGTT  GATGATGEGG  AGGAGGGCGG
551 ACATATTTTC  TGATCGGGGC  GGAGAATGCC  TGTGTGTCCT  GTTGACGCTT
601 ATTTTACAGG  CTAA
```

This corresponds to the amino acid sequence <SEQ ID 1960; ORF 613.a>:

```
a613.pep
1  MSRSSRSRRS  LRRSTPSRSL  LISSRQSARA  SLPMFADSGS  RENLPICSAM
51  FLPICLMPCP  MSAARLPMSA  CVPKIRANSS  DARERRLPSR  DSTAMPRMRS
101 PSSPMSPAPG  SPPWRIFCTA  LLRKVISVSA  KPFPAESKPS  SVMRPASFPN
151 AMFRVSVLPA  KAASSERLSG  LCRIRRLMMG  RRADIFSDRG  GECLLLLLTL
201 ILQA*
```

m613/a613 98.0% identity in 204 aa overlap

	10	20	30	40	50	60
m613.pep	MSRSSRSRRSLRRSTPSRSLISSRQSARASLPMFADSDSRENPPICSAMFLPICLMPCP					
a613	MSRSSRSRRSLRRSTPSRSLISSRQSARASLPMFADSDSRENPPICSAMFLPICLMPCP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m613.pep	MSAARLPMSACVPKIRANSSDARERRLPSRDSTAMPRMRSPSSPMSPAPGSPPWRICTA					
a613	MSAARLPMSACVPKIRANSSDARERRLPSRDSTAMPRMRSPSSPMSPAPGSPPWRICTA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m613.pep	LLRKVISVSAKPFPAESKPSSVMRPASFSPAMFRVSVLPAAKASSERLSGLCRIRRLMMG					
a613	LLRKVISVSAKPFPAESKPSSVMRPASFNPAMFRVSVLPAAKASSERLSGLCRIRRLMMG					
	130	140	150	160	170	180
	190	200				
m613.pep	RRADIFSDRGGECLLLLLPLILQAX					
a613	RRADIFSDRGGECLLLLLTLILQAX					
	190	200				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1961>:

982

g614.seq

```

1   AtggcTgcgt  tcAacgcctt  ggacggcaaa  aaagaagaca  acgggcaaat
51  cgaaTATTCT  CAGTTCATCC  GACAGGTCAA  CAACGGCGAA  GTATCCGGCG
101 TCAACATCGA  AGGATCCGTC  GTCAGCGGTT  ACCTGATTAA  AGGCGAGCGC
151 ACCGACAAAA  GCACCTTCTT  CACCAACGCG  CCCTTGGATG  ACAACCTGAT
201 TCAAACCTT  TTGAACAAAA  ACGTCCGCGT  AAAAGTAACG  CCGGAAGAAA
251 AACCGAGCGC  GCTGACTGCC  CTGTTTACA  GCCTGCTGCC  CGTCTGCTG
301 CTGATTGGCG  CATGGTTCTA  CTTTATGCGT  ATGCAGGCGG  GCGGCGGCGG
351 AAAAGGCGGC  GCATTCTCCT  TCGGCAAAAG  CCGCGCCCGC  CTGCTGGACA
401 AAGATGCCAA  CAAAGTTACC  TTTGCCGATG  TCGCCGGCTG  CGACGAAGCC
451 AAAGAAGAAG  TGCAGGAAAT  CGTCGATTAC  CTCAAAGCAC  CGAACCGCta
501 tcaAAGcctc  ggcggccgtg  ttcCGCGCGG  CATCCTgCtg  gcgGgcagcc
551 CGGGAaccgg  taaAACACTC  TTGGCGAAAG  CCATTGCAGG  CGAGGCCGCG
601 GTGCCGTCT  TCAGCATTTT  CGGTTCCGAT  TTTGTGCAAA  TGTTCGTCGG
651 TGTCCGTGCA  AGCCGCGTCC  GCGATATGTT  CGAGCAGGCA  AAGAAAAACG
701 CCCCATGCAT  TATCTTTATC  GACGAGATTG  ACGCGGTAGG  CCGCCAACGC
751 GGCGCAGgTT  TGGGCGGCGG  CAATGATGAG  CGCGAGCAAA  CATTAACCA
801 ATTATTGGTT  GAAATGGACG  GTTTTGAAG  CAATCAGACT  GTAATTGTGA
851 TTGCGGCAAC  CAACCGCCCC  GACGTACTCG  ATCCTGCGCT  GCAACGCCCC
901 GGCCGCTTCG  ACCGCCAAGT  CGTCGTCCCC  CTGCCGGACA  TCCGGGGGCG
951 CGAACAGatn  ttGAACGTCC  ATTCTaaAAA  AGTGCcttTG  gacgaATCTg
1001 tggattTTATT  GTCCCTCGCG  CGCGGCACGC  ccggtttTtc  cggcgcgat
1051 tTggcgaaac  tgggtcaacga  agccccctg  tttgcccggc  gccgcaacaa
1101 agtgaaagtc  gatcaaagcg  attTGAAGAC  GCCAAAGACA  AAATCTATAT
1151 GGGTCCGAA  CGCCGCAGTA  TGGTGA

```

This corresponds to the amino acid sequence <SEQ ID 1962; ORF 614.ng>:

g614.pep

```

1   MAAFNALDGK  KEDNGQIEYS  QFIRQVNNGE  VSGVNIEGSV  VSCYLIKGER
51  TDKSTFTFNA  PLDDNLIQTL  LNKNVVRVKV  FEEKPSALTA  LFYSLLPVLL
101 LIGAWFYFMR  MQAGGGGKGG  AFSFGKSRAR  LLDKDANKVT  FADVAGCDEA
151 KEEVQEIVDY  LKAPNRYQSL  GGRVPRGILL  AGSPGTGKTL  LAKAIAGEAG
201 VPFFSISGSD  FVEMFVGVA  SRVRDMFEQA  KKNAPCIIFI  DEIDAVGRQR
251 GAGLGGGNDE  REQTLNQLLV  EMDGFESNQT  VIVIAATNRP  DVLDPALQRP
301 GRFDRQVVVP  LPDIRGREQX  LNVHSKVVPL  DESVDLLSLA  RGTPGFSGAD
351 LAKLVNEAPL  FAGRRNKVKV  DQSDLKTPKT  KSIWVRNAAV  W*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1963>:

m614.seq

```

1   ATGGCTGCGT  TCAACGCTTT  AGACGGTAAA  AAAGAAGACA  ACGGGCAAAT
51  CGAATACTCT  CAGTTCATCC  AACAGGTCAA  CAACGGCGAA  GTATCCGGCG
101 TCAACATCGA  AGGATCCGTC  GTCAGCGGCT  ACCTGATTAA  GGGCGAGCGC
151 ACCGACAAAA  GCACCTTCTT  CACCAACGCG  CCTTGGACG  ACAACCTAAT
201 TAAAACACTG  CTCGACAAAA  ACGTCCGCGT  AAAAGTAACG  CCGGAAGAAA
251 AACCGAGCGC  GCTGGCTGCC  CTGTTTACA  GCCTGCTGCC  CGTCTGCTG
301 CTGATTGGCG  CATGGTTCTA  CTTTATGCGT  ATGCAGACGG  GCGGCGGCGG
351 AAAAGGCGGC  GCATTCTCAT  TCGGTAAAAG  CCGCGCCCGC  CTGCTGGACA
401 AAGATGCCAA  CAAAGTGACC  TTTGCCGATG  TCGCCGGCTG  CGACGAAGCC
451 AAAGAAGAAG  TACAGGAAAT  CGTCGATTAC  CTCAAAGCGC  CGAACCGCTA
501 TCAAAGCCTG  GCGGGGCGCG  TGCCGCGCGG  CATCCTGCTG  GCGGCGAGCC
551 CGGGTACGGG  TAAGACGCTT  TTGGCGAAAG  CGATTGCAGG  CGAAGCCGGC
601 GTGCCGTTCT  TCAGCATTTT  AGGTTCCGAC  TTTGTGCAAA  TETTCGTCGG
651 TGTCCGTGCG  AGCCGCGTCC  GCGATATGTT  CGAGCAGGCG  AAGAAAAACG
701 CCCCTGCAT  CATCTTTATC  GACGAGATTG  ACGCAGTCGG  CCGCCAACGC
751 GGCGCAGGTT  TGGGCGGCGG  CAATGATGAG  CGCGAGCAAA  CATTAACCA
801 ATTGTTGGTT  GAAATGGACG  GTTTTGAAG  CAATCAGACT  GTAATTGTGA
851 TTGCGGCAAC  CAACCGCCCC  GACGTACTCG  ATCCTGCGCT  GCAACGCCCC
901 GGCCGTTTCG  ACCGCCAAGT  GGTGTCCCC  CTGCCGGACA  TCCGAGGGCG
951 CGAACAGATT  TTGAACGTCC  ATTCTAAAAA  AGTGCCTTTG  GACGAATCTG
1001 TGGATTATT  GTCCCTCGCG  CGCGGCACGC  CGGGTTTTTC  CGGCGCGGAT
1051 TTGGCGAACT  TGGTCAACGA  AGCCGCCCTG  TTTGCCGGCC  GCCCAATAA
1101 AGTCAAAGTC  GATCAGAGCG  ATTTGAAGAC  GCCAAAGACA  AAATCTATAT
1151 GGGTCCGAA  CGCCGCAGTA  TGGTGA

```

This corresponds to the amino acid sequence <SEQ ID 1964; ORF 614>:

983

```

m614.pep
  1  MAAFNALDGK KEDNGQIEYS QFIQQVNNGE VSGVNIEGSV VSGYLIKGER
 51  TDKSTFFTNA PLDDNLIKTL LDKNVRVKVT PEEKPSALAA LFYSLLPVLL
101  LIGAWFYEMR MQTGGGGKGG AFSFGKSRAR LLDKDANKVT FADVAGCDEA
151  KEEVQEIVDY LKAPNRYQSL GGRVPRGILL AGSPGTGKTL LAKAIAAGEAG
201  VPFFSISGSD FVEMFVGVA SRVRDMFEQA KKNAPCIIFI DEIDAVGRQR
251  GAGLGGGNDE REQTLNQLLV EMDGFESNQT VIVIAATNRP DVLDPALQRP
301  GRFDRQVVVP LPDIRGREQI LNVHSHKKVPL DESVDLLSLA RGTPGFGSAD
351  LANLVNEAAL FAGRRNKVKV DQSDLKTPKT KSIWVRNAAV W*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m614/g614 98.0% identity in 391 aa overlap

	10	20	30	40	50	60
m614.pep	MAAFNALDGKKEDNGQIEYSQFIQQVNNGEVSGVNIEGSVVSGYLIKGERTDKSTFFTNA					
g614	MAAFNALDGKKEDNGQIEYSQFIQQVNNGEVSGVNIEGSVVSGYLIKGERTDKSTFFTNA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m614.pep	PLDDNLIKTL LDKNVRVKVTPEEKPSALAA LFYSLLPVLL LIGAWFYFMRMQTGGGGKGG					
g614	PLDDNLIQTLLNKNVRVKVTPEEKPSALTALFYSLPVLL LIGAWFYFMRMQAGGGGKGG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m614.pep	AFSEFGKSRARLLDKDANKVTFADVAGCDEAKEEVQEIVDY LKAPNRYQSLGGRVPRGILL					
g614	AFSEFGKSRARLLDKDANKVTFADVAGCDEAKEEVQEIVDY LKAPNRYQSLGGRVPRGILL					
	130	140	150	160	170	180
	190	200	210	220	230	240
m614.pep	AGSPGTGKTL LAKAIAAGEAGVPFFSISGSD FVEMFVGASRVRDMFEQA KKNAPCIIFI					
g614	AGSPGTGKTL LAKAIAAGEAGVPFFSISGSD FVEMFVGASRVRDMFEQA KKNAPCIIFI					
	190	200	210	220	230	240
	250	260	270	280	290	300
m614.pep	DEIDAVGRQRGAGLGGGNDE REQTLNQLLV EMDGFESNQT VIVIAATNRP DVLDPALQRP					
g614	DEIDAVGRQRGAGLGGGNDE REQTLNQLLV EMDGFESNQT VIVIAATNRP DVLDPALQRP					
	250	260	270	280	290	300
	310	320	330	340	350	360
m614.pep	GRFDRQVVVPLPDIRGREQILNVHSHKKVPLDESVDLLSLARGTPGFGSADLANLVNEAAL					
g614	GRFDRQVVVPLPDIRGREQILNVHSHKKVPLDESVDLLSLARGTPGFGSADLAKLVNEAPL					
	310	320	330	340	350	360
	370	380	390			
m614.pep	FAGRRNKVKVDQSDLKTPKTKSIWVRNAAVWX					
g614	FAGRRNKVKVDQSDLKTPKTKSIWVRNAAVWX					
	370	380	390			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1965>:

```

a614.seq
  1  ATGGCTGCGT TCAACGCTTT AGACGGTAAA AAAGAAGACA ACGGGCAAAT
 51  CGAATATTCT CAGTTCATCC AACAGGTCAA CAACGGCGAA GTATCCGGCG
101  TCAACATCGA AGGATCCGTC GTCAGCGGCT ACCTGATTAA GGGCGAGCGC
151  ACCGACAAAA GCACCTTCTT CACCAACGCG CCTTGGACG ACAACCTGAT
201  TAAACACTG CTCGACAAAA ACGTCCGTGT AAAAGTAACG CCGGAAGAAA
251  AACCGAGCGC GCTGGCTGCC CTGTTTACG GCCTGCTGCC CGTCCTGCTG

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984

```

301 CTGATTGGCG CGTGGTTCTA CTTTATGCGT ATGCAGACGG GCGGCGGCGG
351 AAAAGGCGGC GCATTCTCAT TCGGCAAAAG CCGCGCCCGC CTAAGGACAA
401 AAGATGCCAA CAAAGTTACC TTTGCCGATG TCGCCGGCTG CGACGAAGCC
451 AAAGAAGAAG TGCAGGAAAT CGTCGATTAC CTCAAAGCGC CGAACCCTTA
501 TCAAAGCCTG GCGGGGCGCG TCGCGCGCGG CATCCTGCTG GCGGGCAGCC
551 CCGGTACGGG TAAGACGCTT TTGGCGAAAG CGATTGCAGG CGAAGCCGGC
601 GTGCCGTTCT TCAGCATTTT AGGTTCCGAC TTTGTGCGAA TGTTCTGTCG
651 TGTCGGTGCA AGCCGCGTCC GCGATATGTT CGAGCAGGCG AAGAAAAACG
701 CCCCTGTCAT CATCTTTATC GACGAGATTG ACGCAGTCGG CCGCCAACGC
751 GCGCGAGGTT TGGGCGGCGG TAATGATGAG CGCGAGCAGG CATTAAACCA
801 ATTGTTGGTT GAAATGGACG GTTTTGAGAG CAATCAGACT GTAATTGTGA
851 TTGCGGCAAC CAACCGCCCC GACGACTCG ATCCTGCGCT GCAACGCCCC
901 GGCGGTTTCG ACCGCCAAGT GGTGTGTCCTG CTGCCGGACA TCCGGGGGCG
951 CGAACAGATT TTGAACGTCC ACTCTAAAAA AGTGCTTTG GACAAATCTG
1001 TGGATTTATT GTCCCTCGCG CCGGCGACGC CGGGTTTTTC CGGCGCGGAT
1051 TTGGCGAACT TGGTCAACGA AGCCGCCCTG TTGCGCGGCC GCCGCAATAA
1101 AGTCAAAGTC GATCAGAGCG ATTTGAAGAC GCCAAAGACA AAATCTATAT
1151 GGTCCGGAA CGCCGCACTA TGTGTA

```

This corresponds to the amino acid sequence <SEQ ID 1966; ORF 614.a>:

```

a614.pep
1  MAAFNALDGK KEDNGQIEYS QFIQQVNNGE VSGVNIIEGVS VSCYLIKGER
51  TDKSTFFFTNA PLDDNLIKTL LKKNVRVKVT PEEKPSALAA LFYSLLPVLL
101 LIGAWFYFMR MQTGGGGKGG AFSFGKSRAR LLDKDANKVT FADVAGCDEA
151 KEEVQEIVDY LKAPNRYQSL GGRVPRGILL AGSPGTGKTL LAKAIAEAG
201 VPFFSISGSD FVEMFVGVA SRVRDMFEQA KKNAPCIIFI DEIDAVGRQR
251 GAGLGGGNDE REQTLNQLLV EMDGFESNQT VIVIAATNRP DVLDPALQRP
301 GRFDRQVVVP LPDIRGREQI LNVHKKVPL DKSVDLLSLA RGTGPGFSGAD
351 LANLVNEAAL FAGRRNKVKV DQSDLKTPKT KSIWVRNAAV W*

m614/a614 99.7% identity in 391 aa overlap

          10      20      30      40      50      60
m614.pep  MAAFNALDGKKEDNGQIEYSQFIQQVNNGEVSGVNIIEGSVVSGYLIKERTDKSTFFFTNA
a614      MAAFNALDGKKEDNGQIEYSQFIQQVNNGEVSGVNIIEGSVVSGYLIKERTDKSTFFFTNA
          10      20      30      40      50      60

          70      80      90      100     110     120
m614.pep  PLDDNLIKTL LDKNVRVKVT PEEKPSALAA LFYSLLPVLL LIGAWFYFMR MQTGGGGKGG
a614      PLDDNLIKTL LDKNVRVKVT PEEKPSALAA LFYSLLPVLL LIGAWFYFMR MQTGGGGKGG
          70      80      90      100     110     120

          130     140     150     160     170     180
m614.pep  AFSFGKSRARLLDKDANKVT FADVAGCDEAKEEVQEIVDY LKAPNRYQSL GGRVPRGILL
a614      AFSFGKSRARLLDKDANKVT FADVAGCDEAKEEVQEIVDY LKAPNRYQSL GGRVPRGILL
          130     140     150     160     170     180

          190     200     210     220     230     240
m614.pep  AGSPGTGKTL LAKAIAEAG VPFFSISGSD FVEMFVGVA SRVRDMFEQA KKNAPCIIFI
a614      AGSPGTGKTL LAKAIAEAG VPFFSISGSD FVEMFVGVA SRVRDMFEQA KKNAPCIIFI
          190     200     210     220     230     240

          250     260     270     280     290     300
m614.pep  DEIDAVGRQR GAGLGGGNDE REQTLNQLLV EMDGFESNQT VIVIAATNRP DVLDPALQRP
a614      DEIDAVGRQR GAGLGGGNDE REQTLNQLLV EMDGFESNQT VIVIAATNRP DVLDPALQRP
          250     260     270     280     290     300

          310     320     330     340     350     360
m614.pep  GRFDRQVVVP LPDIRGREQI LNVHKKVPL DESVDLLSLARGT PGFSGAD LANLVNEAAL
a614      GRFDRQVVVP LPDIRGREQI LNVHKKVPL DESVDLLSLARGT PGFSGAD LANLVNEAAL

```

985

	310	320	330	340	350	360
	370	380	390			
m614.pep	FAGRRNKVKVDQSDLKTPKTKSIWVRNAAVWX					
a614	FAGRRNKVKVDQSDLKTPKTKSIWVRNAAVWX					
	370	380	390			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1967>:

```

g615.seq
1  ATGTGGAAAC GGCGGCGGCG CGGTGtcggC AGCTTtgaag agcagcGaAT
51  agatgCCGCC GGCAAACAC AATGCCGAAa gcaggCtgaa gcGGTTgcgcC
101 GGCagcTTca tGCCGCCTCC TcGTCCaGCC ACgtttGgca gattttggac
151 agggcgAGga ATTTGCcgCc gcgtgcggCA agtatgtcgc gcCAttgtgc
201 cacttcttcg gcggacggTG cttcgtcgaT gctgCATTCG TACagcagga
251 aatcgagggT tcttcgatg acggGgatgg AttccgTTTG GataAgCTgc
301 ttgagttcgt tcatgactGt TCgGATAcgg aaatcgggaa aatgccgtct
351 gAaagggctt CAGACGGCat tggATTATTT GCTGTGCAGG AAgcgcggtt
401 cctcttccca tttgcCGGAA AtgATGTCGg gtacggcctg cAGGGATttg
451 gCGACGGcat cgtcgatttg ccgGcggtgc ttCgcgcctc ggtttGTTca
501 agacgtagcc gaCGACGagg ttgcggtcGC CGGGGtggcC GATGCCGAGG
551 CGCAGGCGGt aatagtctgc CGTGCCGAGT TTTGCctgAA TGTCTTTCAA
601 GCCGTTGTGT CcgCGTtgc cgcCGCCGAG TTTGAATTtG ATCCGTCCGC
651 AAGGGATGTC GAGTTCGTCG TGGACGACGA GGATTCTTC GGGTTTGATT
701 TTGTAGAACT GTGCAAGCGC GGCAACCGCC TGTCCGGAAC GGTTCATGAA
751 CGTGGCCGGT TTGAGCAGCC AAACATCGCC GTCGGGCAGG GCGGCGCGGG
801 CAACTTCGCC GAAGAATTTT TTTTCTCTT TAAACGAAGC CTTCCATTTC
851 CACGCCAGTT CGTCGAGGAA CCAAAAGCCC GCATTGTGGC GGGTCTGTTC
901 GTATTCTTTG CCCGGGTTGC CCAAGCCGAC AACCATTTTG ATTGTGttcg
951 acatgataTT TtccgtgTTT CTgTCGaag cggtCtgaAG GCTTCAGacg
1001 gcatggTtaT TCTTCTTgaT TttgaACgcg tgtgcggCGC GCTTCTTTGG
1051 GGTTCGATCAA CAGCGGGCGG TACACTTCGA TGCGGTCECC GTCGCGCAGC
1101 GCGGTGTCGT CTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1968; ORF 615.ng>:

```

g615.pep
1  MWKRRRRGVG SFEEQRIDAA GKPOCGKQAE AVARQLHAAS SSSHVWQILD
51  RRRNLPPRAA SMSRHCATSS ADGASSMLHS YSRKSRVSSM TGMDSVWISC
101 LSSFMTVRIR KSGKCRLLKGL QTALDYLLCR KRVASSHLPE MMSGTACRDL
151 ATASSICRRR FRARFVQDVA DDEVAVAGVA DAEAQAVIVC RAEFCLNVFQ
201 AVVSAVAAAE FEFDPSARDV EFVVDDEDFE GFDFVELCKR GNRLSGTVHE
251 RGRFEQPNIA VQGGGAGNFA EEEFFFFKRS LPFPRQFVEE PKARIVAGLF
301 VEFARVAQAD NHFDCVRHDI FRVSVECGLK ASDGMVILLD FERVCGALLW
351 GRSTAGGTLR CGRRRAAACR L*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1969>:

```

m615.seq Length: 1116
1  ATGCGGAAAA GGCGGTGGCG CGGTTTCGGC AGCTTTGAAA AGCAGTGAGT
51  AAATGCTGCC TGCAAACAC AATGCCGAGA GCAGGATAAA GCGGTTGCGT
101 GGCAGATTCA TGCTTGTTC TCTTCAAGCC ATGTCTGGCA TAGTTTGGAT
151 AGGCGCAGGA ATTTTCGGCC GCGTGC GGCC AGCATATCGC GCCAAACGGC
201 AATTTCTTCG GCGGAGGGGG CATCGTCTAT GCTGCATTTC TAGAGCAGGA
251 AATCGAGGGT TTCTTCGATG ACGGGGATGG ATTCCGTTTG GATAAGCTGC
301 TTGAGTTCGG TCATGACTGT TCGGATATGG AAATCGGGAA CATGCCGTCT
351 GAAAGGGCTT CAGACGGCAT CGGGTCATT GCTGTGCAGG AAGCGGGTTG
401 CTTCTTCCCA TTGCGCGGCA AGGATGTCGG GTATGGCTTG CAGGGATTG
451 GCGACGGCAT CGTCAATCTG TCGGCGGTGT .TCCGTA CTG GGTTTGTTCA
501 GGACATAGCC GACGACGAGG TTGCGGTGCG CCGGGTGGCC GATGCCGAGG
551 CGCAGGCGGT AATAGTCTGC CGTGCCGAGT TTTGCCTGAA TGTCTTTCAA
601 GCCGTTGTGT CCGCCGTTGC CGCCGCCGAG TTTGAATTG ATCCGTCCGC
651 AGGGAATGTC GAGTTTCGTC TGGACGACGA GGATTCTTC GGGTTTGATT
701 TTGTAGAACT GTGCAAGCGC GGCAACTGCC TGTCCGGAAC GGTTCATGAA
751 CGTGGCAGGT TTGAGCAGCC AAACGTCGCC GTCGGGCAGG GCGGACGGG

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986

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801 CGACTTCGCC GAAGAATTTT TTTTCTTCTT TAAATGAAGC CTTCATTTC
851 CACGCCAGTT CGTCGAGGAA CAAAAAAGCC GCATTGTGGC GTGTCTGTTC
901 GTATTCTTTG CCCGGGTTGC CCAAGCCGAC AACCATTTTG ATGTGTGTTG
951 ACATGATATT TTCCGTGTTT CTGTCGAATG CTGTCTGAAG GCTTCAGACG
1001 GCATGGTTAT TCTTCTTGAT TTGAACGCG TTGCGGCGC GCTTCTTTGG
1051 GGTGATCAA CAGCGGCGG TACACTTCGA TGCGGTCGCC GTCGCGCAGC
1101 GCGGTGTCGT CTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1970; ORF 615>:

```

m615.pep Length: 372
1 MRKRRWRGFG SFEKQXVNA CXPQCREQDK AVAWQIHACS SSSHVWHS LD
51 RRRNFPPRAA SISRQTAISS AEGASSMLHS XSRKSRVSSM TGMDSVWISC
101 LSSVMTVRIW KSGTCRLKGL QTASGHLLCR KRVASSHLPA RMSGMACRDL
151 ATASSICRRC XRTGFVQDIA DDEVAVARVA DAEAQAVIVC RAEFCLNVFQ
201 AVSAVAAAE FEFDP SAGNV EFVDDDEFF GFDFVELCKR GNCLSGTVHE
251 RGRFEQPNVA VGQGGTGDEA EEEEEFFKXS LPFPRQFVEE PKTRIVACLF
301 VFFARVAQAD NHFDCVXHDI FRVSVECLK ASDGMVILLD FERVCGALLW
351 GRSTAGGTLR CGRRRAACRLX L*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m615/g615 86.8% identity in 371 aa overlap

m615.pep	10	20	30	40	50	60
	MRKRRWRGFGSFEKQXVNAACKPQCREQDKAVAWQIHACSSSHVWHS LDRRRNFPPRAA					
g615	10	20	30	40	50	60
	MWKRRRRGVGSFEEQRIDAAGKPQCGKQAEAVARQLHAASSSHVWQILD RRRLPPRAA					
m615.pep	70	80	90	100	110	120
	SISRQTAISSAEGASSMLHSXSRKSRVSSMTGMDSVWISCLSSVMTVRIWKSGTCRLKGL					
g615	70	80	90	100	110	120
	SMSRHCAITSSADGASSMLHSYSRKS RVSSMTGMDSVWISCLSSFM TVRIKSGKCR LKGL					
m615.pep	130	140	150	160	170	180
	QTASGHLLCRKRVASSHLPARMSGMACRDLATASSICRRCXRTGFVQDIADDEVAVARVA					
g615	130	140	150	160	170	180
	QTALDYLLCRKRVASSHLPENMSGTACRDLATASSICRRCFRARFVQDVADDEVAVAGVA					
m615.pep	190	200	210	220	230	240
	DAEAQAVIVCRAEFC LN VFQAVVSAVAAAEFEFDP SAGNVEFVDDDEFFGFDFVELCKR					
g615	190	200	210	220	230	240
	DAEAQAVIVCRAEFC LN VFQAVVSAVAAAEFEFDP SARDVEFVDDDEFFGFDFVELCKR					
m615.pep	250	260	270	280	290	300
	GNCLSGTVHERGRFEQPNVAVGQGGTGDFAE EEEEEFFKXSLPFPRQFVEE PKTRIVACLF					
g615	250	260	270	280	290	300
	GNRLSGTVHERGRFEQPNIAVGQGGAGNFAE EEEEEFFKXSLPFPRQFVEE PKARIVAGLF					
m615.pep	310	320	330	340	350	360
	VFFARVAQADNHFDCVXHDI FRVSVECLKASDGMVILLDFE EFCGALLWGRSTAGGTLR					
g615	310	320	330	340	350	360
	VFFARVAQADNHFDCVRHDI FRVSVECLKASDGMVILLDFE EFCGALLWGRSTAGGTLR					
m615.pep	370					
	CGRRRAACRLX					
g615	370					
	CGRRRAACRLX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1971>:

```
a615.seq
1  ATGCGGAAAC GCGGCGGCG CGGTGTCGGC AGCTTTGAAG AGCAGCGAAT
51  AGATGCCGCC GGCAAACCAC AATGCGGAAA GCAGGCTGAA GCGGTTGCGC
101 GGCAGCTTCA TGCCGCTCC TCGTCCAGCC ACGTTTGGCA GATTTTGGAC
151 AGGCGCAGGA ATTTGCCGCC CGGTGCGGCA AGTATGTCGC GCCATTGTGC
201 CACTTCTTCG GCGGATGCTG CGTCGTCGAT GCTGCATTTC TACAGCAGGA
251 AATCGAGGGT TTCTTCGATG ACGGGGATGG ATTCGGTTTG GATAAGCTGC
301 TTGAGTTCCG TCATGACTGT TCGGATATGG AAATCGGGAA CATGCCGTCT
351 GAAAGGGCTT CAGACGGCAT CGGTCATTG GCTGTGCAGG AAGCGGGTTG
401 CCTCTTCACA TTTGCCGSCA AGGATGTCGG GTATGGCTTG CAGGGATTTC
451 GCGACGGCAT CGTCAATCTG TCGGCGGTG. TTCCGTACTG GGTTGTTC
501 GGACATAGCC GACGACGAGG TTGCGGTCGC CCGGGTGGCC CATGCCGAGG
551 CGCAGGCGGT AATAGTCTGC CGTGCCGAGT TTTGCCGTA TGTCTTTCAA
601 GCCGTTGTGT CCACCGTTGC CGCCGCCGAG TTTGAATTTC ATCCGTCGCG
651 AGGGAATGTC GAGTTCGTCG TGGACGACGA GGATTCTTC GGGTTTGATT
701 TTATAAAACT GCGCAAGGGC GGCAACTGCC TGTCGGGAAC GGTTTCATGAA
751 CTTGGTCTGGC TTGAGCAGCC AGACATCGCC GTCGGGCGAG GTAGCAGCGG
801 CGACTTCGCC GAAGAATTTT TTTTCTTCTT TAAATGAAGC CTTCATTTC
851 CACGCCAGTT CGTCGAGGAA CAAAAACCC GCATTGTGGC GTGTCTGTTC
901 GTATTCTTTG CCCGGGTTGC CCAAGCCGAC AACCATTTTG ATGTGTGTTG
951 ACATGATATT TTCCGTGTTT CTGCCGAATG CCGTCTGAAG GCTTCAGACG
1001 GCATGGTTAT TCTTCTTGT TTTGAACGCG TTTGCGGCGC GCTTCTTTGG
1051 GGTGATCAA CAGCGGGCGG TACACTTCGA TCGGTCGCC GTGCGCAGC
1101 GCGGTGTCGT CTTTGA
```

This corresponds to the amino acid sequence <SEQ ID 1972; ORF 615.a>:

```
a615.pep
1  MRKRRRRGVG SFEEQRIDAA GKPCGKQAE AVARQLHAAS SSSHVWQILD
51  RRRNLPPRAA SMSRHCATSS ADGASSMLHS YSRKSRVSSM TGMDSVWISC
101 LSSVMTVRIW KSGTCRLKGL QTASGHLLCR KRVASSHLPA RMSGMACRDL
151 ATASSICRRX FRTGFVQDIA DDEVAVARVA DAEAQAVIVC RAEFCLNVFQ
201 AVVSTVAAAE FEFDPAGNV EFVVDDEDF GFDKIKLRKG GNCLSGTVHE
251 RGRLEQPDIA VGQSTGDEA EEEFFFK*S LPFRQFVEE PKTRIVACLF
301 VFFARVAQAD NHFDCV*HDI FRVSAECLK ASDGMVILLD FERVCGALLW
351 GRSTAGGTLR CRRRAAACR L*
```

m615/a615 90.3% identity in 371 aa overlap

	10	20	30	40	50	60
m615.pep	MRKRRWRGFGSFEKQXVNAACKPQCREQDKAVAWQIHACSSSSHVWHS	SLDRRNFPPRAA				
a615	MRKRRRRGVGSFEEQRIDAAAGKPCGKQAEAVARQLHAASSSSHVWQILD	RRRNLPPRAA				
	10	20	30	40	50	60
m615.pep	SISRQTAISSAEGASSMLHSXSRKSRVSSMTGMDSVWISCLSSVMTVRIW	KSGTCRLKGL				
a615	SMSRHCATSSADGASSMLHSYSRKSRVSSMTGMDSVWISCLSSVMTVRIW	KSGTCRLKGL				
	70	80	90	100	110	120
m615.pep	QTASGHLLCRKRVASSHLPARMSGMACRDLATASSICRRCXRTGFVQDIA	DDEVAVARVA				
a615	QTASGHLLCRKRVASSHLPARMSGMACRDLATASSICRRCXRTGFVQDIA	DDEVAVARVA				
	130	140	150	160	170	180
m615.pep	DAEAQAVIVCRAEFCLNVFQAVVSAVAAAEFEFDPAGNV	EFVVDDEDFGFDKIKLRKG				
a615	DAEAQAVIVCRAEFCLNVFQAVVSAVAAAEFEFDPAGNV	EFVVDDEDFGFDKIKLRKG				
	190	200	210	220	230	240
m615.pep	GNCLSGTVHE					
a615	GNCLSGTVHE					
	250	260	270	280	290	300

988

```

m615.pep  GNCLSGTVHERGRFEQPNVAVQGSGTGF AEEFFFFFKXSLPFPRQFVEEPKTRIVACLF
          |||||:||||:||||:|||||
a615       GNCLSGTVHERGRLEQPDIAVGQSGTGF AEEFFFFFKXSLPFPRQFVEEPKTRIVACLF
          250      260      270      280      290      300

          310      320      330      340      350      360
m615.pep  VFFARVAQADNHFDVCXHDIFRVSV EECCLKASDGMVILLDFERVCGALLWGRSTAGGTLR
          |||||:||||:||||:|||||
a615       VFFARVAQADNHFDVCXHDIFRVSA ECRCLKASDGMVILLDFERVCGALLWGRSTAGGTLR
          310      320      330      340      350      360

          370
m615.pep  CGRRRAAACRLX
          |||||
a615       CGRRRAAACRLX
          370

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1973>:

```

g616.seq
1  atgtcgaaCA CAATCAAAAT GGTGTGCGGC TTGGGCAACC CGGGCAAAGA
51  ATACGAACAG ACCCGCCACA ATGCGGGCTT TTGGTTCCTC GACGAACTGG
101 CGTGGAATG GAAGGCTTCG TTAAAGAAG AAAAAAATT CTTCGGCGAA
151 GTTGCCCGCG CCGCCCTGCC CGACGGCGAT GTTGGCTGC TCAAACCGGC
201 CACGTTTATG AACCGTTCCG GACAGGCGGT TGCCGCGCTT GCACAGTTCT
251 ACAAAATCAA ACCCGAAGAA ATCCTCGTCG TCCACGACGA ACTCGACATC
301 CCTTGGCGGAC GGATCAAAAT CAAACTCGGC GcgggcaaCG gcgGACACAA
351 CGGCTTGAAA GACATTcagG CAAACTCGG CACGGcagac tattaCCGCC
401 TGCGCCTCGG CATCGgccaC CCGGCGgacc gcaacctCGT CGtcggctac
451 gtcttgAACA aaccgagcgc gGaaGcaccg Ccgggaaatc gacgatgCCG
501 TCGccaaATC CCTGcaggcc gtaccCGACA TcaTTTCCGg caaatgggaa
551 gaggcaacgc gCTTCCTGCA CAGCAAAATA TccaatGCCG TCTGaaGccc
601 ttTcagacgg cattttcccg atttcgTAT CcGAaCagtc atgaacgaac
651 tcaagcAGcT tatCCAAAcg gaatccatcc ccgtcatcga agaaaccctc
701 gatttcctgc tGTACGAATG cagcAtcgac gaagCACCgt ccgccgaaga
751 agtggcacaa TGgcygcgaca tactTGccgc acgcyGcgGC AAATtcCTgc
801 gcctgtccaa aatctgcCaa aCGTGGCTGG ACgAGGAGGC GGCatgAAgc
851 tGCGGcgCAA CcgcttcaGc ctgctTTCCG CATGTGgGT TGCCGGCGGc
901 atcATtLgc tgctcttcaa AGCTGccgaC ACCGCGCGCG CGCCGTTTCC
951 ACATTTtcgaC AAAGCAGCAC ACCTTGCCCT GTTTTTCGCA CAaatCTTgt
1001 tTctGGCCAA AGCATTCAA ACCGGAAGAA ITCCCATCCC CTACCCGAGC
1051 CTGATTGCGT TCGCCTTCTG TTTTGCCGTC GGCAGCGAAT GCGCGCAGGC
1101 ATGGTTTACC GCAACGCGAA CCGGCAGTTT GGGCGATGTC CTTGCCgACC
1151 TGACSGGCGC AGCCCTTGCC CTCTTTGCCG CGGCTTCTGC CTGCCGcccg
1201 gactaa

```

This corresponds to the amino acid sequence <SEQ ID 1974; ORF 616.ng>:

```

g616.pep
1  MSNTIKMVVG LGNPGKEYEQ TRHNAGFWFL DELANKWKAS FKEEKFFGE
51  VARAALPDGD VWLLKPATFM NRSQAVAAAL AQFYKIPKEE ILVHVHDELDI
101 PCGRIKFKLG GNGGGHNLK DIQAKLGTAD YYRLRLGIGH PGDRNLVVG
151 VLNKPSAEAP PANRRCRRQI FAGRTRHHFR QMGRGNALPA QQIIQCRLLP
201 FQAFSREFPY PNSHRTQAA YPNGIHPRHR RNPRFPAVRM QHRRSTVRRR
251 SGTMARHTCR TRRQIPAPVQ NLPNVAGRGG GMKLPRNRFS LLSALWFAGG
301 IYSLLFKAAD TAPPPFPHFD KAAHLALFFA QILFLAKAFK TGKLPPIYRS
351 LIAFAFCFAV GSECAQAWFT ATRTGS LGDV LADLTGAALA LFAARSACRP
401 D*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1975>:

```

m616.seq
1  ATGTCAAACA CAATCAAAAT GGTGTGCGGC TTGGGCAACC CGGGCAAAGA
51  ATACGAACAG ACACGCCACA ATGCGGGTTT TTGGTTCCTC GACGAACTGG
101 CGTGGAATG GAAGGCTTCA TTAAAGAAG AAAAAAATT CTTCGGCGAA
151 GTCGCCCCTG CCGCCCTGCC CGACGGCGAC GTTGGCTGC TCAAACCTGC
201 CACGTTTATG AACCGTTCCG GACAGGCGAGT TGCCGCGCTT GCACAGTTCT
251 ACAAAATCAA ACCCGAAGAA ATCCTCGTCG TCCACGACGA ACTCGACATT
301 CCTTGGCGGAC GGATCAAAAT CAAACTCGGC GCGGGCAACG GCGGACACAA
351 CGGCTTGAAA GACATTcagG CAAACTCGG CACGGCAGAC TATTACCGCC
401 TGCGCCTCGG CATCGGCCAC CCGGGCGACC GCAACCTCGT CGTCGGCTAT
451 GTCTGAACA AACCCAGTAC GGAACA.CCG CCGACAGATT GACGATGCCG
501 TCGCCAAATC CTGCAAGACC ATACCCGACA TCCTTGCCCG CAAATGGGAA

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989

```

551 GAAGCAACCC GCTTCCTGCA CAGCAAATGA CCCGATGCCG TCTGAAGCCC
601 TTTCAGACGG CATGTTCCCG ATTTCCATAT CCGAACAGTC ATGACCGAAC
651 TCAAGCAGCT TATCCAAACC GAATCCATCC CCGTCATCGA AGAAACCCCTC
701 GATTTCCTGC TCTACGAATG CAGCATAGAC GATGCCCCCT CCGCCGAAGA
751 AATTGCCGTT TGGCGCGATA TGCTGGCCGC ACGCCGCCGA AAATTCCTGC
801 GCCTATCCAA ACTATGCCAG ACATGGCTTG AAGAGGAACA AGCATGAATC
851 TGCCACGCAA CCGCTTTATC CTGCTCTCGG CATTGTGTTT TGCAGGCAGC
901 ATTTACTCAC TGCTTTTCAA AGCTGCCGAA ACCGCCGCAC CGCCTTTTCC
951 GCATTTTGAC AAAGTGGCGC ACCTGCCCTT GTTTTTCGCA CAAATCTGGC
1001 TTCTGACCAA AGCATTGAGA ACCGACAACC GCCCATCCC CTATCGCAGC
1051 CTGATGGTCT TTGCCCTCTG TTTCGCCCTC TTCAGCGAAT GCGCGCAGGC
1101 ATGGTTTACC GCAACGAGAA CCGGCAGTTT GGGCGATGTC CTTGCCGACC
1151 TGACGGGCGC AGCCCTTGCC CTCTTACCG CGCGAGCTGC CTGCCGCCCG
1201 GACTAA

```

This corresponds to the amino acid sequence <SEQ ID 1976; ORF 616>:

```

m616.pep
1 MSNTIKMVVG LGNPGKEYEQ TRHNAGFWFL DELAWKNKAS FKEEKKFFGE
51 VARAALPDGD VWLLKPATFM NRSQQAVAL AQFYKIKPEE ILVVHDELDI
101 PCGRIKFKLG GNGGHNGLK DIQAKLGTD YRLRLGIGH PGDRNLVVG
151 VLNKPSTEXP PTDXRRCRQI PASHTRHPCR CMGRSNPLPA QMTRCRLKP
201 FQTACSRFPY PSHDRTOAA YPNRIHPRHR RNPRFPALRM QHRRCPLERR
251 NCRLARYAGR TRRKIPAPIQ TMPDMAXRGT SMNLPNRNFI LLSALWFAGS
301 IYSLLFKAAE TAPPPPHFD KVAHLALFFA CIWLLTKAFR TDNRPIPYRS
351 LMVFALCFAL FSECAQAWFT ATRTGLSDV LADLTGAALA LFTARAACRP
401 D*

```

m616/g616 86.0% identity in 401 aa overlap

m616.pep	10	20	30	40	50	60
	MSNTIKMVVGLGPNPGKEYEQTRHNAGFWFLDELAWKNKASFKEEKKFFGEVARAALPDGD					
g616	MSNTIKMVVGLGPNPGKEYEQTRHNAGFWFLDELAWKNKASFKEEKKFFGEVARAALPDGD					
	10	20	30	40	50	60
m616.pep	70	80	90	100	110	120
	VWLLKPATFMNRSQQAVALAQFYKIKPEEILVVHDELDIPCGRIKFKLGNGGHNGLK					
g616	VWLLKPATFMNRSQQAVALAQFYKIKPEEILVVHDELDIPCGRIKFKLGNGGHNGLK					
	70	80	90	100	110	120
m616.pep	130	140	150	160	170	180
	DIQAKLGTDYRLRLGIGHPGDRNLVVGVLNKPSTEXPPTDXRRCRQIPASHTRHPCR					
g616	DIQAKLGTDYRLRLGIGHPGDRNLVVGVLNKPSTEXPPTDXRRCRQIPASHTRHPCR					
	130	140	150	160	170	180
m616.pep	190	200	210	220	230	240
	QMGRSNPLPAQOMTRCRLKPFQTACSRFPYPNSHRTQAAYPNRIHPRHRNPFPALRM					
g616	QMGRSNPLPAQOMTRCRLKPFQTACSRFPYPNSHRTQAAYPNRIHPRHRNPFPALRM					
	190	200	210	220	230	240
m616.pep	250	260	270	280	290	300
	QHRRCPLERRNCRLARYAGRTRRKIPAPIQTMPDMAXRGTSMNLPNRNFI LLSALWFAGS					
g616	QHRRCPLERRNCRLARYAGRTRRKIPAPIQTMPDMAXRGTSMNLPNRNFI LLSALWFAGS					
	250	260	270	280	290	300
m616.pep	310	320	330	340	350	360
	IYSLLFKAAETAPPPPHFDKVAHLALFFAQIWLTKAFRTDNRPIPYRSLMVFALCFAL					
g616	IYSLLFKAAETAPPPPHFDKVAHLALFFAQIWLTKAFRTDNRPIPYRSLMVFALCFAL					
	310	320	330	340	350	360
m616.pep	370	380	390	400		
	FSECAQAWFTATRTGLSDVLADLTGAALALFTARAACRPDX					
g616	FSECAQAWFTATRTGLSDVLADLTGAALALFTARAACRPDX					
	370	380	390	400		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1977>:

990

a616.seq

```

1   ATGTCAAACA CAATCAAAT GGTGTGCGGC TTGGGCAACC CSGGCAAAGA
51  ATACGAACAG ACACGCCACA ATGCGGGTTT TTGGTTCCCTC GACGAACTGG
101 CGTGGAAATG GAAGGCTTCA TTAAAGAAG AAAAAAATT CTTCGGCGAA
151 GTCGCCCCGTG CTACCTTGCC CGACGGCGAT GTCTGGCTGC TCAAGCCGAC
201 CACGTTTCATG AACCGTTCCG GACAGGCAGT TGCCGCCCTT GCGCAGTTT
251 ATAAATCAA ACCGAAGAA ATCCTCGTCG TCCACGACGA ACTCGACATT
301 CCCTGCGGAC GGATCAAAT CAAACTCGGC GCGGGCAACG GTGGACACAA
351 CGGCTTGAAA GACATTCAGG CAAACTUGG CACGGCAGAC TATTACCGCC
401 TGCGCCTCGG CATCGGCCAC CCGGGCGACC GCAACCTCGT CGTCGGCTAT
451 GTCCTGAACA AACCCAGTAC GGAA.CACCG CCGACAGATT GACGATGCCG
501 TCGCCAAATC CCTGCAAGCC ATACCCGACA TCCTTGCCGG CAAATGTGAA
551 GAGGCAACCC GCTTCCTGCA CAGCAAATGA CCCGATGCCG TCTGAAGCCC
601 TTTGAGACGG CATGTTCCCG ATTCCATAT CCGAACAGTC ATGACCGAAC
651 TCAAGCAGCT TATCCAAACC GAATCCATCC CCGTCATCGA AGAAACCTC
701 GATTTCCTGC TGTACGAATG CAGCATCGAC GACGCACCAT CCGCCGAGAA
751 AGTGGCACAA TGGCGCGACA TACTTGCCGC ACGCGGCGGC AAATTCCTGC
801 GCCTGTCCAA AATCTGCCAA ACGTGGCTGG ACGAGGAGGC GGCATGAAGC
851 TGCCGCGCAA CCGCTTCAGC CTGCTTCCG CATTGTGGTT TGCCGCGGCG
901 ATCTATTGCG TGCTTTCAA AGCTGCCGAC ACGCGCGCGC CGCCGTTTCC
951 GCATTTGAC AAAGCAGCAC ACCTTGCCCT*GTTTTGCGA CAAATCTGGC
1001 TTTTGACCAA AGCATTCAAA ACCGAAAAC TTCCCATCCC CTACCGCAGC
1051 CTGATGGTCT TTGCCCTCTG TTTCGCCCTC TTCAGCGAAT GCGCGCAGGC
1101 ATGATTTACC GCAACGAGAA CCGGCAGTTT GGGCGATGTT CTTGCCGATA
1151 TGGCAGGTAC GGTCTCGCA CTCTTGCCG CCCGCGCCGC CGACCGCCCG
1201 GACTGA

```

This corresponds to the amino acid sequence <SEQ ID 1978; ORF 616.a>:

a616.pep

```

1   MSNTIKMVVG LGNPGKEYEQ TRHNAGFWFL DELAWKWKAS FKEEKKFFGE
51  VARATLPDGD VWLLKPPTFM NRSGQAAVAL AQFYKIKPEE ILVVHDELDI
101 PCGRIKFKLG GNGGHNCLK DIQAKLGTAD YYRLRLGIGH PGDRNLVVG
151 VLNKPSTEXP PTD*RCRRQI PASHTRHPCR QM*RGNPLPA QMTRCRLKP
201 FQTACSRFPY PNSHDTQAA YPNRIHPRHR RNPRFPAVRM QHRRRTIRRR
251 SGTMARHTCR TRRQIPAPVQ NLPNVAGRGG GMKLPRNRFS LLSALWFAGG
301 IYSLLFKAAD TAPPPFPHFD KAAHLALFFA QIWLTKAFK TGKLPPIYRS
351 LMVFALCFAL FSECAQA*FT ATRTGS LGDV LADMAGTVLA LFAARAADRP
401 D*

```

m616/a616 90.0% identity in 401 aa overlap

	10	20	30	40	50	60
m616.pep	MSNTIKMVVGLGNGPGKEYEQTRHNAGFWFLDELAWKWKASFKEEKKFFGEVARAALPDGD					
a616	MSNTIKMVVGLGNGPGKEYEQTRHNAGFWFLDELAWKWKASFKEEKKFFGEVARATLPDGD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m616.pep	VWLLKPATFMNRSGQAAVALAQFYKIKPEEILVVHDELDIPCGRIKFKLGGGNGGHNGLK					
a616	VWLLKPPTFMNRSGQAAVALAQFYKIKPEEILVVHDELDIPCGRIKFKLGGGNGGHNGLK					
	70	80	90	100	110	120
	130	140	150	160	170	180
m616.pep	DIQAKLGTADYYRLRLGIGHPGDRNLVVGYYLNKPSTEXPPTDXRCRRQIPASHTRHPCR					
a616	DIQAKLGTADYYRLRLGIGHPGDRNLVVGYYLNKPSTEXPPTDXRCRRQIPASHTRHPCR					
	130	140	150	160	170	180
	190	200	210	220	230	240
m616.pep	QMGRSNPLPAQMTRCRLKPFQTACSRFPYPNSHDTQAAYPNRIHPRHRRNPRFPALRM					
a616	QMXRGNPLPAQMTRCRLKPFQTACSRFPYPNSHDTQAAYPNRIHPRHRRNPRFPVRM					
	190	200	210	220	230	240
	250	260	270	280	290	300

991

```

m616.pep      QHRRCP LRRRNCRLARYAGRTRRKIPAPIQTMPD MAXRGTS MNLP RNR FILL S ALWFAGS
a616           QHRRRT IRRRSGT MARHTCRTRRQIPAPVQNL PNVAGRG GGMKLP RNR F S L S ALWFAGG
                250      260      270      280      290      300

                310      320      330      340      350      360
m616.pep      IY S L L F K A A E T A P P P F P H D K V A H L A L F F A Q I W L L T K A E R T D N R P I P Y R S L M V F A L C F A L
a616           IY S L L F K A A D T A P P P F P H D K A A H L A L F F A Q I W L L T K A F K T G K L P I P Y R S L M V F A L C F A L
                310      320      330      340      350      360

                370      380      390      400
m616.pep      F S E C A Q A W F T A T R T G S L G D V L A D L T G A A L A L F T A R A A C R P D X
a616           F S E C A Q A X F T A T R T G S L G D V L A D M A G T V L A L F A A R A A D R P D X
                370      380      390      400

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1979>:

```

g619.seq
1  ATGCCGCTCTG AAAAAAATAT CGGTTTATG GCAGGAAGCA GCCGTCGGTT
51  GCGGGTCGCC TTTGCGCTGT TGCTGGTTTC CTGCATCCTG TTTATGACGC
101 TCAACGTCAA AGGAGATTGG GACTTTGTCT TGCACCTGCG CCTGACCAAG
151 CTTGCCGCGC TGCTGATGGT CGCCTATGCG STCGGCGTGT CCACTCAACT
201 CTTCCAAACG CTGACCAACA ACCCGATTCT GACCCCTTCG ATTTTGGGTT
251 TCGATTTCGT GTATGTGTTT TTGCAGACCT TGCTGgtGTT TACGTtcgGC
301 GCGGTGGGCT ATAcatccct gccgttgacg jGCAAATTCG GCTTTGAACT
351 GGTGTTATG ATGGGCGGCT CGCTGCTGCT GTTTTACACG CTCATCCGTC
401 AGGGCGGGCG CGATTTGCCG CACATGATT TAATCGGCGT GATTTTCGGG
451 ATTTTGTTCC GCAGCCTTTC CTCGCTGCTT TCGCGCATGA TAGACCCCGA
501 AGAATTACG GCCGCGCAGG CGAATATGTT TGCCGGATTC AATACCGTCC
551 GCAGCGAGCT TTTAGGCATA GCGCGCTGG TCCTGCTCGT CAGCGCGGCG
601 GTCGTTTGGC ACGAACGCTA CCGCTCGGAC GTACACCTTT TGGGGCGCGA
651 CCAAGCCGTC AATTGGGCA TCAGCTACAC GCGCAACACC TTATGGATAC
701 TGCTTTGGAT TGCCGCATTG GTGGCGACGG CGACCGCGGT GTGCGGCCCC
751 GTGAGCTTTT TCGGGCTTCT CGCCGCTCGC CTTGCCAACC ACTTTTCCCC
801 gtCCGTGCGC CATTCCGTCC GCCTGCCgat gacggtttGC gtcgGcggCA
851 TCCTCTTggt cggCggacaA ACCGTATTCT AACACTTCTT GGGCATGAag
901 gCggTATTAA GCGTGGTGGt cgaATTTCGg ggcggactcG TTTCTCTCTA
951 TCTCGTTTTA AAACACAAA AATGA

```

This corresponds to the amino acid sequence <SEQ ID 1980; ORF 619.a>:

```

g619.pep
1  MPSEKNIGFM AGSSRPLRVA FALLLVSCIL FMTLNVKGDW DFVLHLRLTK
51  LAALLMVAYA VGVSTQLFQT LTNNPILTPS ILGFDSLTVF LQTLVFTFG
101 LVGYTSLPLT GRFGFELVVM NGGSLLLFYT LIRQGGRDLP HMILIGVIFG
151 ILFRSLSSLL SRMIDPEEFT AAQANMFAGF NTVRSELLGI GALVLLVSAA
201 VVWHERYRSD VHLLGRDQAV NLGISYTRNT LWILLWIAAL VATATAVVGP
251 VSFFGLLAAS LANHFSPSVR HSVRLPMTVC VGGILLVGGQ TVFEHFLGMK
301 AVL SVVVEFA GGLVFLYLVL KHKK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1981>:

```

m619.seq
1  ATGCCGCTCTG AAAAAAATAT CGGTTTATG GCAGGAAGCA GCCGCCCGTT
51  GTGGGTCGCC TTTGCGCTGT TGCTGGTTTC CTGCGTCCTG TTTATGACGC
101 TCAACGTCAA AGCGGATTGG GATTTTGTTT TGCAACTGCG GCTGACCAAA
151 CTTGCCGCGC TGCTGATGGT CGCCTATGCG GTCGGCGTGT CCACGCAACT
201 CTTCCAAACG CTGACCAATA ATCCGATTCT GACCCCTTCA ATTTTGGGTT
251 TCGATTTCGT GTATGTGTTT TTGCAGACCT TGCTGGTGT TACGTTCCGC
301 GCGGTGGGCT ATGCTTCCCT GCCGTGACG GGCAAATTCG GCTTTGAACT
351 GGTGTCATG ATGGGCGGCT CGCTGCTGCT GTTCTACACG CTCATCAAAC
401 AGGGCGGACG CGATTGTGCG CGCATGATT TAATCGGCGT GATTTTCGGG
451 ATTTTGTTCC GCAGCCTGTC GTCGCTGCTT TCGCGCATGA TCGATCCCGA
501 AGAATTACG GCCGCGCAGG CGAATATGTT TGCCGGATTC AATACCGTCC
551 ACAGCGAGCT TTTGGGCATA GCGCGCTGA TTCTGCTCGT CAGCGCGGCG
601 GTCGTTTGGC GCGAACGCTA CCGCTTGGAC GTTTACCTTT TGGGGCGTGA
651 CCAAGCCGTC AATTGGGCA TCAGCTACAC GCGCAACACC TTATGGATAC
701 TGCTTTGGAT TGCCGCATTG GTGGCGACGG CGACCGCGGT GGTGCGCCCC
751 GTAAGCTTTT TCGGGCTTCT CGCCGCTCGC CTTGCCAACC ACTTTTCCCC
801 GTCGGTCAA CATTCCGTCC GCCTGCCGAT GACGGTTTGT ATCGGCGGCA
851 TCCTCTTGGT CGGCGGACAG ACCGTGTTCT AACACTGCT CGGTATGCAG

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901 GCAGTGTGA GCGTAGTAGT AGAATTGCC GCGGACTCG TTTCTCTA
 951 TCTCGTTTA AACACAAAA AATGA

This corresponds to the amino acid sequence <SEQ ID 1982; ORF 619>:

m619.pep
 1 MPSEKNIGFM AGSSRPLWVA FALLLVSCVL FMTLVNKGDW DFVLQRLTK
 51 LAALLMVAYA VGVSTQLFQT LTNNPILTPS ILGFDSLTVF LQTLVFTFG
 101 GVGYASLPLT GKFGFELVVM MGGSLLLFYT LIKQGRDLS RMILIGVIFG
 151 ILFRSLSSLL SRMIDPEEFT AAQANMFAGF NTVHSELLGI GALILLVSAA
 201 VVWRERYRLD VYLLGRDQAV NLGISYTRNT LWILLWIAAL VATATAVVG
 251 VSFFGLLAAS LANHFSPSVK HSVRLPMTVC GIGILLVGGQ TVFEHLLGMQ
 301 AVLSVVVEFA GGLVFLYLVL KHKX*

m619/g619 95.1% identity in 324 aa overlap

	10	20	30	40	50	60
m619.pep	MPSEKNIGFMAGSSRPLWVAFALLLVSCVLFMTLVNKGDWDFVLQRLTKLAALLMVAYA					
g619	MPSEKNIGFMAGSSRPLRVAFALLLVSCILFMTLVNKGDWDFVLHLRLTKLAALLMVAYA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m619.pep	VGVSTQLFQTLTNNPILTPSILGFDSLTVFLQTLVFTFGGVGYASLPLTGKFGFELVVM					
g619	VGVSTQLFQTLTNNPILTPSILGFDSLTVFLQTLVFTFGGVGYTSLPLTGKFGFELVVM					
	70	80	90	100	110	120
	130	140	150	160	170	180
m619.pep	MGGSLLLFYTLIKQGRDLSRMILIGVIFGILFRSLSSLLSRMIDPEEFTAAQANMFAGF					
g619	MGGSLLLFYTLIRQGRDLPHMILIGVIFGILFRSLSSLLSRMIDPEEFTAAQANMFAGF					
	130	140	150	160	170	180
	190	200	210	220	230	240
m619.pep	NTVHSELLGIGALILLVSAVVWRERYRLDVYLLGRDQAVNLGISYTRNTLWILLWIAAL					
g619	NTVRSSELLGIGALVLLVSAVVWHERYRSDVHLLGRDQAVNLGISYTRNTLWILLWIAAL					
	190	200	210	220	230	240
	250	260	270	280	290	300
m619.pep	VATATAVVGVPVSFFGLLAASLANHFSPSVKHSVRLPMTVCIGIGILLVGGQTVFEHLLGMQ					
g619	VATATAVVGVPVSFFGLLAASLANHFSPSVRHSVRLPMTVCVGGILLVGGQTVFEHFLGMK					
	250	260	270	280	290	300
	310	320				
m619.pep	AVLSVVVEFAGGLVFLYLVLKHKX					
g619	AVLSVVVEFAGGLVFLYLVLKHKX					
	310	320				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1983>:

a619.seq
 1 ATGCCGTCTG AAAAAATAT CGGTTTTATG GCAGGAAGCA GCCGTCCGTT
 51 GTGGGTTGCC TTGCGCTGT TGCTGGTTTC CTGCATCCTG TTTATGACGC
 101 TCAACGTCAA AGGCGATTGG GATTTTGTTC TGCACCTCCG CCTGACCAAG
 151 CTTGCCGCGC TGCTGATGGT CGCCTATGCG GTCGGCGITT CGACCCAGCT
 201 TTTTCAAACG CTGACCAACA ATCCGATTCT GACCCCTTCG ATTTTGGGTT
 251 TCGATTCGCT GTATGTGTTT TTGCAGACCT TGCTGGTGTT TACGTTCGGC
 301 GCGGTGGGCT ATGCTTCCCT GCCGTGACG GGCAAAATCG GCTTTGAACT
 351 GGTCGTTATG ATGGGCGGCT CGCTGCTGCT GTTTTACACG CTCATCAAAC
 401 AGGGCGGGCG CGATTGCGG CGTATGATTT TAATCGGCGT GATTTTCGGG
 451 ATTTTGTTCG CAGCCTGTC GTCGCTGCTT TCGCGCATGA TCGACCCCGA
 501 AGAATTTACG GCGGCGCAGG CGAATATGTT TGCCGATTTC AATACCGTCC
 551 ACAGCGAGCT TTTAGGCATA GGCGCGCTGA TTCTGCTCGT CAGCGCGGCG
 601 GTCGTTTGGC GCGAACGCTA CCGCTTGGAC GTACACCTTT TGGGGCGCGA
 651 CCAAGCCATA AATTTGGGCA TCAGCTACAC GCGCAACACC TTATGGATAC
 701 TGCTTTGGAT TGCCGCGCTG GTGGCGACGG CGACCGCCGT TGTCGGCCCC

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751  GTAAGCTTTT TCGGGCTTCT CGCGCCTCG CTTGCCAACC ACITTTCCCC
801  GTCGGTCAAA CATTCCGTCC GCCTGCCGAT GACGGTTTGT GTCGGCGGCA
851  TCCTCTTGGT CGGCGGACAG ACCGTATTCT AACACTTCTT GGGCATGAAG
901  GCGGTATTAA GCGTGGTGGT CGAATTTCG GCGGGACTCG TTTCTCTTA
951  TCTCGTTTTA AGACACAAAA AATGA

```

This corresponds to the amino acid sequence <SEQ ID 1984; ORF 619.a>:

```

a619.pep
1  MPSEKNIGFM AGSSRPLWVA FALLLVSCIL FMTLNVKGDW DFVLHLRLTK
51  LAALLMVAYA VGVSTQLFQT LTNNPILTPS ILGFDSLTVF LQTLVFTFG
101 GVGYASLPLT GKFGFELVVM MGSLLLFYT LIKQGGRLP RMILIGVIFG
151 ILFRSLSSL SRMIDPEEFT AAQANMFAGF NTVHSELLGI GALILLVSAA
201 VVWRERYRLD VHLLGRDQAI NLGISYTRNT LWILLWIAAL VATATAVVG
251 VSFFGLLAAS LANHFSPSVK HSVRLPMTVC VGGILLVGGQ TVFEHFLGMK
301 AVLSVVVEFA GGLVFLYLVL RHKK*

m619/a619 97.2% identity in 324 aa overlap

m619.pep      10      20      30      40      50      60
MPSEKNIGFMAGSSRPLWVAFALLLVSCVLFMTLNVKGDWDFVLQRLTKLAALLMVAYA
|||||
a619          10      20      30      40      50      60
MPSEKNIGFMAGSSRPLWVAFALLLVSCILFMTLNVKGDWDFVLHLRLTKLAALLMVAYA
|||||

m619.pep      70      80      90     100     110     120
VGVSTQLFQTLTNNPILTPSILGFDSLTVFLQTLVFTFGGVGYASLPLTGKFGFELVVM
|||||
a619          70      80      90     100     110     120
VGVSTQLFQTLTNNPILTPSILGFDSLTVFLQTLVFTFGGVGYASLPLTGKFGFELVVM
|||||

m619.pep     130     140     150     160     170     180
MGSLLLFYTLIKQGGRLDSRMILIGVIFGILFRSLSSLSRMIDPEEFTAAQANMFAGF
|||||
a619         130     140     150     160     170     180
MGSLLLFYTLIKQGGRLDPRMILIGVIFGILFRSLSSLSRMIDPEEFTAAQANMFAGF
|||||

m619.pep     190     200     210     220     230     240
NTVHSELLGIGALILLVSAAVVWRERYRLDVYLLGRDQAVNLGISYTRNTLWILLWIAAL
|||||
a619         190     200     210     220     230     240
NTVHSELLGIGALILLVSAAVVWRERYRLDVHLLGRDQAINLGISYTRNTLWILLWIAAL
|||||

m619.pep     250     260     270     280     290     300
VATATAVVGVPVSFFGLLAASLANHFSPSVKHSVRLPMTVCIGGILLVGGQTVFEHLLGMQ
|||||
a619         250     260     270     280     290     300
VATATAVVGVPVSFFGLLAASLANHFSPSVKHSVRLPMTVCVGGILLVGGQTVFEHFLGMK
|||||

m619.pep     310     320
AVLSVVVEFAGGLVFLYLVLKHKXX
|||||
a619         310     320
AVLSVVVEFAGGLVFLYLVLKHKXX
|||||

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1985>:

```

g620.seq
1  ATGAAGAAAA CCCTGTTGGc AATTGTTGCC gttttCGCCT TAAGTGCTG
51  CCGGcaggcg gaAGaggcac cgccgCCTTT ACCCCGGCAG AtTAGCGacc
101 gttcggtcgg aCACTAttgC Agtatgaacc tgaccgaaca caacggcccc
151 aaagcccaga ttttttgaa cGGCAAAACC GATCAGCCCG TTTGGTTCTC
201 CACCGTcaag cagatgttcg GCTATACCA GCTGCCCGAA GAGCCCAAAG
251 GCATCCGCGT GATTACGTT ACCGATATGG GCAATGTTAC CGATTGGACG
301 AATCCTAATG CCGACACGGA GTGGATAGAT GCGAAAAAAG CCTTTTACGI
351 CATCGACAGC GGCTTTATCG GCGGTATGGG CGCGGAAGAC GCGCTGCCGT
401 TCGGCAACAA GGAGCAGGCT GAAAAATTG CAAAGGATAA AGGCGGCAAG
451 GTCGTCGGTT TTGACGATAT GCCCGATGCT TACATTTTCA AGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1986; ORF 620.ng>:

```
g620.pep
1  MKKTLAIVA VFALSACRQA EEAPPPLPRQ ISDRSVGHYC SMNLTEHNGP
51  KAOIFLNGKP DQPVWFSTVK QMFGYTKLPE EPKGIRVIYV TDMGNVTDWT
101 NPNADTEWID AKKAFYVIDS GFIGGMAED ALPFGNKEQA EKFAKDKGGK
151 VVGFDMPDA YIFK*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1987>:

```
m620.seq
1  ATGAAAAAAA CCCTGTTGGC AATTGTTGCC GTTCCGCCT TAAGTGCCTG
51  CCGGCAGGCG GAAGAGGGAC CGCCGCCTTT ACCCCGGCAG ATTAGCGACC
101 GTTCGGTCGG AACTATTGCG AGTATGAACC TGACCGAACA CAACGGCCCC
151 AAAGCCCAGA TTTTCTTGAA CGGCAAACCC GATCAGCCCG TTTGGTTCTC
201 CACCATCAAG CAGATGTTCC GCTATACCAA GCTGCCCGAA GAGCCTAAAG
251 GCATCCGCGT GATTACGTT ACCGATATGG GCAATGTTAC CGATTGGACG
301 AATCCCAATG CCGACACGGA GTGGATGGAT GCGAAAAAAG CCTTTACGT
351 CATCGACAGC GGCTTTATCG GCGGTATGGG TCGGGAAGAC GCGCTGCCGT
401 TCGGCAACAA AGAGCAGGCT GAGAAATTG CAAAGGATAA AGGCGGTAAG
451 GTTGTCGGTT TCGACGATAT GCCTGATACC TATATTTTCA AATAA
```

This corresponds to the amino acid sequence <SEQ ID 1988; ORF 620>:

```
m620.pep
1  MKKTLAIVA VSALSACRQA EEGPPPLPRQ ISDRSVGHYC SMNLTEHNGP
51  KAOIFLNGKP DQPVWFSTIK QMFGYTKLPE EPKGIRVIYV TDMGNVTDWT
101 NPNADTEWMD AKKAFYVIDS GFIGGMAED ALPFGNKEQA EKFAKDKGGK
151 VVGFDMPDT YIFK*
```

m620/g620 97.0% identity in 164 aa overlap

	10	20	30	40	50	60
m620.pep	MKKTLAIVAVSALSACRQAEEGPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP					
g620	MKKTLAIVAVFALSACRQAEEAPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m620.pep	DQPVWFSTIKQMFGYTKLPEEPKGIRVIYVTDMGNVTDWTPNADTEWMDAKKAFYVIDS					
g620	DQPVWFSTVKQMFGYTKLPEEPKGIRVIYVTDMGNVTDWTPNADTEWIDAKKAFYVIDS					
	70	80	90	100	110	120
	130	140	150	160		
m620.pep	GFIGGMAEDALPFGNKEQAEKFAKDKGGKVVGFDMPDTYIFKX					
g620	GFIGGMAEDALPFGNKEQAEKFAKDKGGKVVGFDMPDAYIFKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1989>:

```
a620.seq
1  ATGAAAAAAA CCCTGTTGGC AATTGTTGCC GTTCCGCCT TAAGTGCCTG
51  CCGGCAGGCG GAAGAGGGAC CGCCGCCTTT ACCCCGGCAG ATTAGCGACC
101 GTTCGGTCGG AACTATTGCG AGTATGAACC TGACCGAACA CAACGGCCCC
151 AAAGCCCAGA TTTTCTTGAA CGGCAAACCC GATCAGCCCG TTTGGTTCTC
201 CACCATCAAG CAGATGTTCC GCTATACCAA GCTGCCCGAA GAGCCTAAAG
251 GCATCCGCGT GATTACGTT ACCGATATGG GCAATGTTAC CGATTGGACG
301 AATCCCAATG CCGACACGGA GTGGATGGAT GCGAAAAAAG CCTTTACGT
351 CATCGACAGC GGCTTTATCG GCGGTATGGG TCGGGAAGAC GCGCTGCCGT
401 TCGGCAACAA AGAGCAGGCT GAGAAATTG CAAAGGATAA AGGCGGTAAG
451 GTTGTCGGTT TCGACGATAT GCCTGATACC TATATTTTCA AATAA
```

This corresponds to the amino acid sequence <SEQ ID 1990; ORF 620.a>:

```
a620.pep
1  MKKTLAIVA VSALSACRQA EEGPPPLPRQ ISDRSVGHYC SMNLTEHNGP
51  KAOIFLNGKP DQPVWFSTIK QMFGYTKLPE EPKGIRVIYV TDMGNVTDWT
101 NPNADTEWMD AKKAFYVIDS GFIGGMAED ALPFGNKEQA EKFAKDKGGK
151 VVGFDMPDT YIFK*
```

995

m620/a620 100.0% identity in 164 aa overlap

	10	20	30	40	50	60
m620.pep	MKKTLAIVAVSALSACRQAEEGPPPLRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP					
a620	MKKTLAIVAVSALSACRQAEEGPPPLRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m620.pep	DQPVWFSTIKQMFYTKLPPEPKGIRVIYVTDMGNVTDWTPNADTEWMDAKKAFYVIDS					
a620	DQPVWFSTIKQMFYTKLPPEPKGIRVIYVTDMGNVTDWTPNADTEWMDAKKAFYVIDS					
	70	80	90	100	110	120
	130	140	150	160		
m620.pep	GFIGGMAEDALPFGNKEQAEKFAKDKGGKVVGFDMPDTYIFKX					
a620	GFIGGMAEDALPFGNKEQAEKFAKDKGGKVVGFDMPDTYIFKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1991>:

g622.seq

```

1  ATGCAactta  ccgctgtcgg  ACTCAATCAT  CAAACCGCAC  CTTTAAGCAT
51  ACGGGAAAag  ctggCGTTTG  CCGCCGCCGC  CCTGCCAGAA  gccgTccgCA
101 ATCTTGCCCG  AAGCAATGCG  GCAACGGAGG  CGGTAATCCT  TTCTACCTGC
151 AACCGCACCG  AGCTTTACTG  CGTCGCCGAT  TCGGAAGaaa  TCATCCGATG
201 GCTTGCCGAT  TACCACAGTT  TGCCGATTGA  AGAAATCCGT  CCGTATCTGT
251 ACACGCTGGA  TATGCAGGAA  ACCGTGCGCC  ACGCCTTCCG  CGTTGCCTGC
301 GGCTTGGAAT  CGATGGTTT  GGGCGAGCCG  CAGATTTTGG  GGCAGATTAA
351 AGATGCGGTG  CGTGCGGCTC  AAGAACAGGA  AAGTATGGGG  GCAAAACTCA
401 ATGCCCTGTT  CCAAAAAACC  TTTTCCGTG  CTAAGAAGT  CCGTACCGAT
451 ACCGCTGTGC  GCGAAAATTC  GGTTCGATG  GCTTCCCGGT  CCGTCAAGTT
501 GCGGGAACAG  ATTTTCCCG  ACATCGGCGA  TTTGAACGTA  TTGTTTATCG
551 GCGCAGGCGA  AATGATTGAG  CTGGTTGCCA  CTTATTTTGC  CGCCAAAAAT
601 CCCC GGCTGA  TGACGGTTGC  CAACCGGACG  CTGGCGCGTG  CACAGGAGTT
651 GTGCGACAAG  CTCGGTGTTA  ACGCCGAACC  GTGCCTGCTG  TCCGATCTGC
701 CTGCCATTCT  GCACGATTAC  GACGTGGTGG  TTTCTTCAAC  GGCGAGCCAG
751 CTTCCGATAG  TCGGCAAAGG  CATGGTCGAA  CGCGCATTTA  AACAGCGTCA
801 GAGTATGCCG  TTGTTTATGC  TTGACTTGCG  CGTCCGCCGC  GATATTGAAG
851 CGGAAGTCGG  CGATTGAAC  GATGCGTATC  TTTATACGGT  GGACGATATG
901 GTCACATCG  TCCAAAGCG  caaggaggca  aggcagaaag  ccgccgcCgc
951 cgccgaaacg  ctggTGTCGG  AAAAGGTTGC  CGAATTGTGC  AGGCAGCAGC
1001 AGGGCAGGCA  GagggttcCG  CTGATTAAGG  CCTTCGGGGA  CGAGGGCGAG
1051 AAAGCGCGCA  AGCAGGTGTT  GGAAAATGCG  ATGAAACAGC  TTGCCAAAGG
1101 CGcaacGGCG  GAAGagggtt  TGgaacggct  gtccgtcCAA  CTGACCAACA
1151 AGCTGCTGCA  TTCGCCAACT  CAAACCTTGA  ATAAGCGGG  GGAAGAAGAT
1201 AAAGatttGG  TTCATGCCgt  cGCGCAGATt  tatcatttGG  ACAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1992; ORF 622.ng>:

g622.pep

```

1  MQLTAVGLNH  QTAPLSIREK  LAFAAAAALPE  AVRNLARSNA  ATEAVILSTC
51  NRTELYCVGD  SEEIIRWLAD  YHSLPIEEIR  PYLYTLDMQE  TVRHAFRVAC
101 GLDSMVLGEP  QILGQIKDAV  RAAQEQESMG  AKLNALFQKT  FSVAKEVRTD
151 TAVGENSVSM  ASASVKLAEO  IFPDIGDLNV  LFIGAGEMIE  LVATYFAAKN
201 PRLMTVANRT  LARAQELCDK  LGVNAEPCLL  SDLPAILHDY  DVVVSSTASQ
251 LPIVGKGMVE  RALKQROSM  LFMLDLAVPR  DIEAEVGLDN  DAYLYTVDDM
301 VNIVQSGKEA  RQKAAAAAET  LVSEKVAEFV  RQQQGRQSV  LIKALRDEGE
351 KARKQVLENA  MKQLAKGATA  EEVLERLSVQ  LTNKLLHSPT  QTLNKAGEED
401 KDLVHAVAQI  YHLDK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1993>:

m622.seq

```

1  ATGCAACTTA  CCGCTGTCCG  ACTCAATCAT  CAAACCGCAC  CTTTAAGCAT
51  ACGGGAAAAG  CTGGCGTTTG  CCGCCGCCGC  CCTGCCATAA  GCCGTCCGCA
101 ATCTTGCCCG  AAGCAATGCG  GCAACGGAGG  CGGTAATCCT  TTCTACCTGC
151 AACCGCACCG  AGCTTTACTG  CGTCGGTGAT  TCGGAAGAAA  TCATCCGATG
201 GCTTGCCGAT  TACCACAGTT  TGCCGATTGA  AGAAATCCGT  CCGTATCTGT
251 ACGCGCTGGA  TATGCAGGAG  ACTGTGCGCC  ATGCTTTCCG  CGTCGCTGTC

```

```

301 GGGCTGGATT CGATGGTGT GGGCGAGCCG CAGATTTTAG GACAGATTAA
351 GGATGCCGTT AGGGTTGCTC AAGAGCAGGA AACTATGGGT AAGAACTCA
401 ATGCCCTGTT CCAAAAAACC TTTTCCGTG CTAAAGAGGT CCGTACCGAT
451 ACTGCCGTCG GCGAAAACTC GGTTCATG GCTTCGCTT CCGTCAAAAT
501 GGCAGAACAG ATTTTCCCG ACATCGGCGA TTTGAATGTC TTGTTTATCG
551 GCGCAGCCGA AATGATTGAG CTGGTIGCCA CTATTITGTC CGCCAAAAGT
601 CCCCCTGTA TGACGGTTGC CAACCGGACG CTGGCGGTG CACAGGAGTT
651 GTGCGACAAG CTCGGTGTCA ACGCCGAACC GTGCTGTCTG TCCGATCTGC
701 CTGCCATTCT GCACGATTAC GACGTAGTGG TTCTTCAAC GGCAAGCCAG
751 TTGCCATTG TCGGCAAAGG CATGGTGGAG CGTGCATTGA AACAAAGGCA
801 GAGTATGCCG TTGTTTATGC TTGATTGGC AGTGCCGCTG GACATTGAAG
851 CGGAAGTCGG CGATTGAAT GATGCCTATC TTATACGGT GGACGATATG
901 GTCAATATCG TCCAAAGCGG CAAGGAGGCA AGGCAGAAG CCGCCGCCG
951 CGCCGAAACG CTGGTGTCCG AGAAAGTTGC CGAATTGTG AGGCAGCAGC
1001 AGGGCAGGCA GAGTGTCCCT TTGATTAAAG CGTTGCGGGA CGAGGGCGAG
1051 AAAGCGCGCA AACAGGTGTT GGAAATGCC ATGAACAGC TTGCCAAAGG
1101 CGCAACGGCA GAAGAGGTTT TGGACGGCT GTCCGTCCAA CTGACCAACA
1151 AGCTGCTGCA TTCGCCGACC CAAACCTGA ATAAGGCGGG GGAAGAAGAT
1201 AAAGATTGGT TTCATGCCGT CGCGCAGATT TATCATTGG ACAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1994; ORF 622>:

```

m622.pep
1  MQLTAVGLNH QTAPLSIREK LAFAAAAALPK AVRNLARSNA ATEAVILSTC
51  NRTELYCVGD SEEIRWLAD YHSLPIEIR PYLYALDMQE TVRHAERVAC
101 GLDSMVLGEP QILGQIKDAV RVAQEESMG KKLNALFQKT FSVAKEVRTD
151 TAVGENSVSM ASASVKLAEQ IFPDIGDLNV LFIGAGEMIE LVATYFAAKS
201 PRLMTVANRT LARAQELCDK LGVNAEPCLL SLPAILHDY DVVVSSTASQ
251 LPIVGKGMVE RALKQSQMP LFMLDLAVPR DIEAEVGLND DAYLYTVDDM
301 VNIVQSGKEA RQKAAAAAET LVSEKVAEFV RQQQGRQSVPLIKALRDEGE
351 KARKQVLENA MKQLAKGATA EEVLERLSVQ LTNKLLHSPT QTLNKAGEED
401 KDLVHAVAQI YHLDK*

```

m622/g622 98.8% identity in 415 aa overlap

m622.pep	10	20	30	40	50	60
	MQLTAVGLNHQTAPLSIREKLAFAAAAALPKAVRNLARSNAATEAVILSTCNRTELYCVGD					
g622	10	20	30	40	50	60
	MQLTAVGLNHQTAPLSIREKLAFAAAAALPEAVRNLARSNAATEAVILSTCNRTELYCVGD					
m622.pep	70	80	90	100	110	120
	SEEIRWLADYHSLPIEIRPYLYALDMQETVRHAERVACGLDSMVLGEPQILGQIKDAV					
g622	70	80	90	100	110	120
	SEEIRWLADYHSLPIEIRPYLYTLDMQETVRHAERVACGLDSMVLGEPQILGQIKDAV					
m622.pep	130	140	150	160	170	180
	RVAQEESMGKKLNALFQKTFVSAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV					
g622	130	140	150	160	170	180
	RAAQEESMGAKLNALFQKTFVSAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV					
m622.pep	190	200	210	220	230	240
	LFIGAGEMIELVATYFAAKSPRLMTVANRTLARAQELCDKLGVNAEPCLLSDLPAILHDY					
g622	190	200	210	220	230	240
	LFIGAGEMIELVATYFAAKNPRLMTVANRTLARAQELCDKLGVNAEPCLLSDLPAILHDY					
m622.pep	250	260	270	280	290	300
	DVVVSSTASQLPIVGKGMVERALKQSQMPLEFMLDLAVPRDIEAEVGLNDAYLYTVDDM					
g622	250	260	270	280	290	300
	DVVVSSTASQLPIVGKGMVERALKQSQMPLEFMLDLAVPRDIEAEVGLNDAYLYTVDDM					
m622.pep	310	320	330	340	350	360
	VNIVQSGKEARQKAAAAAETLVSEKVAEFVRQQQGRQSVPLIKALRDEGEKARKQVLENA					
g622	310	320	330	340	350	360
	VNIVQSGKEARQKAAAAAETLVSEKVAEFVRQQQGRQSVPLIKALRDEGEKARKQVLENA					
m622.pep	370	380	390	400	410	
	MKQLAKGATAEEVLERLSVQLTNKLLHSPTQTLNKAGEEDKDLVHAVAQIYHLDKX					
g622	MKQLAKGATAEEVLERLSVQLTNKLLHSPTQTLNKAGEEDKDLVHAVAQIYHLDKX					

997

370 380 390 400 410

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1995>:

```
a622.seq
1  ATGCAACTTA CCGCTGTCGG ACTCAATCAT CAAACCGCAC CTTTAAGCAT
51  ACGGAAAAAG CTGGCGTTTG CCGCGGCCTG CCTGCCCGAA GCCGTCCGCA
101 ATCTTGCCCG AAGCAATGCG GCAACGGAGG CGGTAATCCT TTCTACCTGC
151 AACCGTACCG AGCTTTACTG TGTAGGTGAT TCGGAAGAAA TCATCCGTG
201 GCTCGCAGAC TATCACAGCC TTCCCATAGA AGAAATCAGC CCCTACCTTT
251 ATACTTTGGG GATGCAGGAG ACTGTGCGCC ATGCTTTCCG CGTCGCCTGC
301 GGCTTGATT CGATGGTGTT GSGCGAGCCG CAGATTTTAG GACAGATTAA
351 GGATGCGGTC AGGGTTGCTC AAGAGCAGGA AAGTATGGGT AAGAACTCA
401 ATGCCCTGTT CCAAAAAACC TTTTCTGTTG CTAAAGAGGT CCGTACCGAT
451 ACTGCCGTCG GCGAAAACTC GGTTCCTATG GCTTCCGCTT CCGTCAAGTT
501 GGCAGAGCAG ATTTTCCCGG ACATCGGCGA TTGAATGTC TTGTTTATCG
551 GTGCGGGTGA GATGATTGAG CTGGTTGCCA CTTATTTTGC CGCCAAAAGT
601 CCCCGGCTGA TGACGGTTGC CAACCGGACG CTGGCGCGTG CACAGGAGTT
651 GTGCGACAAG CTCGGTGTCA ACGCCGAACC GTGCCTGCTG TCCGATCTGC
701 CTGCCATTTT GCATGAGTAC GACGTGGTGG TTTCTTCAAC GSCAAGCCAG
751 TTGCCCATTT TCGGCAAAGG TATGGTGGAG CGCGCATTGA AACAAAGGCA
801 GAGTATGCCG TTGTTTATGC TTGACTTGGC CGTGCCGCGA GACATTGAGG
851 CGGAAGTCGG AGATTTGAAC GATGCCTATC TTTATACGGT GGACGATATG
901 GTCAATATCG TCCAAAGCGG CAAGGAGGCA AGGCAGAAGG CCGCCGCCGC
951 CGCCGAAACG CTGGTGTCCG AGAAGGTTGC CGAATTGTGC AGGCAGCAGC
1001 AGGCGAGGCA GAGTGTCCCG TTAATCAGGG CATTGAGGGA TGAGGGAGAG
1051 AAAGCGCGCA AACAGGTCTT GGAAATGCG ATGAAACAGC TTGCCAAAGG
1101 CGCAACGCGA GAAGAGGTTT TGGAAAGGCT GTCGATCCAA CTGACCAACA
1151 AGCTGCTGCA TTCGCCGACC CAAACCTTGA ATAAGGCGGG GGAAGAAGAT
1201 AAAGATTGGT TTCACGCCGT CGCGCAGATT TATCATTGGG ACAAATAA
```

This corresponds to the amino acid sequence <SEQ ID 1996; ORF 622.a>:

```
a622.pep
1  MQLTAVGLNH QTAPLSIREK LAFAAACLPE AVRNLARSNA ATEAVILSTC
51  NRTELYCVGD SEEIIRWLAD YHSLPIEEIS PYLYTLGMQE TVRHAFRVAC
101 GLDSMVLGEP QILGQIKDAV RVAQEQESMG KKLNALFQKT FSVAKEVRTD
151 TAVGENSVSM ASASVKLAEQ IFPDIGDLNV LFIGAGEMIE LVATYFAAKS
201 PRLMTVANRT LARAQELCDK LGVNAEPCLL SDLPAIHLEY DVVVSSTASQ
251 LPIVGKGMVE RALKQRQSMF LFMLDLAVPR DIEAEVGLN DAYLYTVDDM
301 VNIVQSGKEA RQKAAAAAET LVSEKVAEFV RQQQGRQSV LIRALRDEGE
351 KARKQVLENA MKQLAKGATA EEVLRLSIQ LTNKLLHSPT QTLNKAGEED
401 KDLVHVAQI YHLDK*
```

m622/a622 98.1% identity in 415 aa overlap

	10	20	30	40	50	60
m622.pep	MQLTAVGLNHQTAPLSIREKLAFAAAALPKAVRNLARSNAATEAVILSTCNRTELYCVGD					
a622	MQLTAVGLNHQTAPLSIREKLAFAAACLPEAVRNLARSNAATEAVILSTCNRTELYCVGD					
	10	20	30	40	50	60
m622.pep	SEEIIRWLADYHSLPIEEIRPYLYALDMQETVRHAFRVACGLDSMVLGEPQILGQIKDAV					
a622	SEEIIRWLADYHSLPIEEISPYLYTLGMQETVRHAFRVACGLDSMVLGEPQILGQIKDAV					
	70	80	90	100	110	120
m622.pep	RVAQEQESMGKKLNALEQTFVSAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV					
a622	RVAQEQESMGKKLNALEQTFVSAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV					
	130	140	150	160	170	180
m622.pep	RVAQEQESMGKKLNALEQTFVSAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV					
a622	RVAQEQESMGKKLNALEQTFVSAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV					

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	190	200	210	220	230	240
m622.pep	LFIGAGEMIELVATYFAAKSPRLMTVANRTLARAQELCDKLGVNAEPCLLSDLPAILHDY					
a622	LFIGAGEMIELVATYFAAKSPRLMTVANRTLARAQELCDKLGVNAEPCLLSDLPAILHEY					
	190	200	210	220	230	240
	250	260	270	280	290	300
m622.pep	DVVVSSTASQLPIVGKGMVERALKQRQSMPLFMLDLAVPRDIEAEVGDNDAYLYTVDDM					
a622	DVVVSSTASQLPIVGKGMVERALKQRQSMPLFMLDLAVPRDIEAEVGDNDAYLYTVDDM					
	250	260	270	280	290	300
	310	320	330	340	350	360
m622.pep	VNIVQSGKEARQKAAAAAETLVSEKVAEFVRQQQGRQSVPLIKALRDEGEKARKQVLENA					
a622	VNIVQSGKEARQKAAAAAETLVSEKVAEFVRQQQGRQSVPLIRALRDEGEKARKQVLENA					
	310	320	330	340	350	360
	370	380	390	400	410	
m622.pep	MKQLAKGATAEEVLERLSVQLTNKLLHSPQTQTLNKAGEEDKDLVHAVAQIYHLDKX					
a622	MKQLAKGATAEEVLERLSIQLTNKLLHSPQTQTLNKAGEEDKDLVHAVAQIYHLDKX					
	370	380	390	400	410	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1997>:

g624.seq
 1 ATGATCCGTT ATCTTTTAAT TGCCTGCGGC GGCATCTCCC TGCTGTTGGG
 51 GATAATCGGC ATTTTTTTCG CGCTGTTGCC GACCACGCCG TTCGTAACAC
 101 TCTCCGCCCG CTGCTGGGCA AAGGCATCCC cgcgcTTTCa ccgCTGGCTG
 151 CACcgGCacc gCTATTTCGG CCGATGGTT CATAACTGGG AACAAAACGG
 201 CGCAGTGCCG CGCAAAGCCA AGATTTCGCG CATCAGCATG AtaaccgcAt
 251 cctgcctcat gatctTTtg CatTTTCccc aacnctggtg ggtcGGGGCG
 301 GTTTCATCGG TTTTGTGTC CCTGTGcAc ATacggatgt gGcacAGacC
 351 cgaatCTTGA

This corresponds to the amino acid sequence <SEQ ID 1998; ORF 624.ng>:

g624.pep
 1 MIRYLLIACG GISLLLLGIIG IFLPLLPTTP FVLLSAACWA KASPRFHRWL
 51 HRHRYFGPMV HNWEQNGAVP RKAKIFAISM ITASCLMIFW HFQXWWVGA
 101 VSSVFCSLVT IRMWHRPES*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1999>:

m624.seq
 1 ATGATACGTT ATCTTTTAAT TGCCTGCGGC TGCATTTCCT TACTGTTGGG
 51 TATCATCGGC ATTTTTTTCG CGCTGTTGCC GACCACGCCG TTCGTAACAC
 101 TCTCCGCCCG CTGCTGGGCA AAGGCATCCC CGCGCTTTTA CCGCTGGCTG
 151 CACCGGCACC GCTATTTCGG CCGATGGTT CATAACTGGG AACAAAACGG
 201 CGCAGTGCCG CGCAAAGCCA AAATATTCGC CATCAGTATG ATGACCGCAT
 251 CCTSCCTGAT AATGTTTTCG CAGTTTCCCC AACGCTGGTG GGTGCGGGCG
 301 GTTTCATCGG TTTTGTGTC CCTGTGCGCC ATATGGATGT GGCAGAGGCC
 351 CGAATCTTGA

This corresponds to the amino acid sequence <SEQ ID 2000; ORF 624>:

m624.pep
 1 MIRYLLIACG CISLLLLGIIG IFLPLLPTTP FVLLSAACWA KASPRFYRWL
 51 HRHRYFGPMV HNWEQNGAVP RKAKIFAISM MTASCLMIFW QFPQRWWVGA
 101 VSSVFCSLVA IWMWRPES*

m624/g624 91.6% identity in 119 aa overlap

	10	20	30	40	50	60
m624.pep	MIRYLLIACGCGISLLLLGIIGIFLPLLPTTPFVLLSAACWAKASPRFYRWLHRHRYFGPMV					
g624	MIRYLLIACGCGISLLLLGIIGIFLPLLPTTPFVLLSAACWAKASPRFYRWLHRHRYFGPMV					
	10	20	30	40	50	60

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	70	80	90	100	110	120
m624 . pep	HNWEQNGAVPRKAKIFAISM	MTASCLIMFWQFPQRWWVGAVSSVFCSLVAIWMWRRPESX				
g624	HNWEQNGAVPRKAKIFAISM	MTASCLIMFWQFPQRWWVGAVSSVFCSLVTIRMWHRPESX				
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2001>:

```
a624 . seq
1  ATGATACGTT ATCTTTTAAT TGCCTGCGGC TGCATTTCCC TGCTGTGGG
51  TATCATCGGC ATTTTTTTGC CGCTGTTGCC GACCACGCCG TTCGTACTGC
101 TCTCCGCCGC CTGCTGGGCA AAGGCATCCC CGCGCTTCA CCGCTGGCTG
151 CACCGGCACC GCTATTTCCG TCCGATGGTT CATAACTGGG AACAAACGG
201 CGCAGTCCCG CGCAAAGCCA AAATATTCGC CATCAGTATG ATGACCGCAT
251 CCTGCCTGAT AATGTTTGG CAGTTTCCCC AACGCTGGTG GGTCCGGGGC
301 GTTTCATCGG TTTTGTTC CCTTGTGCC ATATGGATGT GCGCAGGCC
351 CGAATCTTGA
```

This corresponds to the amino acid sequence <SEQ ID 2002; ORF 624.a>:

```
a624 . pep
1  MIRYLLIACG CISLLGLIIG IFLLPLPTTP FVLLSAACWA KASPRFHRWL
51  HRHRYFGPMV HNWEQNGAVP RKAKIFAISM MTASCLIMFW QFPQRWWVGA
101 VSSVFCSLVA IWMWRRPES*
```

m624/a624 99.2% identity in 119 aa overlap

	10	20	30	40	50	60
m624 . pep	MIRYLLIACGCISLLGLIIGIFLPLPTTPFVLLSAACWAKASPRFYRWLHRHRYFGPMV					
a624	MIRYLLIACGCISLLGLIIGIFLPLPTTPFVLLSAACWAKASPRFHRWLHRHRYFGPMV					
	10	20	30	40	50	60

	70	80	90	100	110	120
m624 . pep	HNWEQNGAVPRKAKIFAISM	MTASCLIMFWQFPQRWWVGAVSSVFCSLVAIWMWRRPESX				
a624	HNWEQNGAVPRKAKIFAISM	MTASCLIMFWQFPQRWWVGAVSSVFCSLVAIWMWRRPESX				
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2003>:

```
a625 . seq
1  ATGTTTGCAA CCAGGAAAT GAAGAAGATG ACGATGTGCA CGCGGCGGGT
51  ACGGTTTGG TTGGCTTTCA GCAGCGGACG AATCATCAGC ATTGCTGCGC
101 CGGTCGTTCC CATGATAGAG GCAAGTGCCG TACCGACGGC AAGCAGGGCG
151 GTGTTGAGCT TGGGTGTGCC GTTCAAGTCG CCCCAAACCA AAATGCCGCC
201 TGAATGGTG TACAGGGCAA GCAGCAGCAG GATGAAAGGG ATGTATTCTT
251 CAACGAGTGC GTGTGCGACG GTATGGATAC CGGCGGACGC GCCAAAACCC
301 AAACGAACG GGATGAGGAA GAGCAATGTC CAAAAGCGCG TAATTTTGCC
351 GTAA
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2004>:

```
g625 . seq
1  atgtttgcaa ccaggaaat gaagaagatg acgatgtgca cgcgcggggt
51  acggctttgg ttggctttca gcagcggacg aatcatcagc attgccgscg
101 cggtcggttc catgatagag gcaagtgcgc tacccgacgc aagcagggcg
151 gtgttgagct tgggtgtgcc gttcaagtcg ccccaaacca aaatgccgcc
201 tgaatggtg tacagggcaa gcagcagcag gatgaagggg atatatictt
251 caacgagtcg gtgtgacgac gtatggatgc cggcggacgc gccaaaacc
301 aaactgaacg ggatgaggaa gagcaatgtc caaagcgcg tgattttgcc
351 gtaa
```

This corresponds to the amino acid sequence <SEQ ID 2005; ORF 625.ng>:

```
g625 . pep
1  NFATRKMKKM TMCTRRVRSW LAFSSGRIIS IAAPVVPME ASAVPTASRA
```


1000

51 VLSLGVPFKS PQTMPPEMV YRASSSRMKG IYSSTSACAT VWIPADAPKT
101 KLNGMRKSNV QKAVILP*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2006>:

m625.seq
1 ATGTTTGCAA CCAGGAAAAT GAAGAAGATG ACGATGTGCA CGCGGCGGGT
51 ACGGTTTGG TTGGCTTTCA GCACCGGACG AATCATCAGC ATTGCTGCGC
101 CGGTCGTTCC CATGATAGAG GCAAGTGCCG TACCGACGGC AAGCAGGGCG
151 GTGTTGAGCT TGGGTGTGCC GTTCAAGTCG CCCCAAACCA AAATGCCGCC
201 TGAATGGTG TACAGGGCAA GCAGCAGCAG GATGAAAGGG ATGTATTCTT
251 CAACGAGTGC GTGTGCGACG GTATGGATAC CGCGGACGCG GCCAAAACCC
301 AAACGAACG GGATGAGGAA GAGCAATGTC CAAAAGGCGG TAATTTTGCC
351 GTAA

This corresponds to the amino acid sequence <SEQ ID 2007; ORF 625>:

m625.pep
1 MFATRKMKKM TMCTRRVRFW LAFSSGRIIS IAAPVVPMIE ASAVPTASRA
51 VLSLGVPFKS PQTMPPEMV YRASSSRMKG MYSSTSACAT VWIPADAPKT
101 KLNGMRKSNV QKAVILP*

m625/g625 98.3% identity in 117 aa overlap

	10	20	30	40	50	60
m625.pep	MFATRKMKKMTMCTRRVRFWLAFSSGRIISIAAPVVPMIEASAVPTASRAVLSLGVPFKS					
g625	MFATRKMKKMTMCTRRVRFWLAFSSGRIISIAAPVVPMIEASAVPTASRAVLSLGVPFKS					
	10	20	30	40	50	60
	70	80	90	100	110	
m625.pep	PQTMPPEMVYRASSSRMKG MYSSTSACATVWIPADAPKTKLNGMRKSNVQKAVILPX					
g625	PQTMPPEMVYRASSSRMKG MYSSTSACATVWIPADAPKTKLNGMRKSNVQKAVILPX					
	70	80	90	100	110	

This corresponds to the amino acid sequence <SEQ ID 2008; ORF 625.a>:

a625.pep
1 MFATRKMKKM TMCTRRVRFW LAFSSGRIIS IAAPVVPMIE ASAVPTASRA
51 VLSLGVPFKS PQTMPPEMV YRASSSRMKG MYSSTSACAT VWIPADAPKT
101 KLNGMRKSNV QKAVILP*

m625/a625 100.0% identity in 117 aa overlap

	10	20	30	40	50	60
m625.pep	MFATRKMKKMTMCTRRVRFWLAFSSGRIISIAAPVVPMIEASAVPTASRAVLSLGVPFKS					
a625	MFATRKMKKMTMCTRRVRFWLAFSSGRIISIAAPVVPMIEASAVPTASRAVLSLGVPFKS					
	10	20	30	40	50	60
	70	80	90	100	110	
m625.pep	PQTMPPEMVYRASSSRMKG MYSSTSACATVWIPADAPKTKLNGMRKSNVQKAVILPX					
a625	PQTMPPEMVYRASSSRMKG MYSSTSACATVWIPADAPKTKLNGMRKSNVQKAVILPX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2009>:

g627.seq
1 ATGTCCGCC TTTGGAACCG CGAACACCCG GGATTGAAA TCCTCGGCAG
51 CCGTTACGCC CTGCAAAACC TTGTCCGCGA TGTCATCCTG ATTACATTEA
101 CCGCCGTATC TATGGCAATC ACGCCCAAAC AAGTCGCGC AGGCAACGAA
151 TTCAACTTTG AATCCATCGC CGAAGTGGGC AAATCTTCC TCGGCATCTT
201 CATCACCATC TTCCCGTCC TGAGCATTCT GAAAGCAGGC GAGGCAGGCG
251 CGCTGGGCGG GGTGGTATCG CTGGTTCACG ATACGGCAGG TCATCCGATT
301 AATACGATGT ATTTCTGGAT GAGCGGCATA TTGTCGGCAT TCTTGGATAA
351 CGCGCCCACT TATCTCGTGT TTTTCAATAT GGCGGGCGGC GATGCCCAAG
401 CCTTAATGAC GGGTCCCTCG TTTTCAATAT TGCTGGCGGT TTCTAtgggT
451 tCGGTATTCA TGGGCGCACT GaccTACATc gGCAAcgcac cgaactTCAT

1001

```

501  GGTcaaggcc aTTGCCGaaC agcgcgGCgt accgaTGCcg actTTCTTcc
551  ggtaTAtgat gtggtcggtc gcCTTCCTGa caCCCGTCTT CAtcgTACAT
601  ACCCTcgtCT TTTTcgTTtt cAAACTACTg taa

```

This corresponds to the amino acid sequence <SEQ ID 2010; ORF 627.ng>:

```

g627.pep
1  MSGLWKPEHP GFEILGSRYA LQNLVRDVIL ITLTAVSMAI TPKQVRAGNE
51  FNFEPIAEVG KLFLGIFITI FPVLSILKAG EAGALGGVVS LVHDTAGHPI
101 NTMYFWMSGI LSAFLDNAPT YLVFFNMAGG DAQALMTGPL FHSLLAVSMG
151 SVFMGALTYI GNAPNFMVKA IAEQRGVPMP TFFRYMMWSV AFLTPVFIVH
201 TLVFFVFKLL *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2011>:

```

m627.seq
1  ATGTCCGGCC TTTGGAAACC CGAACACCCG GGATTGAAA TCCTCGGCAG
51  CCGTTACGCC CTGCAAAACC TCGTCCGCGA TGTCATCCTG ATTGCATTGA
101 CCGCCGTATC TATGGCAATC ACGCCCAAAC AAGTCCGCGC AGGCAACGAA
151 TTCAACTTTG AACCATCGC CGAAGTGGGC AAATCTTTC TCGGCATCTT
201 CATCACCATC TTCCCGTCC TGAGCATTCT GAAAGCAGGC GAGGCAGGCG
251 CGCTGGGCGG GGTGGTATCG CTGGTTCACG ATACGGCAGG TCATCCGATT
301 AATGTGATGT ATTTTGGAT GAGCGGCATA TTGTCGGCAT TCTTGGATAA
351 CGCCCCCACT TATCTCGTTT TTTTCAATAT GGCGGGCGGC GATGCCCAAG
401 CCTTGATGAC GGGTACCCTG TTTCATTTCG TGCTGGCGGT TTCTATGGGT
451 TCGGTATTCA TGGGCGCACT GACCTACATC GGCAACGCAC CGAACTTCAT
501 GGTCAAGGCC ATTGCCGAAC AGCGCGGCGT ACCGATGCCG ACTTCTTCG
551 GCTATATGAT GTGGTCGGTC GCCTTCCTGA CACCCGTCTT CATCGTACAT
601 ACCCTTATCT TTTTCGTTTT CAACTGCTG TAA

```

This corresponds to the amino acid sequence <SEQ ID 2012; ORF 627>:

```

m627.pep
1  MSGLWKPEHP GFEILGSRYA LQNLVRDVIL IALTAVSMAI TPKQVRAGNE
51  FNFEPIAEVG KLFLGIFITI FPVLSILKAG EAGALGGVVS LVHDTAGHPI
101 NVMYFWMSGI LSAFLDNAPT YLVFFNMAGG DAQALMTGTL FHSLLAVSMG
151 SVFMGALTYI GNAPNFMVKA IAEQRGVPMP TFFGYMMWSV AFLTPVFIVH
201 TLIFFVFKLL *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m627/g627 97.6% identity in 210 aa overlap

	10	20	30	40	50	60
m627.pep	MSGLWKPEHPGFEILGSRYALQNLVRDVIL	IALTAVSMAITPKQVRAGNEFNFEPIAEVG				
g627	MSGLWKPEHPGFEILGSRYALQNLVRDVIL	ITLTAVSMAITPKQVRAGNEFNFEPIAEVG				
	10	20	30	40	50	60

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	70	80	90	100	110	120
m627.pep	KLFLGIFITIFPVLSILKAGEAGALGGVVSIVHDTAGHPINVMYFWMSGILSAFLDNAPT					
g627	KLFLGIFITIFPVLSILKAGEAGALGGVVSIVHDTAGHPINTMYFWMSGILSAFLDNAPT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m627.pep	YLVFFNMAGGDAQALMTGTLFHSLLAVSMGVSVMGALTYIGNAPNFMVKAIAEQRGVPMP					
g627	YLVFFNMAGGDAQALMTGTLFHSLLAVSMGVSVMGALTYIGNAPNFMVKAIAEQRGVPMP					
	130	140	150	160	170	180
	190	200	210			
m627.pep	TFFGYMMWSVAFLTPVFIVHTLIFFVFKLLX					
g627	TFFRYMMWSVAFLTPVFIVHTLVFVFKLLX					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2013>:

```
a627.seq
1  ATGTCCGCC  TTGGAAACC  CGAACACCCG  GGATTGAAA  TCCTCGGCAG
51  CCGTTACGCC  CTGCAAAACC  TCGTCCGCGA  TGTCATCCTG  ATTGCATTGA
101 CCGCCGTATC  TATGGCAATC  ACGCCCAAAC  AAGTCCGCGC  AGGCAACGAA
151 TTCAACTTGT  AACCACATCG  CGAAGTGGGC  AAACCTCTCC  TCGGCATCTT
201 CATCACCATC  TTTCCCGTCC  TGAGCATTCT  GAAAGCAGGC  GAGGCAGGCG
251 CGCTGGGCGG  GGTGGTATCG  CTGGTTCACG  ATACGGCAGG  TCATCCGATT
301 AATGTGATGT  ATTTTGGAT  GAGCGGCATA  TTGTCGGCAT  TCTTGGATAA
351 CGCGCCCACT  TATCTCGTTT  TTTTCAATAT  GGCGGCGGCG  GATGCCCAAG
401 CCTTGATGAC  GGGTTCCTCG  TTTCAATCGC  TGCTGGCGGT  TTCTATGGGT
451 TCGGTATTCA  TGGGCGCACT  GACCTACATC  GGCAACGCAC  CGAACTTCAT
501 GGTCAAGGCC  ATTGCCGAAC  AGCGCGGCGT  ACCGATGCCG  ACTTCTCTCG
551 GCTATATGAT  GTGGTCGGTC  GCCTTCTCTG  CACCCGTCTT  CATCGTACAT
601 ACCCTTATCT  TTTTCGTTTT  CAAACTGCTG  TAA
```

This corresponds to the amino acid sequence <SEQ ID 2014; ORF 627.a>:

```
a627.pep
1  MSGLWKPEHP  GFEILGSRYA  LQNLVRDVIL  IALTAVSMAI  TPKQVRAGNE
51  FNFEPIAEVG  KLFLGIFITI  FVLSILKAG  EAGALGGVVS  LVHDTAGHP
101 NVMYFWMSGI  LSAFLDNAPT  YLVFFNMAGG  DAQALMTGSL  FHSLLAVSMG
151 SVFMGALTYI  GNAPNFMVKA  IAEQRGVPMP  TFFGYMMWSV  AFLTPVFIVH
201 TLIFFVFKLL *
```

m627/a627 99.5% identity in 210 aa overlap

	10	20	30	40	50	60
m627.pep	MSGLWKPEHPGFEILGSRYALQNLVRDVILIALTAVSMAITPKQVRAGNEFNFEPIAEVG					
a627	MSGLWKPEHPGFEILGSRYALQNLVRDVILIALTAVSMAITPKQVRAGNEFNFEPIAEVG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m627.pep	KLFLGIFITIFPVLSILKAGEAGALGGVVSIVHDTAGHPINVMYFWMSGILSAFLDNAPT					
a627	KLFLGIFITIFPVLSILKAGEAGALGGVVSIVHDTAGHPINVMYFWMSGILSAFLDNAPT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m627.pep	YLVFFNMAGGDAQALMTGTLFHSLLAVSMGVSVMGALTYIGNAPNFMVKAIAEQRGVPMP					
a627	YLVFFNMAGGDAQALMTGSLFHSLLAVSMGVSVMGALTYIGNAPNFMVKAIAEQRGVPMP					
	130	140	150	160	170	180
	190	200	210			
m627.pep	TFFGYMMWSVAFLTPVFIVHTLIFFVFKLLX					

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a627 TFFGYMMWSVAFLTFVFIVHTLIFFVFKLLX
190 200 210

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2015>:

g628.seq
1 ATGTGCGTGC CACTCAAGCC GGCAGGATGC GGGCCGCCAA ATTCATGTGT
51 TTCGATATTG GCAGCATTTT CAGACGGCAC GTCTGCCCTT GCTGCTTTAC
101 ACACATGGAT TTTACGTTTC GTCAGGCGGC TCAATACCAA CAGGCCGCGT
151 TTGAAGTCTT CGGCGGCTTC TTTGATGATG ACCGTACGGT CGGCAGCCAG
201 CGGATTGGTG TCCATCGCAT TGACGAAGAT GGCGAACGGC TCGGCATCTA
251 CGGCAGGGAT TTTGCTGAAC GGACGGGTGC GAAGCGCAGT CCATAAGCCT
301 GATTGAATCA GGTTGCGGCG CACTTTTTCG CTGCTCAATT TTGCCAGCGC
351 TTCAGGTacg TAG

This corresponds to the amino acid sequence <SEQ ID 2016; ORF 628.ng>:

g628.pep
1 MCVPLKPAGC GPPNSCVSIL AAFSDGTSAP AALHTWILRS VRRNTNRP
51 LKSSAASLMM TVGSAASGLV SIALTKMANG SASTAGILLN GRVRSVHKP
101 D*IRLRRTFS LLNFASASGT *

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2017>:

m628.seq
1 ATGTGCGTGC CACTCAAACC GGCAGGATGC GGGCCGCCGA ATTCATGTGT
51 TTCGATGTTG GCAGCATTTT CAGACGGCAC GTCTGCGCCA GCTGCCTTAC
101 AAACATGGAT TTTGCGTTTC GTCAAACGGC TCAATACCAA CAGGCCGCGT
151 TTGAAATCCT CGGCGGCTTC TTTGATAATG ACCGTAGGGT CGGCAGCCAG
201 CGGATTGGTG TCCATCGCAT TGACGAAGAT GGCGAACGGC TCGGCATCGA
251 CGGCAGGAAT TTTGCTGAAC GGACGGGTGC GCAGCGCAGT CCACAAACCG
301 GATTGGATCA GGTTGCGGCG CACTTCTTCG CCGCTTAAGT TTGCCAGCGC
351 TTCAGGTGCG TAG

This corresponds to the amino acid sequence <SEQ ID 2018; ORF 628>:

m628.pep
1 MCVPLKPAGC GPPNSCVSML AAFSDGTSAP AALQWILRS VKRLNTNRP
51 LKSSAASLIM TVGSAASGLV SIALTKMANG SASTAGILLN GRVRSVHKP
101 DWIRLRRTSS PLKFASASGA *

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m528/g628 93.3% identity in 119 aa overlap

	10	20	30	40	50	60
m628.pep	MCVPLKPAGCGPPNSCVSMLAAFS	DGTSAPAAALQWILRSVKRLNTNRP	RLKSSAASLIM			
g628	MCVPLKPAGCGPPNSCVSILAAFS	DGTSAPAAALHTWILRSVRRNTNRP	RLKSSAASLMM			
	10	20	30	40	50	60
	70	80	90	100	110	120
m628.pep	TVGSAASGLVSIALTKMANGSASTAGILLN	GRVRSVHKPDWIRLRRTSSPLKFASASGA				
g628	TVGSAASGLVSIALTKMANGSASTAGILLN	GRVRSVHKPDWIRLRRTSSPLKFASASGT				
	70	80	90	100	110	120
m628.pep	X					
g628	X					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2019>:

1004

```

a628.seq
1  ATGTGCGTGC  CACTCAAACC  GGCCGGATGC  GGGCCGCCGA  ATTCATGTGT
51  TTCGATGTTG  GCAGCATTTT  CAGACGGCAC  GTCTGCGCCA  GCTGCCTTAC
101 ACACATGGAT  TTTACGCTCG  GTCAAACGGC  TCAATACCAG  CAAACCTCGT
151 CTGAAATCCT  CGGCGGCTTC  TTTGATCACA  ACCACAGGGT  CTGCCGCCAG
201 CGGATTGGTG  TCCATCGCAT  TGACGAAGAT  GGCGAACGGC  TCGGCATCGA
251 CGGCAGGGAT  TTTGCTGAAC  GGACGGGTAC  GCAGCGCAGT  CCACAAACCG
301 GATTGGATCA  GATTGCGGCG  CACTTCTTCG  CCGCTTAAGT  TTGCCAACGC
351 TTCGGGCGCG  TAG

```

This corresponds to the amino acid sequence <SEQ ID 2020; ORF 628.a>:

```

a628.pep
1  MCVPLKPAGC  GPNNSCVSML  AAFSDGTSAP  AALHTWILRS  VKRLNTSKPR
51  LKSSAASLIT  TTGSAASGLV  SIALTKMANG  SASTAGILLN  GRVRSVHKP
101 DWIRLRRTSS  PLKFANASGA  *

```

m628/a628 95.0% identity in 120 aa overlap

	10	20	30	40	50	60
m628.pep	MCVPLKPAGCGPPNSCVSMLAAFS DGT SAPAALQTWILRSVKRLNTNRPRLKSSAASLIM					
a628	MCVPLKPAGCGPPNSCVSMLAAFS DGT SAPAALHTWILRSVKRLNTSKPRLKSSAASLIT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m628.pep	TVGSAASGLVSIALTKMANGSASTAGILLNGRVRSVHKPDWIRLRRTSSPLKFASASGA					
a628	TTGSAASGLVSIALTKMANGSASTAGILLNGRVRSVHKPDWIRLRRTSSPLKFANASGA					
	70	80	90	100	110	120

```

m628.pep      X
               |
a628           X

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2021>:

```

g629.seq
1  ATGACTGCca  aacCTTTTTC  CCTCAACCTG  GCcaaCCTCC  TGCTGCCggc
51  ggtattGTTT  GCCGTCAGcc  tGtccgTCCG  cattgccgaT  TTCCGCTGGT
101 CGGATGTGTT  TTCGCTGTCC  GACAGCCAGC  AAGTGATGTT  CATCAGCCGC
151 CTGCCGCGCA  CGTTTGcgaT  TGTGTTGACG  GGCgcgtcga  tagcgGtggc
201 gGGGatgatt  atgcagATTC  TGATGCGCAA  CcgtTTGTGTC  GAGCCTtcta
251 tggcgGGTGC  GGGCCAAAGt  gcgGCTTTGG  GTttgcttct  gAtgtccctg
301 ctgctgcctg  CgcGccgct  gccgtcaAA  ATGTCGTag  Cgcgccgtgc
351 CGCGCTGATC  GGGATGTTGG  cctTtatgct  gctaataccgC  Cgcctgccac
401 cgacggcgca  gctgatgGTg  ccgCTGGTGG  Gg.ttACTTT  CGGCGGCGTG
451 GttgaGGCGG  TGGCGACGTT  TGTCGCGTAT  GAGTTTGAGA  TGCTGCAAAT
501 GTTGGGCGTG  TGGCAGCAGG  GCGACTTTTC  AAGCGTGCTG  CTGGGGCGGT
551 ACGAGCTGCT  TTGGATTACG  GCGGGTTTGG  CGGTGTTTGC  CTACCTGATT
601 GCCGACCGGC  TGACGATTTT  GGGGCTGGGC  GAGACGGTGA  GCGTGAATTT
651 GGGTTTGAAc  CGGACGGCGG  TGTGTGGTGC  GGGTTTGATT  ATTGTGGCAC
701 TGATTACATC  GCTGGTCATT  GTAACGGTCG  GCAATATTCC  GTTTATCGGG
751 CTGGTCGTGC  CGAATAACGT  CAGCCGCCTG  ATGGGCGACA  GGCTGCGCCA
801 AAGCTGCCT  GCGGTCGCCC  TCTTGGGCGC  GTCTTTGGTT  TTATTGTGCG
851 ACATTATCGG  ACGCATGATT  GTGTTTCCGT  TTGAAATTCC  GGTCTCCACG
901 GTTTTGGTG  TGTGGGTAC  GGCTTTGTTT  TTGTGGCTTT  TGTTGAGGAA
951 ACCCGCTAT  GCCGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2022; ORF 629.ng>:

```

g629.pep
1  MTAKPFSLNL  ANLLPVLV  AVLSVGIAD  FRWSDVFSLS  DSQQVMFISR
51  LPRTEAIVLT  GASIAVAGMI  MQILMRNRFV  EPSMAGAGQS  AALGLLMLSL
101 LLPAAPLPVK  MSVAAVAALI  GMLVFMLLIR  RLPPTAQLMV  PLVGXIFGGV

```

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151 VEAVATFVAY EFEMLOMLGV WQOGDFSSVL LGRYELLWIT GGLAVFAYLI
 201 ADRLTILGLG ETVSVNLGLN RTAVLWSGLI IVALITSLVI VTVGNIPFIG
 251 LVVPNIIVSRL MGDRLRQSLP AVALLGASLV LLCDIIGRMI VFPEIPVST
 301 VEGVLGTALF LWLLLRKPAY AV*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2023>:

m629.seq
 1 ATGACTGCCA AACCTTTTTC CCTCAACCTG ACCAACCTGC TGCTGCTGGC
 51 GGTGTTGTTT GCGTCAGCC TGTCGGTGGG CGTTGCCGAT TTCCGCTGGT
 101 CTGATGTGTT TTCACGTGCC GACAGCCAGC AGGTCATGTT CATCAGCCGC
 151 CTGCCGCGCA CGTTTGGCAT TGTGCTGACG GCGCGCTCGA TGGCGGTGGC
 201 CCGCATGATT ATGCAGATTT TGATGCGCAA CCGTTTGTGC GAACCGTCGA
 251 TGGTGGGCGC AAGCCAAAGC GCGGCTTAG GTTTGCTGCT GATGACCCTG
 301 CTGCTGCGCG CCGCGCCGCT GCCGGCGAAA ATGTCGGTTG CCGCGGTTGC
 351 CCGCTGATC GGGATGTTGG TCTTTATGCT GCTGATCCGC CGCCTGCCGC
 401 CGACCGCGCA ACTGATGGTG CCTTTGGTCG GGATTATTTT CCGCGGTGTG
 451 ATTGAGGCGG TAGCCACCTT TATCGCGTAT GAAACGAAA TGGTGCAAAT
 501 GCTCGGCGTG TGSCAGCAGG GCGATTTTTC GAGCGTGCTG CTGGGCGGCT
 551 ACGAGCTGCT TTGGATTACG GCGGGTTTGG CCGTGTGTC CTATCTGATT
 601 GCCGACCGGC TGACGATTTT GGGGCTGGGC GAAACGGTAA GCGTGAATTT
 651 GGGTTTGAAC CGGACGGCGG TGTGTGGTC GGGTTTGATT ATTGTGGCTT
 701 GEATTACGTC GCTGGTTATC GTTACGGTCG GCAATATTCC GTTTATCGGG
 751 CTGGTCTGTC CGAACATCAT CAGCCGCTG ATGGGCGACA GGTTCGCCCA
 801 AAGCCTGCCT GCSGTGGCCT TGCTGGGCGC ATCTTTGGTG TGTCTGTGCG
 851 ACATTATCGG ACGCGTGATT GTGTTCCGT TTGAAATCC GGTCTCTACG
 901 GTTTTGGTG TATTGGGTAC GGCTTGTTT TTGTGGCTTT TGTGAGGAA
 951 ACCCGCTAT GCCGTCTGA

This corresponds to the amino acid sequence <SEQ ID 2024; ORF 629>:

m629.pep
 1 MTAKPFSLNL TNLLLLAVLF AVSLSVGVAD FRWSDVFSLS DSQQVMFISR
 51 LPRTFAIVLT GASMAVAGMI MQILMRNRFV EPSMV GASQS AALGLLMLTL
 101 LLPAAPLPAK MSVAAVAALI GMLVFMLLIR RLPPTAQLMV PLVGIFGGV
 151 IEAVATFIAY ENEMLOMLGV WQOGDFSSVL LGRYELLWIT GGLAVFAYLI
 201 ADRLTILGLG ETVSVNLGLN RTAVLWSGLI IVALITSLVI VTVGNIPFIG
 251 LVVPNIISRL MGDRLRQSLP AVALLGASLV LLCDIIGRVI VFPEIPVST
 301 VEGVLGTALF LWLLLRKPAY AV*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m629/g629 95.7% identity in 322 aa overlap

	10	20	30	40	50	60
m629.pep	MTAKPFSLNLTNLLLLAVLFAVSLSVGVADFRWSDVFSLSDSQQVMFISRRLPRTFAIVLT					
g629	MTAKPFSLNLNANLLPAVLFAVSLSVGIADFRWSDVFSLSDSQQVMFISRRLPRTFAIVLT					
	10	20	30	40	50	60
m629.pep	GASMAVAGMIMQILMRNRFVEPSMV GASQS AALGLLMLTLLPAAPLPAKMSVAAVAALI					
g629	GASIAVAGMIMQILMRNRFVEPSMAGAGQSAALGLLMSLLLPAAPLPVKMSVAAVAALI					
	70	80	90	100	110	120
m629.pep	GMLVFMLLIRRLPPTAQLMVPLVGIIIFGGVIEAVATFIAYENEMLOMLGVWQOGDFSSVL					
g629	GMLVFMLLIRRLPPTAQLMVPLVGXIFGGVVEAVATFVAYEFEMLOMLGVWQOGDFSSVL					
	130	140	150	160	170	180
m629.pep	LGRYELLWITGGLAVFAYLIADRLTILGLGETVSVNLGLNRTAVLWSGLIIVALITSLVI					
g629	LGRYELLWITGGLAVFAYLIADRLTILGLGETVSVNLGLNRTAVLWSGLIIVALITSLVI					
	190	200	210	220	230	240
m629.pep	LGRYELLWITGGLAVFAYLIADRLTILGLGETVSVNLGLNRTAVLWSGLIIVALITSLVI					
g629	LGRYELLWITGGLAVFAYLIADRLTILGLGETVSVNLGLNRTAVLWSGLIIVALITSLVI					

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```

g629      LGRYELLWITGGLAVFAYLIADRLTILGLGETVSVNLGLNRTAVLWSGLIIVALITSLVI
           190      200      210      220      230      240

           250      260      270      280      290      300
m629.pep  VTVGNIPFIGLVVFNIIISRLMGDRLRQSLPAVALLGASLVLLCDIIGRVIVFPFEIPVST
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g629      VTVGNIPFIGLVVFNIVSRLMGDRLRQSLPAVALLGASLVLLCDIIGRMIVFPFEIPVST
           250      260      270      280      290      300

           310      320
m629.pep  VFGVLGTALFLWLLLRKPAYAVX
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g629      VFGVLGTALFLWLLLRKPAYAVX
           310      320

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2025>:

```

a629.seq
1  ATGACTGCCA AACCTTTTTC CCTCAACCTG ACTAACCTCC TGCTGCTGGC
51 GGTGTTGTTT GCCGTGAGCC TGTCGGTGGG CGTTGCCGAT TTCCGCTGGT
101 CGGATGTGTT TTCGCTGTCG GACAGCCAGC AGGTTATGTT CATCAGCCGC
151 CTGCCGCGCA CGTTTGCGAT TGTGTTGACG GGCGCGTCGA TGGCGGTGGC
201 GGGGATGATT ATGCAGATTG TGATGCGTAA CCGTTTGTC GAGCCTTCTA
251 TGGCGGGCGC GGGTCAGAGT GCGGCTTTGG GTTTGCTTCT GATGTCCCTG
301 CTGCTGCCTG CCGCGCCGCT GCCGGTCAAA ATGTCGGTTG CCGCCGTTGC
351 CGCGTTAATC GGGATGTTGG TGTATTATGAT GCTTATCCGC CGCCTGCCGC
401 CGACGGCGCA ACTGATGGTG CCTTTGGTCG GGATTATTTT CGGCGGCGTG
451 GTTGAGGCGG TGGCCACCTT TATTGCGTAT GAAAACGAAA TGCTGCAAAAT
501 GCTGGGCGTG TGGCAACAGG GCGATTTTTC CGGCGTGTG CTCGGACGGT
551 ATGAACTGTT GTGGGCAACG GGGATTTTGG CTTTGTTCG CTATTGATT
601 GCCGACCAGC TGACGATTTT GGGTTTGGGC GAAACGGTAA GCGTGAACCTT
651 GGGGCTGAAC CGGACGGCGA TTCTGTGTC GGGGCTGATT ATTGTGGCTT
701 TGATTACGTC GCTGGTTATC GTTACGGTCG GCAATATTCC GTTTATCGGG
751 CTGGTCGTGC CGAACATCAT CAGCCGCTG ATAGGCGACA GGCTGCGCCA
801 AAGCCTGCCT GCGGTGGCTT TGCTGGGTGC GTCTTGGTT TTATTGTGCG
851 ACATTATCGG ACGAGTGATT GTGTTCCGT TTGAAATTCC GGTATCGACC
901 GTCTTCGGCG TATTGGGTAC GGCCTTGTTT TTATGGCTTT TGTAAAGGAA
951 ACCTGCTCAT GCCGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2026; ORF 629.a>:

```

a629.pep
1  MTAKPFSNLN TNLLLLAVLF AVSLSVGVAD FRWSDVFSLS DSQQVMFISR
51 LPRTFAIVLT GASMAVAGMI MQILMRNRFV EPSMAGAGQS AALGLLMSL
101 LLPAAPLPVK MSVAAVAALI GMLVFMLIR RLPPTAQLMV PLVGIIFFGV
151 VEAVATFIAY ENEMQLMLGV WQQGDFSGVL LGRYELLWAT GILALFAYLI
201 ADQLTILGLG ETVSVNLGLN RTAILWSGLI IVALITSLVI VTVGNIPFIG
251 LVVFNIIISRL IGDRLRQSLP AVALLGASLV LLCIDIIGRVI VFPFEIPVST
301 VFGVLGTALF LWLLLRKPAH AV*

```

m629/a629 95.7% identity in 322 aa overlap

```

           10      20      30      40      50      60
m629.pep  MTAKPFSNLNLTNLLLLAVLFAVSLSVGVADFRWSDVFSLSDSQQVMFISRLPRTFAIVLT
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a629      MTAKPFSNLNLTNLLLLAVLFAVSLSVGVADFRWSDVFSLSDSQQVMFISRLPRTFAIVLT
           10      20      30      40      50      60

           70      80      90      100     110     120
m629.pep  GASMAVAGMIMQILMRNRFVEPSMVGASQAALGLLMTLLLPAAPLPKMSVAAVAALI
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a629      GASMAVAGMIMQILMRNRFVEPSMAGAGQAALGLLMSLLLPAAPLPVKMSVAAVAALI
           70      80      90      100     110     120

           130     140     150     160     170     180
m629.pep  GMLVFMLLIRRLPPTAQLMVPLVGIIFFGVIEAVATFIAYENEMQLMLGVWQQGDFSSVL
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

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```

a629      GMLVFMMILIRRLPPTAQLMVLVGIIFGGVVEAVATFIAYENEMLQMLGVWQQGDFSGVL
           130      140      150      160      170      180

           190      200      210      220      230      240
m629.pep  LGRYELLWITGGLAVFAYLIADRLTILGLGETVSVNLGLNRTAVLWSGLIIVALITSLVI
           ||||| || ||:|||||:|||||:|||||:|||||:|||||:|||||
a629      LGRYELLWATGILALFAYLIADQLTILGLGETVSVNLGLNRTAILWSGLIIVALITSLVI
           190      200      210      220      230      240

           250      260      270      280      290      300
m629.pep  VTVGNIPFIGLVVPNIISRLMGDRLRQSLPAVALLGASLVLLCDIIGRVIVFPFVIPVST
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a629      VTVGNIPFIGLVVPNIISRLIGDRLRQSLPAVALLGASLVLLCDIIGRVIVFPFVIPVST
           250      260      270      280      290      300

           310      320
m629.pep  VFGVLGTALFLWLLLRKPAYAVX
           |||||:|||||:|||||:|||||
a629      VFGVLGTALFLWLLLRKPAHAVX
           310      320

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2027>:

```

g630.seq (partial)
1  aTgatGATTT TGGTGTGGCT ggctttgttt ccccccatgt tttacggcat
51  gtacaacgtc GCGGCACAGG CATTCGGTGC CTTAACGCCC GAtttgctgc
101 aacaaagcat cgcccacgac ggcaattacg ccctcgccaa cgctttgggc
151 atcaatatgt cccccgaaGc gggcgtgtTg ggcaaaatgc tgttcgGCGC
201 GATttacttc ctgccgattt acgcgaccgt aTTTATTCGT GCGggttct
251 ggGaagtCTT GTTCGCATCc gtACGCAAAc ACGAAATCAa CGAAGGTTTC
301 TTCGTTACTT CGATTCTGTT TGCCTTAATC GTTCCGCCCA CGCTGCCGCT
351 GTGGCAGGCG GCTTTGGGTA TTTCTTTCGG CGTTGTGTTT GCGAAAGAAG
401 TATTCGGCGG TACAGGTAAa AACTTCATGA ACCCTGCGCT GGCAGGCCCG
451 GCCTTCCTGT TCTTCGCCTA CCGCGCCAAC TTGAGCGGCG ATGCGGTTTG
501 GACGGCGGTT GACGGCTATT CCGGCGCAAC CGCGCTGGCG CAATGGGCGG
551 CACACGGTGC AGACGGCCTG AAAAAcGCGG TAACCGGTCA AACCATCACT
601 TGGATGGACG CGTTTATCGG CAAACTGCCG GGCTCCATCG GCGAAGTCTC
651 CACTTTGGCA CTCTTAATCG GCGGCGCGTT TATCGTGTTC GCCCGCATCG
701 CTTcttgGCG CATTATTGCC ggCGTGATGA TCGGTatGat tGcgatgTCT
751 tcgctgatta acttcatCGg ttctgacacc aaagctatgt ttgcatgca
801 cttggtacat ggcacttggT GGAaagatGa ttAtcactca ctgtacatta
851 aa.....

```

This corresponds to the amino acid sequence <SEQ ID 2028; ORF 630.ng>:

```

g630.pep
1  MMILVWLALF PPMFYGMYNV GAQAFGALTP DLLQOSIAHD GNYALANALG
51  INMSPEAGVL GKMLFGAIYF LPIYATVFIV GGFWEVLFA VRKHEINEGF
101 FVTSLIFALI VPPTLPLWQA ALGISFGVVV AKEVFGGTGK NFMNPALAGR
151 AFLEFFAYFAN LSGDAVWTAV DGYSGATALA QWAAHGADGL KNAVGTQTIT
201 WMDAFIGKLP GSIGEVSTLA LLIGGAFIVE ARIASWRIIA GVMIGHMIAMS
251 SLINFIGSDT KAMFAMHLVH GTWWKDDYHS LYIK....

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2029>:

```

m630.seq
1  AIGATGATTT TGGTGTGGCT GGCTTTGTTC CCTGCCATGT TCTACGGTAT
51  GIACAAcGTC GCGCGCAGG CATTCGGTGC GTTAACGCCCT GATTtGCTGC
101 AACAAAACAT CGCCAACGAC TGGCATTACG CCTTTGCCAA CGCTTTGGGC
151 AICAAATATGT CGTCTGAAGC GGGCGTGTCTG GACAAAATGC TGTtTGGCGC
201 GATTtACTTC CTGCCGATTt ACGCGACTGT ATTTGTtGTG GCGGgTTTCT
251 GGGAAAGTTTt GTTCGCCACC GTGCGCAAAc ACGAAATCAa CGAAGGTTTC
301 TTCGTTACTT CGATTCTGTT TGCCTTAATC GTTCCGCCCA CGCTGCCGCT
351 GTGGCAGGCG GCTTTGGGTA TTTCTTTCGG CGTTGTGTTT GCGAAAGAAG
401 TATTCGGCGG TACAGGTAAa AACTTCATGA ACCCTGCGCT GGCAGGCCGT
451 GCTTTCCTGT TCTTCGCCTA CCGTGCcAAC TTGAGCGGCG ATGCGGTTTG
501 GACGGCGGTT GACGGCTATT CCGGCGCAAC CGCACTGGCG CAATGGGCGG
551 CACACGGTGC AGACGGCCTG AAAAAcGCGG TAACCGGTCA AACCATCACT
601 TGGATGGACG CGTTTATCGG CAAACTGCCG GGCTCCATG GCGAAGTCTC
651 CACTTTGGCA CTCTTAATCG GCGGCGCGTT TATCGTGTTC GCCCGCATCG
701 CTTCTTGGCG CATTATTGCC GCGGTGATGA TCGGTATGAT TGCGATGTCT
751 TCGCTGTFALI ACTTCATCGG TTCGGACACC AACCGTATGT TTGCTATGCC

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801 TTGCTACTGG CACTTGGTGG TCGGCGGCTT CGCCATCGGT ATGCTGTTTA
851 TGGGACCGCA CCCTGTTTCC GCTTCCTTTA CCAATGTCGG CAAATGGTGG
901 TACGGCGCAC TGATCGGTGT GATGTGCGTA TTAATCCGCG TGGTCAATCC
951 GGCTTACCCC GAAGGCATGA TGTGGCGAT TCTGTTGCC AACCTGTTTG
1001 CCCCAGATTT CGACTATTTC GTCGCACAAG CGAACATCAA ACGCAGAAAG
1051 GCGCGCAGCA ATGGCTAA

```

This corresponds to the amino acid sequence <SEQ ID 2030; ORF 630>:

```

m630.pep
1  MMILVWLALF PAMFYGMYNV GAQAFGALTP DLLQONIAND WHYAFANALG
51  INMSSEAGVS DKMLFGAIYF LPIYATVFVV GGFWEVLFAT VRKHEINEGF
101 FVTSILFALI VPPTLPLWQA ALGISFGVVV AKEVFGGTGK NFMNPALAGR
151 AFLFFAYPAN LSGDAVWTAV DGYSGATALA OWAAGADGL KNAVGTQTIT
201 WMDAFIGKLP GSIGEVSTLA LLIGGAFIVF ARIASWRIIA GVMIGMIAMS
251 SLFNFIGSDT NAMFAMPWYW HLVVGGFAIG MLFMATDPVS ASFTNVGKWW
301 YGALIGVMCV LIRVVPAYP EGMMLAILFA NLFAPIDYF VAQANIKRRK
351 ARSNG*

```

m630/g630 93.5% identity in 275 aa overlap

	10	20	30	40	50	60
m630.pep	MMILVWLALFPAMFYGMYNVGAQAFGALTPDLLQONIANDWHYAFANALGINMSSEAGVS					
g630	MMILVWLALFPMPFYGMYNVGAQAFGALTPDLLQQSIAHDGNALANALGINMSPEAGVL					
	10	20	30	40	50	60
m630.pep	DKMLFGAIYFLPIYATVFVVGGFWEVLFATVRKHEINEGFFVTSILFALIVPPTLPLWQA					
g630	GKMLFGAIYFLPIYATVFIVGGFWEVLFASVRKHEINEGFFVTSILFALIVPPTLPLWQA					
	70	80	90	100	110	120
m630.pep	ALGISFGVVVAKEVFGGTGKNFMNPALAGRAFLFFAYPANLSGDAVWTAVDGYSGATALA					
g630	ALGISFGVVVAKEVFGGTGKNFMNPALAGRAFLFFAYPANLSGDAVWTAVDGYSGATALA					
	130	140	150	160	170	180
m630.pep	QWAAGADGLKNAVGTQTITWMDAFIGKLP GSIGEVSTLALLIGGAFIVFARIASWRIIA					
g630	QWAAGADGLKNAVGTQTITWMDAFIGKLP GSIGEVSTLALLIGGAFIVFARIASWRIIA					
	190	200	210	220	230	240
m630.pep	GVMIGMIAMSSLFNFIGSDTNAMFAMPWYHVLVGGFAIGMLFMATDPVSASFNTVGKWW					
g630	CVMIGMIAMSSLINFIGSDTKAMFAM----HLVHCTWKKDDYHSLYIK.					
	250	260	270	280	290	300
m630.pep	YGALIGVMCVLIRVVPAYPEGMMLAILFANLFAPIFDYFVAQANIKRRKARSNGX					
g630						
	310	320	330	340	350	
m630.pep						

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2031>:

```

a630.seq
1  ATGATGATTT TGGTGTGGCT GGCTTTGTTC CCTGCCATGT TCTACGGTAT
51  GTACAACGTC GCGGCACAGG CATTGCGTGC GTTAACGCCG GATTTGCTGC
101 AACAAAGCAT CGCCAACGAC TGGCATTACG CCCTTGCCAA CGCTTTGGGC
151 ATCAATATGT CGTCTGAAGC GGGCGTGTG GGCAAAATGC TGTTGCGCGC
201 GATTTACTTC CTGCCGATTT ACGCGACCGT ATTTATGTGC GCGGTTTCT
251 GGGAAGTTT GTTCGCCACC GTGCGCAAAC ATGAAATCAA CGAAGTTTC
301 TTTGTTACCT CGATTCTGTT TGCCCTAATC GTTCCGCCCA CGCTGCCGCT
351 GTGGCAGGCA GCTTTGGGTA TTTCTTTCGG CGTTGTGGTT GCGAAAGAAG
401 TATTCGGCGG TACAGGTAAA AACTTCATGA ACCCTGCGCT GGCAGGCCGT
451 GCCTTCCTGT TCTTCGCCTA CCCTGCCAAC TTGAGCGGCG ATGCGGTTTG
501 GACGGCGGTT GACGGCTATT CCGGCACAAC CGCGCTGGCG CAATGGGCGG
551 CACACGGTGC AGACGGCTG AAAAAACGCCA TAACCGGTCA AACCATCACT
601 TGGATGGATG CGTTTATCGG CAAACTGCCG GGCTCCATCG GCGAAGTCTC
651 CACTTTGGCA CTCTTAATCG GCGGCGCGTT TATCGTGTTC GCCCGCATCG

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701 CTTCTTGGCG CATTATTGCC GCGGTGATGA TCGGTATGAT TGCCATGTCT
751 TCGCTGTTCA ACTTCATCGG TTCGGACACC AACGCTATGT TTGCTATGCC
801 TTGGTACTGG CATTGGGTCG TCGGCGGCTT CGCCATCGGT ATGCTGTTTA
851 TGGCGACCGA CCCCCTTTCC GCTTCCTTTA CCAATGTCGG CAAATGGTGG
901 TACGGCGCAC TGATCGGTGT GATGTGCGTA TTAATCCGCG TGGTCAATCC
951 GGCTTACCCC GAAGGCATGA TGTGGCGAT TCTGTTTGCC AACCTGTTTG
1001 CCCCATTTC CGACTATTTC GTCGCACAAG CGAACATCAA ACGCAGAAAG
1051 GCGCGCAGCA ATGGCTAA

```

This corresponds to the amino acid sequence <SEQ ID 2032; ORF 630.a>:

```

a630.pep
1  MMILVWLALF PAMFYGMYNV GAQAFGALTP DLLQOSIAND WHYALANALG
51  INMSSEAGVL GKMLFGAIYF LPIYATVFIV GGFWEVLFAT VRKHEINEGF
101 FVTSILEFALI VPPTLPLWQA ALGISFGVVV AKEVFGGTGK NFMNPALAGR
151 AFLFFAYPAN LSGDAVWTAV DGYSGATALA QWAAHGADGL KNAITGQTIT
201 WMDAFIGKLP GSIGEVSTLA LLIGGAFIVE ARIASWRIIA GVMIGMIAMS
251 SLNFIGSDT NAMFAMPWYW HLVVGGFAIG MLEMATDPVS ASFTNVGKWW
301 YGALIGVMCV LIRVVNPAYP EGMMLAILFA NLFAPIFDYF VAQANIKRRK
351 ARSNG*

m630/a630 98.3% identity in 355 aa overlap

      10      20      30      40      50      60
m630.pep MMILVWLALFPAMFYGMYNVGAQAFGALTPDLLQONIANDWHYAFANALGINMSSEAGVS
|||||
a630      MMILVWLALFPAMFYGMYNVGAQAFGALTPDLLQOSIANDWHYALANALGINMSSEAGVL
      10      20      30      40      50      60

      70      80      90      100     110     120
m630.pep DKMLFGAIYFLPIYATVFVVGGEVLFATVRKHEINEGFFVTSILFALIVPPTLPLWQA
|||||
a630      GKMLFGAIYFLPIYATVFIVVGGEVLFATVRKHEINEGFFVTSILFALIVPPTLPLWQA
      70      80      90      100     110     120

      130     140     150     160     170     180
m630.pep ALGISFGVVVAKEVFGGTGKNFMNPALAGRAFLFFAYPANLSGDAVWTAVDGYSGATALA
|||||
a630      ALGISFGVVVAKEVFGGTGKNFMNPALAGRAFLFFAYPANLSGDAVWTAVDGYSGATALA
      130     140     150     160     170     180

      190     200     210     220     230     240
m630.pep QWAAHGADGLKNAVGTGQTITWMDAFIGKLPGSIGEVSTLALLIGGAFIVFARIASWRIIA
|||||
a630      QWAAHGADGLKNAITGQTITWMDAFIGKLPGSIGEVSTLALLIGGAFIVFARIASWRIIA
      190     200     210     220     230     240

      250     260     270     280     290     300
m630.pep GVMIGMIAMSSLENFIGSDTNAMFAMPWYWHLVVGGFAIGMLEMATDPVSASFTNVGKWW
|||||
a630      GVMIGMIAMSSLENFIGSDTNAMFAMPWYWHLVVGGFAIGMLEMATDPVSASFTNVGKWW
      250     260     270     280     290     300

      310     320     330     340     350
m630.pep YGALIGVMCVLIRVVNPAYPEGMMLAILFANLFAPIFDYFVAQANIKRRKARSNGX
|||||
a630      YGALIGVMCVLIRVVNPAYPEGMMLAILFANLFAPIFDYFVAQANIKRRKARSNGX
      310     320     330     340     350

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2033>:

```

g635.seq
1  ATGACCCGGC GACGGGTCGG CAAGCAAAAC CGTATTGCCA TCCACTCCGC
51  GCPATACCGA AAAATGGTCG TCTTTGCGGT ATTTCAGATA CACGATGACG
101 GGGATTTTCA ACTGCGCGAG CTGTTTGAAA GACAGGGCAT AGCCTTTCGC
151 CTCAAAACCC AAATCGGGCA TAATGCGCCG CATATCCTCA AACGACGCGC
201 GCATCTGTTT CTTACCCAGT TTTTCAACA CTTCTTCTTC CGTCAGCTTT
251 TGCCCGTAAA AATTGTTCAA AAGCGTCGCC ACCGAAGCCG CCCCAGGAGA

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301 AAAATCCAAA TCCTGCTTTA CAATATTGAA ATCCCGCCGC GCTTTCCAAC
 351 TCTGCAATTT GATTTTCCG TAAACAACAG GATTATCGTT AAACATCGGT
 401 GCAGCATTC AAGGATAAGA CAAGGCTCTG TACCAGATTA G

This corresponds to the amino acid sequence <SEQ ID 2034; ORF 635.ng>:

g635.pep

1 MTRRRVGKQN RIAIHSQYR KMVFAVFCI HDDGDFQLRE LFERQGIAGR
 51 LKTQIGHNAP HILKRRRAHLF LTOFFQHFFF RQLLPVKIVQ KRRHRSRPAG
 101 KIQILLYNIE IPPRFPTLQF DFSVNNRIIV KHRCSIQTIR QGSVPD*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2035>:

m635.seq

1 ATGACCCAGC GACGGGTCCG CAAGCAAAAC CGTATTGCCG TCTATACCGC
 51 GCAATACCGA GAAATGATCA TCCTTGCGGT ATTCAGATA CACGATGACG
 101 GGGATTTGCA ACTGTGCAAG CTGCTCGAAA GACAGGGCAT AGCCTTTCGC
 151 TTCAAACCC AAATCAGGCA TAATGCGCCG CATATCCTCA AACGACGCGG
 201 GCATCTGCTC CTTATCCAGT TTTTCAACA CGTCCTCTTC CGTCAGCTTT
 251 TGCCCGTGAA AATTGTTCAA AAGCGTCACC ACCGAAGCCG CCCCAGGGA
 301 AAAATCCAAA TCCTGCTTTA CAATATTGAA ATCGCGCCTT TCTTTCCAAC
 351 TCTGCACCTT GATTTTCCA TAAGCAACAG GATTATAGTG GATTAA

This corresponds to the amino acid sequence <SEQ ID 2036; ORF 635>:

m635.pep

1 MTQRRVGKQN RIAVYTAQYR EMILAVFQI HDDGDLQLCK LLERQGIAGR
 51 FKTQIRHNAP HILKRRGHLL LIQFF*HVLV RQLLPVKIVQ KRRHRSRPAG
 101 KIQILLYNIE IAPFFPTLHF DFSISNRIIV D*

m635/g635 80.0% identity in 130 aa overlap

	10	20	30	40	50	60
m635.pep	MTQRRVGKQNRIAVYTAQYREMI	ILAVFQIHDDGDLQLCKLLERQGI	AFRFRKTQIRHNAP			
g635	MTRRRVGKQNRIAIHSQYRKMVFAVFCI	HDDGDFQLREL	FERQGI	AFRLKTQIGHNAP		
	10	20	30	40	50	60
	70	80	90	100	110	120
m635.pep	HILKRRGHLLLIQFFXHVLF	RQLLPVKIVQKRRHRSRPAG	KIQILLYNIEIAPFFPTLHF			
g635	HILKRRRAHLFELTQFFQHF	FRQLLPVKIVQKRRHRSRPAG	KIQILLYNIEIPPRFPTLQF			
	70	80	90	100	110	120
	130					
m635.pep	DFSISNRIIVDX					
g635	DFSVNNRIIVKHRCSIQTIRQGSVPDX					
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2037>:

a635.seq

1 ATGACCCAGC GACGGGTCCG CAAGCAAAAC CGTATTGCCG TCTATACCGC
 51 GCAATACCGA GAAATGATCA TCCTTGCGGT ATTCAGATA CACGATGACG
 101 GGGATTTGCA ACTGTGCAAG CTGCTCGAAA GACAGGGCAT AGCCTTTCGC
 151 CTCAAAACCC AAATCAGGCA TGATGCGCCG CATATCCTCA AACGACGCGC
 201 GCATCTGCTC CTTATCCAGC TTTTCAACA CGTCCTCTTC CGTCAGCTTT
 251 TGCCCGTGAA AATTGTTCAA AAGCGTCGCC ACCGAAGCCG CCCCAGGGA
 301 AAAATCCAAA TCCTGCTTTA CAATATTGAA ATCGCGCCTT TCTTTCCAAC
 351 TCTGCACCTT GATTTTCCA TAAGCAACAG GATTATAGTG GATTAA

This corresponds to the amino acid sequence <SEQ ID 2038; ORF 635.a>:

a635.pep

1 MTQRRVGKQN RIAVYTAQYR EMILAVFQI HDDGDLQLCK LLERQGIAGR
 51 LKTQIRHDAP HILKRRRAHLL LIQLFQHVLF RQLLPVKIVQ KRRHRSRPAG
 101 KIQILLYNIE IAPFFPTLHF DFSISNRIIV D*

m635/a635 95.4% identity in 131 aa overlap

10	20	30	40	50	60
----	----	----	----	----	----

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```

m635.pep      MTQRRVGKQNRIAVYTAQYREMIILAVFQIHDDGDLQLCKLLERQGIARFKTQIRHNAP
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a635          MTQRRVGKQNRIAVYTAQYREMIILAVFQIHDDGDLQLCKLLERQGIARFKTQIRHDAP
              10      20      30      40      50      60

              70      80      90      100     110     120
m635.pep      HILKRRGHLLLIQFFXHVLFROLLPVKIVQKRHRSRPAGKIQILLYNIEIAPFFFTLHF
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a635          HILKRRHLLLIQLFQHVLFROLLPVKIVQKRHRSRPAGKIQILLYNIEIAPFFFTLHF
              70      80      90      100     110     120

              130
m635.pep      DFSISNRIIVDX
|||||:|||||:
a635          DFSISNRIIVDX
              130

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2039>:

```

g638.seq
1  ATGATTGGCG GACAGTTTAT CGTAGTtgGc atTGTAGGCA AAAACGCACT
51  TGCCCGCTTT GTTGATAATA ttgtcGTGAA TAtcGGAATA GTTGACATAG
101 TTGAGCATGA TGCCCTAATC GCGGCTGCCG ACGGCGATAT TGTCGAACAC
151 TTTGAGCCGT TCGGAAAACA TCAGCACATA GCCCATATTG TtgCCACGG
201 AATATTSCC GCTGacttcg ctgtcgTTGG TGTACATATA GTGGACGGCG
251 AAACGCAGGT CGCTGAAGCG GTTGTTTTGA TAGGTGTTGT GCGTGCTGGT
301 ATTGGA AAAA ATGCCGTCCC GCCCTTTGGA AATGTCGTTG ccgACGACCT
351 GCGCgcccgg CgcgtTCCAA ACGGTAACGC CATTGCCGCG CTCATTCACG
401 CGCAAGGTcg catcgCCGAC GATTTTATTC TCGCGCACCA TCGCATCGGC
451 AGAACCATGA AGGTATACGC CGAACGAATT ATCAAAAATA TTGTTGTGTT
501 CAACCAAGGC GCGCGGGGCG GCTTTTTCGA GATAAATACC GGCATCCATT
551 GCTGGCAGGC TCATACCGGA ACGGGTAACG GTCAGGTTGC GGAGCGTTAC
601 GTCCGGCGCG TGTACGGCTA TGGTACGCC GCTCTGTGCC CCTTCGATGG
651 TTGCGGAACG GTCGGCAGGC CCTTCAATCG TAATCGGTTT GTCGATATAA
701 AGTTTGGTTT GATATACGCC GGAAGCCAGT TTGATCGTAT CGCCCGCCCG
751 GCGCGGGGCA AAAATTTCGG CAAGGTTGTC TTGCGGGGAA ACGTGGACGA
801 CCGCTGCCGA TGCCGTCTGA AAAATGCTGC CGGCGGCAAG TATCAGCACG
851 GCCTTCAGCC ATATACGGAG CGCGGATGTG TGCATAGTGT CCCTCTGTTT
901 CTTCTCGTAT GGCCGAACAA AATAAAGCAT CATTCAAATG TGCCTGTTTT
951 TATAGCGAAA CCGCTGAAA CGGTACGGCA AGCGGTTTGG CTATAA

```

This corresponds to the amino acid sequence <SEQ ID 2040; ORF 638.ng>:

```

g638.pep
1  MIGGQFIVVG IVGKNALARF VDNIVVNIGI VDIVEHDALI AAADGDIVEH
51  FEPFGKHQHI AHIVAHGNIA ADFAVVGVHI VDGETQVAEA VVFIGVVVRAG
101 IGKNAVPPFG NVVADDLRAG RVPNGNAIAA LIHAQGRAD DFILAHHRIG
151 RTMKVYAERI IKNIIVFNQG ARGGFEEINT GIHCWQAHTG TGNQVVAERY
201 VRRVYGYGTP ALVPFDGCGT VGRPFNRNRF VDIKFLIYA GSQFDRIARP
251 GAGKNFGKVV LRGNVDDGCR CRLKNAAGGK YQHGLQPYTE RGCVHSVPLF
301 RSVWPNKIKH HSNVPVFIK PPETVRQAVW L*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2041>:

```

m538.seq
1  ATGATTGGCG AAAAGTTTAT CGTAGTTGCG ATTATAGGCA AATACGCACT
51  TCCCTGCCTT GTTGATAATG TTGTCGTGAA TATCGGAATA GTTGACATAG
101 TTGAGCATAA TGCCCTGATC GCGGCTGCCG ACGGCGATAT TGTCGAATAC
151 TTTGAGCCGT TCGGAAAACA TCAGCACATA GCCCATATTG TTGCCACGG
201 AATATTGCC GCTGATTTCC CTGTCGTTGG TGTACATATA GTGGACGGCG
251 AAACGC AAAT CGCTGAAGCG GTTGTTTTGA TAGGTGTTGT GCGTGCTGGT
301 ATTGGA AAAA ATGCCGTCCC GCCCTTTGGA AATGTCGTTG CCGACGACCT
351 GCGCACCGGG TGCGTTCCAA ACGGTAACGC CGTTGCCGCG CTCGTTACG
401 CGCAAGTTCG CTGCGCCGAC GATTTTATTC TCGCGCACCA TCGCATCGGC
451 AGAACCATGC AGATATACGC CGACCGAATT ATCAAAAATA TTGTTGTGTT
501 CAATCAGGGC GCGCGGGGCA GTTCTTTCGA GATAAATACC GGCATCCATT
551 GCGGGCAGGC TCATACCGGA ACGGGTAACG GTCAGGTTGC GGAGCGTTAC
601 GTCCGGCGCG TGTACGGCTA TGGTACGCC GCTCTGTGCG CCTTCGATGG
651 TTGCGGAACG GTCGGCAGGC CCTTCAATCG TAATCGGTTT GTCATGTGA
701 ACTTTGCTTT TATATACGCC GGAAGCCAGT TTGAGCGTAT CGCCCGCCCG
751 GCGCGGGGCA AATGCGGGAT ACCGATCAGC ATAATCGGTT CGTGA

```

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This corresponds to the amino acid sequence <SEQ ID 2042; ORF 638>:

```
m638.pep
  1 MIGEKFIVVG IIGKYALACL VDNVVVNIGI VDIVEHNALI AAADGDIVEY
 51 FEPLGKHQHI AHIVAHGNIA ADFAVVGVHI VDGETQIAEA VVFGVVRAG
101 IGKNAVPPFG NVVADDLRTG CVPNGNAVAA LVHAQSRVAD DFILAHHRIG
151 RTMQIYADRI IQNIVFNQO ARGSFFEINT GIHCGQAHTG TGNGQVAERY
201 VRRVYGYGTP APVAFDGCCT VGRPFNRRNF VNVKFGFIYA GSQFERIARP
251 GAGKCGIPIS IIGS*

m638/g638 88.2% identity in 254 aa overlap

m638.pep      10      20      30      40      50      60
MIGEKFIVVGIIIGRYALACLVDNVVVNIGIVDIVEHNALIAAADGDIVEYFEPLGKHQHI
g638          10      20      30      40      50      60
MIGGQFIVVGIVGKNALAREVDNIVVNIGIVDIVEHDALIAAADGDIVEHFEFPFGKHQHI

m638.pep      70      80      90      100     110     120
AHIVAHGNIAADFAVVGVIHVDGETQIAEAVVFGVVRAGIGKNAVPPFGNVVADDLRTG
g638          70      80      90      100     110     120
AHIVAHGNIAADFAVVGVIHVDGETQVAEAVVFIGVVRAGIGKNAVPPFGNVVADDLRAG

m638.pep      130     140     150     160     170     180
CVPNGNAVALVHAQSRVADDFILAHHEIGRTMQIYADRIIQNIVFNQOARGSFFEINT
g638          130     140     150     160     170     180
RVPNGNAIALIHAQGRIADDFILAHHEIGRTMKVYAERIINKNIVFNQOARGGFFEINT

m638.pep      190     200     210     220     230     240
GIHCGQAHTGTGNGQVAERYVRRVYGYGTPAPVAFDGCCTVGRPFNRRNFVNVKFGFIYA
g638          190     200     210     220     230     240
GIHCWQAHTGTGNGQVAERYVRRVYGYGTPALVPFDGCCTVGRPFNRRNFVDIKFGLIYA

m638.pep      250     260
GSQFERIARPGAGKCGIPISIIIGSX
g638          250     260     270     280     290     300
GSQFDRIARPGAGKNFGKVVLRGNVDDGCRCLKNAAGGKYQHGLQPYTERGCVHSVPLF
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2043>:

```
a638.seq
  1 ATGATTGGCG GACAGTTTAT CGTAGTTGGC ATTGTAGGCA AAAACGCACT
 51 TGCCCGCTTT GTTGATAATG TTGTCGTGAA TATCGGAATA GTTGACATAG
101 TTGAGCATGA TGCCTTGGTC GCGGCTGCCG ACGGCGATAT TGTCAAACAC
151 TTTGAGCCGC TCGGAAAACA TCAGCACATA GCCCATATTG TTGCCACGG
201 AAATATTGCC GCTGATTTCG CTGTCGTTGG TGTACATATA GTGGACGGCG
251 AAACGCAAT CGCTGAAGCG GTTGTTTTGA TAGGTGTTGT GCGTGCTGGT
301 ATTGGAATA ATGCCGTCCC GCCCTTTGGA AATATCGTTG CCGACGACCT
351 GCGCGCCGGG CGCGTTCCAA ACGGTAACGC CATTGCCGCG CTCGTTACG
401 CGCAAAGTCG CGTCGCCGAC GATTTTATTC TCCCGCACCA TCGCATCGGC
451 AGAACCATGC AGATAGACGC CGACCGAATT ATCCAAAATA TTATTGTGTT
501 CAATCAGGGC GCGCGGGGCA GTTCTTTCGA GATAAATACC GGCATCCATT
551 GCGGGCAGGC TCATACCGGA ACGGTAACG GTCAGGTTGC GGAACGTTAC
601 GTCCGCGCGG TGTACGGCTA TGGTACGCCC GCTCCTGTCT CCTTCGATGG
651 TTGCAGAACG GTCGGCAGGC CCTTCAATCG TAATCGGTTT GTCGATGTGA
701 AGTTTGGTTT GATATACGCC GGAAGCCAGT TTGAGCGTAT CGCCCGCCCC
751 GCGCGGGGCA AATGCGGGAT ACCGATCAGC ATAATCGACT CATGGTGA
```

This corresponds to the amino acid sequence <SEQ ID 2044; ORF 638.a>:

```
a638.pep
  1 MIGGQFIVVG IVGKNALARE VDNVVVNIGI VDIVEHDALV AAADGDIVKH
 51 FEPLGKHQHI AHIVAHGNIA ADFAVVGVHI VDGETQIAEA VVFIGVVRAG
101 IGKNAVPPFG NIVADDLRAG RVPNGNAIAA LVHAQSRVAD DFILPHHRIG
151 RTMQIDADRI IQNIVFNQO ARGSFFEINT GIHCGQAHTG TGNGQVAERY
201 VRRVYGYGTP APVSFDGCRT VGRPFNRRNF VDVKEGLIYA GSQFERIARP
```

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251 GAGKCGIPIS IIDSW*

m638/a638 91.3% identity in 264 aa overlap

	10	20	30	40	50	60
m638.pep	MIGEKFIVVGIIGKYALACLV	DNVVVNIGIVDIVEH	NALIAAADGDIVEY	FEPLGKHQHI		
a638	MIGGQFIVVGIIGKALARFV	DNVVVNIGIVDIVEH	DALVAAADGDIVKH	FEPLGKHQHI		
	10	20	30	40	50	60
m638.pep	70	80	90	100	110	120
a638	70	80	90	100	110	120
	130	140	150	160	170	180
m638.pep	130	140	150	160	170	180
a638	130	140	150	160	170	180
	190	200	210	220	230	240
m638.pep	190	200	210	220	230	240
a638	190	200	210	220	230	240
	250	260				
m638.pep	250	260				
a638	250	260				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2045>:

g639-1.seq

```

1  ATGAGCCTGC CAGCAATGGA TGCCGGTATT TATCTCGAAA AAGCCGCCCC
51  GCGCGCCCTG GTTGAACACA ACAATATTTT TGATAATTCG TTCGGCGTAT
101 ACCTTCATGG TTCTGCCGAT GCGATGGTGC GCGAGAATAA AATCGTCGGC
151 GATCGCACTT TGCGCGTGAA TGAGCGCGGC AATGGCGTTA CCGTTTGGA
201 CGCGCCCGGC GCGCAGGTCC TCGGCAACGA CATTTCCTAA GGGCGGGACG
251 GCATTTTTTC CAATACCAGC ACGCACAAAC CCTATAAAAA CAACCGCTTC
301 AGCGACCTGC GTTTCGCCGT CCACTATATG TACACCAACG ACAGCGAAGT
351 CAGCGGCAAT ATTTCCGTGG GCAACAATAT GGGCTATGTG CTGATGTTTT
401 CCGAACGGCT CAAAGTGTTC GACAATATCG CCGTCGGCAG CCGCGATTAG
451 GGCATCATGC TCAACTATGT CAACTATTCC GATATTCACG ACAATATTAT
501 CAACAAAGCG GGCAAGTGCG TTTTGCCTA CAATGCCAAC TACGATAAAC
551 TGTCCGCCAA TCATTTTGAA AACTGCCAAA TCGGCATGCA CTTTACCGCC
601 GCCATCGAAG GCACGTCCCT GCACGACAAT TCCTTTATCA ACAACGGAAG
651 CCAGGTCAAA TATGTCAGTA CGCGCTTTCT CGACTGGAGC GAGGGCGGAC
701 ACGGCAACTA CTGGAGCGAC AACAGCCCGT TCGATTGAA CCGCGACGGC
751 TTCGGAGACA GCGCGTACCG TCCCGACGGC ATCATCGACC AAATCATCTG
801 GCGCGCGCCC GTATCGCGCC TCTTGATGAA CAGTCCCGCA ATCAGCATCG
851 TCAATATGGC GCAGGCGCAG TTTCCCGCCG TTCTGCCCGG CGGCGTGGTG
901 GACAGCAAAC CGCTGATGAA GCCTTATGCC CCCAAATTC AAACCCGTTA
951 TCAGGCGATG AAGGACGAGT TGCTCAAAGA AGCCGAAACG CGGCAGTCGG
1001 AACGGGCGAC GCGGAAAC GGTCTTTGA ACTAG

```

This corresponds to the amino acid sequence <SEQ ID 2046; ORF 639-1.ng>:

g639-1.pep

```

1  MSLPAMDAGI YLEKAAPRAL VEHNIFDMS FGVYLHGSAD AMVRENKIVG
51  DATLRVNERG NGVTVWNPAG AQVVGNDISK GRDGIFNTS THNTYKNNRF
101 SDLRFVHYM YTNDSEVSGN ISVGNMGGV LMFSERLKVF DNIYVSGSRD*
151 GIMLYNVNYS DIHDNIINKA GKCVFAYNAN YDKLSANHFE NCQIGMHFTA
201 AIEGTSLHDN SFINNGSQVK YVSTRFLDWS EGGHGNYSW NSPFDLNGDG
251 FGDSAYRPDG IIDQIIWRAP VSRLMNSPA ISIVKWAQAO FPAVLPGGVV
301 DSKPLMKPYA PKIQTRYQAM KDELLKEAET ROSERGRAEN GSLN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2047>:

1014

m639-1.seq

```

1  ATGAGCCTGC CCGCAATGGA TGCCGGTATT TATCTCGAAG AAAGTGGCCC
51  GCGCGCCCTG ATTGAACACA ACAATATTTT GGATAATTCG GTCGGCGTAT
101 ATCTGCATGG TTCTGCCGAT GCGATGGTGC GCGAGAATAA AATCGTCGGC
151 GACGCGACTT TGCGCGTGAA CGAGCGCGGC AACGGCGTTA CCGTTTGGAA
201 CGCACCCGGT GCGCAGGTGC TCGGCAACGA CATTTCCAAA GGGCGGGACG
251 GCATTTTTC CAATACCAGC ACGCACAACA CCTACAAAAA CAACCGCTTC
301 AGCGATTTCG GTTTCGCGGT CCACTATATG TACACCAACG ACAGCGAAAT
351 CAGCGGCAAT ATTTCCGTGG GCAACAATAT GGGCTATGTG CTGATGTTTT
401 CCCAGCCGCT CAAAGTATTC GACAATATCG CCGTCGGCAG CCGCGATCAG
451 GGCATTATGC TCAACTATGT CAACTATTCC GATATTACAG ACAACATTAT
501 CAACAAGGCA GGCAGTGC G TATTGCCTA TAATGCCAAC TACGATAAAC
551 TTTTCGCCAA TCATTTTGAA AACTGTCAA TCGGCATACA CTTTACCGCC
601 GCCATCGAAG GCACGTCCTT GCATGACAAT TCCTTTATCA ACAACGAAAG
651 CCAGGTCAA TACGTACGCA CGCGCTTCT CGATTGGAGC GAGGGCGGAC
701 ACGGCAACTA TTGGAGCGAC AACAGCGCGT TCGATTGAA CCGGCGCGGC
751 TTCGGAGACA GCGCGTACCG CCCCAACGGC ATCATCGACC AAATCATCTG
801 GCGCGCGCCC GTATCGCGCC TTTTGATGAA CAGTCCCGCA ATCAGCATCG
851 TCAAATGGGC GCAGGCGCAG TTTCCCGCGC TTCTGCCTGG CGGCGTGGTG
901 GACAGCAAAC CGCTGATGAA GCCTTATGCC CCAAAATTC AAACCCGTTA
951 TCAGGCGATG AAGGACGAGC TACTCAAAGA AGTCGAAACG CCGCAGTCGG
1001 AATGGGGCAG GCGGAAAC GGTCTTTGA ACTAG

```

This corresponds to the amino acid sequence <SEQ ID 2048; ORF 639-1>:

m639-1.pep

```

1  MSLPAMDAGI YLEETAPRAL IEHNNILDNS VGVYLHGSAD AMVRENKIVG
51  DATLRVNERG NGVTVWVAPG AQVVGNDISK GRDGIFSNIS THNTYKNNRF
101 SDLRFVHYM YTNDEISGN ISVGNMGYV LMFSERLKVF DNIAVGSRDQ
151 GIMLNYVNY DIHDNIINKA GKCVFAYNAN YDKLFANHFE NCQIGIHFTA
201 AIEGTSLDN SFINNESQVK YVSTRFLDWS EGGHGNYSW NSAFDLNGDG
251 FGDSAYRPNG IIDQIWRAP VSRLLMNSPA ISIVKWAQQAQ FPAVLPGGVV
301 DSKPLMKPYA PKIQTRYQAM KDELLKEVET RQSEWGRAEN GSLN*

```

g639-1/m639-1 95.9% identity in 344 aa overlap

	10	20	30	40	50	60
g639-1.pep	MSLPAMDAGIYLEKAAPRALVEHNNIFDNSFGVYLHGSADAMVRENKIVGDATLRVNERG					
m639-1	MSLPAMDAGIYLEETAPRALIEHNNILDNSVGVYLHGSADAMVRENKIVGDATLRVNERG					
	10	20	30	40	50	60
g639-1.pep	70	80	90	100	110	120
m639-1	NGVTVWVAPGAQVVGNDISKGRDGIFSNIS THNTYKNNRFSDLRFVHYMYTNDSEVSGN					
	70	80	90	100	110	120
g639-1.pep	130	140	150	160	170	180
m639-1	ISVGNMGYVLMFSERLKVF DNIAVGSRDQXGIMLNYVNYSDIHDNIINKAGKCVFAYNAN					
	130	140	150	160	170	180
g639-1.pep	190	200	210	220	230	240
m639-1	YDKLSANHFENCQIGMHFTA AIEGTSLDNSFINNESQVKYVSTRFLDWS EGGHGNYSW					
	190	200	210	220	230	240
g639-1.pep	250	260	270	280	290	300
m639-1	NSPFDLNGDGFSGDSAYRPNGIIDQIWRAPVSRLLMNSPAISIVKWAQQAQ FPAVLPGGVV					
	250	260	270	280	290	300
g639-1.pep	310	320	330	340		
m639-1	DSKPLMKPYAPKIQTRYQAMKDELLKEAETRQSERGRAENGSLNX					
	310	320	330	340		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2049>:

a639-1.seq

1015

```

1  ATGAGCCTGC CCGCAATGGA TGCCGGTATT TATCTCGAAG AAACCTGCCCC
51  GCGCGCCCTG ATTGAACACA ATAATATTTT GGATAATTTCG GTCGGCGTCT
101 ATCTGCATGG TTCTGCCGAT GCGATGGTGC GGGAGAAATAA AATCGTCGGC
151 GACGCGACTT TGCGCGTGAA CGAGCGCGGC AATGGCGTTA CCGTTTGAA
201 CCGCGCCGCG GCGCAGGTGC TCGGCAACGA TATTTCCAAA GGGCGGGACG
251 GCATTTTTC CAATACCAGC ACGCACAACT CCTATAAAA CAACCGCTTC
301 AGCGATTTCG GTTTCGCCGT CCACTATATG TACACCAACG ACAGCGAAAT
351 CAGCGGCAAT ATTTCCGTGG GCAACAATAT GGGCTATGTG CTGATGTTTT
401 CCGAGCGGCT CAAAGTGTTT GACAATATCG CCGTCGGCAG CCGCGACCAA
451 GGCATCATGC TCAACTATGT CAACTATTCC GATATTCACG ACAACATTAT
501 CAACAAAGCG GCAAGTGC TTTTGCCTA CAATGCCAAC TACGATAAAC
551 TGTCCGCCAA TCATTTTGAA AACTGCCAAA TCGGCATACA CTTTACCGCC
601 GCCATCGAAG GCACGTCCCT GCACGACAAT TCCTTTATCA ACAACGAAAG
651 CCAGGTCAA TACGTAGCA CGCGCTTCT CGACTGGAGC GAGGCGGAC
701 ACGGCAACTA TTGGAGGAC AACAGCGCGT TCGATTGAA CCGCGACGGC
751 TTCGGAGACA GCGCGTACCG TCCCAACGGC ATCATCGACC AAATCATCTG
801 GCGCGCACCC GTATCGCGCC TCTTGATGAA CAGTCCCGCA ATCAGCATCG
851 TCAAATGGGC GCAGGCGCAA TTCCCGCCG TTTGCCTGG CCGCGTGGTG
901 GACAGCAAAC CGCTGATGAA GCCTTATGCC CCAAAATTC AAACCCGTTA
951 TCAGGCGATG AAGGACGGGC TGCTCAAAA AGTCGAAACG CGGCAGTTGG
1001 AATGGGGCAG GCGGAAAAC GGTCTTTGA ACTAG

```

This corresponds to the amino acid sequence <SEQ ID 2050; ORF 639-1.a>:

a639-1.pep

```

1  MSLPAMDAGI YLEETAPRAL IEHNNILDNS VGVYLHGSAD AMVRENKIVG
51  DATLRVNERG NGVTVWNPAG AQVVGNDISK GRDGFISNTS THNTYKNNRF
101 SDLRFVHYM YTNDSISGN ISVGNMGGYV LMFSERLKVF DNIAGVSRDQ
151 GIMLNVNYS DIHDNIINKA GKCVFAYNAN YDKLSANHFE NCQIGIHFTA
201 AIEGTSLHNS FINNESQVK YVSTRFLDWS EGGHGNYSW NSAFLNGDG
251 FGDSAYRPNQ IIDQIIWRAP VSRLMNSPA ISIVKWAQAF PAVLPGGVV
301 DSKPLMKPYA PKIQTRYQAM KDGLLKKVET RQLEWGRAEN GSLN*

```

a639-1/m639-1 98.8% identity in 344 aa overlap

	10	20	30	40	50	60
a639-1.pep	MSLPAMDAGIYLEETAPRALIEHNNILDNSVGVYLHGSADAMVRENKIVGDATLRVNERG					
m639-1	MSLPAMDAGIYLEETAPRALIEHNNILDNSVGVYLHGSADAMVRENKIVGDATLRVNERG					
	10	20	30	40	50	60
	70	80	90	100	110	120
a639-1.pep	NGVTVWNPAGAQVVGNDISKGRDGFISNTSTHNTYKNNRFSDLRFVHYMYTNDSEISGN					
m639-1	NGVTVWNPAGAQVVGNDISKGRDGFISNTSTHNTYKNNRFSDLRFVHYMYTNDSEISGN					
	70	80	90	100	110	120
	130	140	150	160	170	180
a639-1.pep	ISVGNMGGYVLMFSERLKVFVFNIAVGSRDQGIMLNVNYSIDIHDNIINKAGKCVFAYNAN					
m639-1	ISVGNMGGYVLMFSERLKVFVFNIAVGSRDQGIMLNVNYSIDIHDNIINKAGKCVFAYNAN					
	130	140	150	160	170	180
	190	200	210	220	230	240
a639-1.pep	YDKLSANHFENCQIGIHFTAAIEGTSLHNSFINNESQVKYVSTRFLDWSSEGGHGNYSW					
m639-1	YDKLFANHFENCQIGIHFTAAIEGTSLHNSFINNESQVKYVSTRFLDWSSEGGHGNYSW					
	190	200	210	220	230	240
	250	260	270	280	290	300
a639-1.pep	NSAFDLNGDGFSDSAYRPNQIIDQIIWRAPVSRLMNSPAISIVKWAQAFPAVLPGGVV					
m639-1	NSAFDLNGDGFSDSAYRPNQIIDQIIWRAPVSRLMNSPAISIVKWAQAFPAVLPGGVV					
	250	260	270	280	290	300
	310	320	330	340		
a639-1.pep	DSKPLMKPYAPKIQTRYQAMKDGLLKKVETRQLEWGRAENGSLNX					
m639-1	DSKPLMKPYAPKIQTRYQAMKDELLKEVETRQSEWGRAENGSLNX					
	310	320	330	340		

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The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2051>:

```

g640.seq
1  ATGATTCATA TAATATCAAT ATTAAGAGT ATCGGTATAT CGGGGATAGC
51  TATGTCCTGT TTTTCAATCC GCGGTATGTC TCGGTTTCGG GCGCGGATAA
101 CGGCGTTTTT TACCGCCTTT GTCTTTTGA CGGcggcACT GCCCGCTTAT
151 GcggAgcgTc tgcctGATTT TCTGgcgAAA ATacAgcctT CGGAAATTTT
201 TCCGGGTGCG GATCGTTACG GCAAGCCGGA aggcAAGCCT AtggtTGCCC
251 GCgtttACAA AGgcgATGAG CAGCTCGGTT TGGTTTATAT CACGACCGAT
301 GCGGTCAATA CGCGCGGTTA TTCGAGCAAA CCGATCGATA CGCTGATGGC
351 TTTGGCAAAC GACGGCACGA TAGCCGGGGC GAAACTGGTC GATCATCACG
401 AACCGATTAT GCTGATCGGT ATCCCGCAAT CGCGTGCGA TAAGTTCATC
451 GACAAATATA TCGGTCTGAA TTTTATTAAA AATCCGCCGA CCCCAGCGCT
501 GCGCGCGGGC GACATCATCA GcggTGCGAC TgttaCACTG ATGGTGGTTA
551 ACGACAGCAT CCAGCGTTCG TACAAGGTCA TGGCCAACCA ATACCGTCTG
601 GGTTCGGACA AGGCCCTTCA GACGGCATCC GCTTCCGATG TTCGGGAAGC
651 CGCGCCTGCG TCAGAAACCC GTCCGCGCCG TATGGCAAAT CCGGACAGC
701 AGGATATTTT GTCTTGGGAC GAACTTTTGA AACAAAGGC CGTCCGCCAT
751 CTGCATATCA CGCTCGATCA AATCAACAAA CTGTTTGAGA AAGGCGGCAA
801 GGCCGGCGTG GCCGATCAGC CCGAACAGGG CGATCCTGAC GATACCTTTA
851 TTGATTTGTA TGTTCCTTG GTGAGCCAGC CTCCATCGG TAAAGCCTG
901 CTGGGTGAGG ACGGCTGGGC GCATCTGCAA AAACGGGTGA AACCCGGGCA
951 GCAGGCGGTT TTGGTTGCCG GAGAGGGCCG TTATTCTTGG AAAGGTCGG
1001 GCTATGTGCG CGCGGGTATT TTCGACCGTA TCGAGATGAT TCAGGGGAG
1051 AACAGCTTCC GTTTTACCGA TGCCCAACAC GAACGCTCG TCGAGCTGTC
1101 TGCGCCGAT GCGCCGCGTT TTAAGAGT TTCTTGGTT ACCATCCCTG
1151 AAGCGTAGC GTTTGACGGT GCGGAGCCGT GCGGCTGTA A

```

This corresponds to the amino acid sequence <SEQ ID 2052; ORF 640.ng>:

```

g640.pep
1  MIHIISILKS IGISGIAMSC FSIRMSAFR ARITAFFTAF VFLTAALPAY
51  AERLPDFLAK IQPSEIFPGA DRYGKPEGKP MVARVYKGDE QLGLVYITTD
101 AVNTRGYSSK PIDTLMALAN DGTIAGAKLV DHHEPIMLIG IPQSRVDKFI
151 DKYIGLNFIK NPPTPSVAPG DIISGATVTL MUVNDSIQRS YKVIANQYRL
201 GSDKALQTAS ASDVREAAFA SETRPRRMAN PDKQDILSWD ELLKQKAVGH
251 LHITLDQINK LFEKGGKAGV ADHAEQGDPD DTFIDLYVAL VSQPSIGKSL
301 LGEDGWAHLQ KRLKPGQQAV LVAGEGRYSW KSGYVRGGI FDRIMIQQE
351 NSFRETDAQH ERVELLSAAD APREKEVSF TIPEGVAFDG AEPWRL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2053>:

```

m640.seq (partial)
1  ATGATTCATA TAATATCAAT ATTAAGAGT ATCGGTATAT CGGGGATAGT
51  CATGTCCTGT TTTTCAATCA AACGTATGTC CGCGTTTCGG GCGCGGATAA
101 CGGCGTTTTT TGCCGCCTTT GTCTTTTGA CGGCGGCACT GCCCGCTTAT
151 GCGGAGCGTC TGCTGATTT TCTGGCGAAA ATACAGCCTT CGGAAATTTT
201 TCCGGGTGCG GACCGTTACG GCAAGCCGGA AGGTAAGCCT ATGGTTGCCC
251 GCGTTTACAA AGGCGATGAG CAGTTGGGCT TGGTCTATAT CACGACCGAT
301 GCGGTCAATA CGCGCGGTTA TTCGAGCAAA CCGATTGATA CGCTGATGGT
351 GTTGGCAAAC GACGGCACGA TAGCCGGGGC GAAACTGGTC GACCATCACG
401 AACCGATTAT GCTGATCGGT ATCCCGCAT...

```

This corresponds to the amino acid sequence <SEQ ID 2054; ORF 640>:

```

m640.pep (partial)
1  MIHIISILKS IGISGIVMSC FSIKRMSAFR ARITAFFAAF VFLTAALPAY
51  AERLPDFLAK IQPSEIFPGA DRYGKPEGKP MVARVYKGDE QLGLVYITTD
101 AVNTRGYSSK PIDTLMVLAN DGTIAGAKLV DHHEPIMLIG IPH...

```

m640/g640 96.5% identity in 143 aa overlap

	10	20	30	40	50	60
m640.pep	MIHIISILKS	IGISGIVMSC	FSIKRMSAFR	ARITAFFAAF	VFLTAALPAY	AERLPDFLAK
g640	MIHIISILKS	IGISGIAMSC	FSIRMSAFR	ARITAFFTAF	VFLTAALPAY	AERLPDFLAK
	10	20	30	40	50	60
	70	80	90	100	110	120

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```

m640.pep      IQPSEIFPGADRYGKPEGKPMVARVYKGDEQLGLVYITTDVAVNTRGYSSKPIDTLMVLAN
                |||||||
g640           IQPSEIFPGADRYGKPEGKPMVARVYKGDEQLGLVYITTDVAVNTRGYSSKPIDTLMALAN
                70      80      90      100     110     120

                130      140
m640.pep      DGTIAGAKLVDHHEPIMLIGIPH
                |||||||
g640           DGTIAGAKLVDHHEPIMLIGIPQSRVDKFIDKYIQLNFIKNPPTPSVAFGDIISGATVTL
                130      140      150      160     170     180

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2055>:

```

a640.seq (partial)
1  ATGATTCATA TAATATCAAT ATTAAAGAGT ATCGGTATA  CGGGGATAGT
51 CATGTCCTGT TTTTCAATCA AACGTATGTC CGCGTTTCGG GCGCGGATAA
101 CGGCGTTTTT TGCCGCCTTT GTCTTTTGA CGGCGGCAC  GCCCGCTTAT
151 GCGGAGCGTC TGCCGTGATT TCTGGCGAAA ATACAGCCT  CGGAAATTGT
201 TCCGGGTGCG GACCGTTACA GCAAGCCGGA AGGTAAGCCT ATGTTGCCCC
251 GCGTTTACAA AGGCGATGAG CAGTTGGGCT TGGTCTATA  CACGACCGAT
301 GCGGTCAATA CGCGCGGTTA TTCGAGCAA CCGATTGATA CGCTGATGGC
351 GTTGGCTAAA GACGGTACGA TAGCCGAGC GAAATTGGT  GATCACCATG
401 AGTCGATTAT SCTGATCGGT ATCCCGCAT...

```

This corresponds to the amino acid sequence <SEQ ID 2056; ORF 640.a>:

```

a640.pep (partial) Length: 143
1  MIHIISILKS IGISGIVMSC FSIKRMSAFR ARITAFFAAF VFLTAALPAY
51  AERLPDFLAK IQPSEIVPGA DRYSKPEGKP MVARVYKGDE QLGLVYITTD
101 AVNTRGYSSK PIDTLMALAK DGTIAGAKLV DHHESIMLIG IPH...

```

m640/a640 96.5% identity in 143 aa overlap

```

                10      20      30      40      50      60
m640.pep      MIHIISILKSIGISGIVMSCFSIKRMSAFRRARITAFFAAFVFLTAALPAYAERLPDFLAK
                |||||||
a640           MIHIISILKSIGISGIVMSCFSIKRMSAFRRARITAFFAAFVFLTAALPAYAERLPDFLAK
                10      20      30      40      50      60

                70      80      90      100     110     120
m640.pep      IQPSEIFPGADRYGKPEGKPMVARVYKGDEQLGLVYITTDVAVNTRGYSSKPIDTLMVLAN
                |||||
a640           IQPSEIVPGAADRYSKPEGKPMVARVYKGDEQLGLVYITTDVAVNTRGYSSKPIDTLMALAK
                70      80      90      100     110     120

                130      140
m640.pep      DGTIAGAKLVDHHEPIMLIGIPH
                |||||||
a640           DGTIAGAKLVDHHEPIMLIGIPH
                130      140

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2057>:

```

g642.seq
1  ATGCGGTATC CGCCGCAATC GCGGTTTTG CAGAAATGCCG CGCGTTGCCT
51  TTGCGCCGC CCGAAATCTG CCTGCCGCCG TATTGCCC GATCCGCAA
101 TATCGGCAGT CCAATATATC TTTGCGGATG TCGTTCAGCA GGAAGGCTGT
151 GGTGTCTTCG TGTTCCTCCT GTACGAAGAC AAAAAGTCGG GCGATGATT
201 TGCCGATGAA GACTTTTTCG AGGCGCAGG CGTCGGTCAG GGTGTGTTC
251 TGCAGGAAGC TGCGGATGTC TTCGGGCAA GCGTAgTcgc gGCAACGGC
301 GGcaaaagcg ACatcggtT Gcacggcgtc gagCAGGgtt tggTTTTGT
351 CCAACTTAAT GCCTGCTTCT TTTCTTCGG CGGTGGCGCG GACGAACTGG
401 TCGTAAATTT CGGCATAAAG CATATCGTTC GGCCTTCAA AAATCGTGAA
451 GGGGCGGATA TCGATGGCGA TATTGCCGGC TGGGTGTCCG CGTTCAAAC
501 CCTTCGCGCC CAAGAGTTT TGCAACATT GCGCGCGGc qTAAGTGAT
551 TCCGTGGCGa ggGTTTGAc gatgTTCGCC TCCATCAATT GATGGGCGAc
601 ggGCGgacg ggCGAAACGG AATGGCAGAC GTAGCGGTAA AGGATTTCCG
651 AAACCTGATG GCGGCGTTGG ATTCGCGGC GTTCGTAATC GACGAATCTG

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```

701 ATATCGTTGC GGACATATCG GTTCAGGTTG TCAACGATGT ATTCCATAAT
751 GCCGTGCGTC ATGCCGATCA GTTGCAGGCG GCTGCGGATA AAGATGTTTT
801 GGAACGCGCG CAAACCGGCA GCGTCGCCCC GGGAGAGTTT CATCACGGCG
851 GTTGCAGGCA TTTCGGCATC GATGCGGTTG ACGGCGTAAC GGACGGCGCG
901 CAGGCCTTCG GATGCGAGGG TTTCGCAGCG GATGTATGTT TTGGGGACGA
951 GCAGCAGGTC GATGactttg gcgagtttgC Cgtttttgcg ctctttggcg
1001 gcaacgaggA GGAAGTCGCT TTGCGAATTG CCCTGCCAGT ATTTCGCGGC
1051 GctgACGTAA ATGGTTtgtt cgtcggataa ttcgtagcag gactgcaTTT
1101 CGCGTGCAAT cgCgcgcgcg gaggtTtcgg gttcggtaAc gcccacacgg
1151 cggctttcgc cttTGAAAAT CATGTCCAAA CCTGTGCGA CTTCGcttc
1201 gccgcggaac tCTTGACAG GCTGCAACAC CAGCGCGCCT TCGATGCCGG
1251 TACGCAGCGT AACGGGCACG CCGTAATGCC CCGCAATCCT TAG

```

This corresponds to the amino acid sequence <SEQ ID 2058; ORF 642.ng>:

```

g642.pep
1 MRYPPQSAVL QNAARCLLRE PKSACRRICP LSAISAVQYI FADV VQOEGC
51 GV FVFLLYED KKS GDDFADE DFLQAGVGQ GVFLQEAADV FGQSVVAGNG
101 GKADIGLHGV EQGLVFEVLN ACFFFFGGGA DELV VNFVGIK HIVRAFKNRE
151 GADIDGDIAG WVS AFKTLRA QEF LQHLRGG VSVFRGEGFD DVLRLHQLMGD
201 GRDGRNGMAD VAVKDFGNLM AALDFAAFVI DESDIVADIS VQVVKDVFHN
251 AVRHADQLQA AADKDV LERA QTGSVAPGEF HHGGCRHFGI DAVDGVTDGA
301 QAFGCEGFAA DVC FGDEQQV DDFGEFAVFA LFGGNEEEVA LRALPVRFG
351 VDVNGLFVGE FVAGLHFACN RRAGGF GFGN AQTA AFEN HVQTLCDLRF
401 AAELLQRLQH QRAFDAGTQR NGHAVMPRNP *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2059>:

```

m642.seq (partial)
1 GCCTGCCGCC GTATTGCCCC GCTACCCGCA ATATCGGCAG TCCAATATAT
51 CTTTGGCGAT GTCGTT CAGC AGGAAGGCTG CCGTGTCTTC GTGTTTCGCC
101 TGTACGAAGA CAAAGAGTCG GCGGATGATT TTGCCGATAA AGACTTTTGT
151 CAGGGCGCAG GCATC3GTCA GGGTGTGTTC CTGCAGGAAG CTGCGGATGT
201 CTTACGGCAA AGTGTAGTCG CGGGCGACGG CGGCAAAGCG GCATCGGTT
251 TGCAGGCGGT CGAGCAGGGT TTGGTTTTTG TCCA ACTTCA TGCCTGCTTC
301 TTTTCTTCG CGCGTGGCGC GGACAACTG GTCGTAAATT TCGGCATAAA
351 GCATATCGTT CGGGCCTTCA AAAATCGTGA AGGGGCGGAT GTCGATAGCG
401 ATATTGCCCG CGGTGTGTCC GCGTTCAAAA CCCTTCGCAC CCAAGAGTTT
451 TTGCAACATT TGCGCGGCGG CGTAAGTGTA TTCCGTGGCG AGGGTTTTGA
501 CGATGTTCGC CTCCATCAGC TGATGGGCGA CGGGGGCAAC AGCGGAAACG
551 GAATGGCAGA CGTAGCGGTA AAGAATCTCG GAAACCTGAT GCGCGCGCCG
601 GATTCGCGG CGTTCGTAAT CGACGAATTT GATGTCGTTG CGGACGTATC
651 GTTCCAGATT TTCAAGGATG TATTCCATAA TGCCGTGCGT CATGCCGATC
701 AGTTGCAGGC GGCTGCGGAT AAAGATGTTT TGGAACGCGC GCAAACCGGC
751 AGCGTCGCTC TGGGAGAGTT TCATCACGGC GGTTCAGGC ATTTCGGCAT
801 GCATGCGGTT GACGGCGTAA CGGACGGCGC GCAAGCCTTC GGATGCGAGG
851 GTTTCGCAGC GGATGTATGT TTTGGGGACG AGCAGCAGGT CGATGACTTT
901 GGCGAGTTTG CCGTTTTTGC GCTCTTTGGC GGCAACGAGG AGGAAGTCGC
951 TTTGCGAGTT GCCCTGCCAG TATTTCGCGG CGTTGACGTA AATGGTTTGT
1001 CCGTCGATAT ATTCTAGTA GGACTGCATT TCGCGTGCAA TCGCCGCGCC
1051 GGAGGTTTCG GGTTCGTAAC CACCCAAACC GCCGCCCTCG CCTTTGAAAA
1101 TCATCTCAA ACCTTGC GCG ACTTGCCTT CATCGCGGAA CTCTTGCACT
1151 GGCTGCAACA CCAGCGCGCC TTCGATGCCG GTACGCAGCG TAACGGGCAC
1201 CCCGTAATGC CCCGCAATCC G

```

This corresponds to the amino acid sequence <SEQ ID 2060; ORF 642>:

```

m642.pep (partial)
1 ACRRICPLPA ISAVQYIFAC VVQEGCGVF VFRLYEDKES GDDFADKDFL
51 QGAGIGQGVF LQEAADVFRQ SVVAGDGGKA GIGLQAVEQG LVFVQLHACF
101 FFFGGGADKL VVNFVGIKHIV RAFKNREGAD VSDIAGGVS AFKTLRTQEF
151 LQHLRGGVSV FRGEGFDDVR LHQLMGDGGN RRNGMADVAV KNLGNLMAAP
201 DFAAFVIDEF DVVADV SFQI FKDV FHNVR HADQLQAAAD KDVLERAQTG
251 SVALGEFHFG GCRHFGIDAV DGVTDGAQAF GCEGFAADVC FGDEQQVDDF
301 GEFAVFALFG GNEEEVALRV ALPVFRGVDV NGLSVDIFVV GLHFACNRRA
351 GGFGFGNTQT AALAFENHLQ TLRDLRFIAE LLQWLQHQRA FDAGTQRNGH
401 AVMPRNP

```

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m642/g642 90.4% identity in 407 aa overlap

m642.pep			10	20	30	
			ACRRICPLPAISAVQYIFADVQQEGCGVFVRLYED			
g642	MRYPPQSAVLQNAARCLLRPKSACRRICPLSAISAVQYIFADVQQEGCGVFVLLYED					
	10	20	30	40	50	60
m642.pep	40	50	60	70	80	90
	KESGDDFADKDFLQGAGIGQGVFLQEAAADVFRQSVVAGDGGKAGIGLQAVEQGLVVFVQLF					
g642	KESGDDFADEDFLQGAGVGQGVFLQEAAADVFGQSVVAGNGGKADIGLHGVEQGLVVFVQLN					
	70	80	90	100	110	120
m642.pep	100	110	120	130	140	150
	ACFFFFGGGADKLNVNFGIKHIVRAFKNREGADVDSIAGGVSAFKTLRTQEFLOHLRGG					
g642	ACFFFFGGGADELNVNFGIKHIVRAFKNREGADIDGDIAGWVSAFKTLRAQEFLOHLRGG					
	130	140	150	160	170	180
m642.pep	160	170	180	190	200	210
	VSVFRGEGFDDVRLHQLMGDGNRRNGMADVAVKNLGNLMAAPDFAAFVIDEFDVVADVS					
g642	VSVFRGEGFDDVRLHQLMGDGRDGRNGMADVAVKDFGNLMAALDFAAFVIDESDIVADIS					
	190	200	210	220	230	240
m642.pep	220	230	240	250	260	270
	FQIFKDVFNHVRHADQLQAAADKDVLERAQTSVALGEFHHGGCRHFGIDAVDGVTDGA					
g642	VQVVKDVFNHVRHADQLQAAADKDVLERAQTSVAPGEFHHGGCRHFGIDAVDGVTDGA					
	250	260	270	280	290	300
m642.pep	280	290	300	310	320	330
	QAFGCEGFAADVCFGDEQQVDDFGEFAVFALFGGNEEEVALRVALPVFRGVDVNGLSVDI					
g642	QAFGCEGFAADVCFGDEQQVDDFGEFAVFALFGGNEEEVALRIALPVFRGVDVNGLFVGI					
	310	320	330	340	350	360
m642.pep	340	350	360	370	380	390
	FVVGHLHFACNRRAGGFGFGNTQTAALAFENHLQTLRDLRFIAELLQWLQHQRAFDAGTQR					
g642	FVAGLHFACNRRAGGFGFGNAQTAAAFENHVOTLCDLRFIAELLQRLQHQRAFDAGTQR					
	370	380	390	400	410	420
m642.pep	400	NGHAVMPRNP				
g642	NGHAVMPRNPX					
	430					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2061>:

a642.seq (partial)

```

1   GCCTGCCGCC GTATTTGCCG GCTATCCGCA ATATCGGCAG TCCAATATGT
51  CTTTGCCGAT GTCGTTCCAG AGGAAGGCTG CGGTGTCTTC GTGTTCCGCC
101 TGTACGAAGA CAAAGAGTCG GCGGATGATT TTGCCGATAA AGACTTTTGT
151 CAGGGCGCAG GCATCGGTCA GGGTGTGTTC CTGCAGGAAG CTGCGGATGT
201 CTTGCGGCAA AGTGTAGTCG CGGGCGACGG CGGCAAAGCG GGCATCGGTT
251 TGCAGGCGGT CGAGCAGGGT TTGGTTTTTG TCCAACCTCA TGCCTGCTTC
301 TTTTCTTCG GCGGTGGCGC GGACAACTG GTCGTAAATT TCGGCATAAA
351 GCATATCGTT CGGGCTTCA AAAATCGTGA AGGGGCGGAT GTCGATAGCG
401 ATATTGCCGG CGGTGTGTCC GCGTTCAAA CCCTTCGCGC CCAAGAGTTT
451 TTGCAACATT TCGCGGCGG CGTAAGTGTA TTCCGTGGCG AGGGTTTTGA
501 CGATGTTCCG CTCCATCAGT TGATGGGCGA CGGTGCAAC GGGCGAAACG
551 GAATGGCAGA CGTAGCGGTA AAGAATCTCG GAAACCTGAT GGCGGCGCCG
601 GATTTCGCGG CGTTCGTAAT CGACGAATCT GATGTCGTTG CGGACGTATC
651 GTTCCAGGTT TTCAAGGGTG TATTCATAA TGCCGTGCGT CATGCCGATC

```

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```

701 AGTTGCAGGC GGCTGCCGAT AAAGATGTTT TGGAACGCGC GCAAACCGGC
751 AGCGTCGCTC TGGGAGAGTT TCATCACGGC GGTTCGAGGC ATTTCCGGCAT
801 CGATGCGGTT GACGGCGTAA CGGACGGCGC GCAAGCCTTC GGATGCGAGG
851 GTTTCGCAGC GGATGTATGT TTTGGGACG AGCAGCAGGT CGATGACTTT
901 GGCGAGTTTG CCGTTTTTGC GCTCTTTGGC GGCAACGAGG AGGAAGTCGC
951 TTTGCGAGTT GCCCTGCCAG TATTTCCGCG CGTTGACGTA AATGGTTTGT
1001 CCGTCGGTAT ATTCGTAGTA AGACTGCATT TCTCGGGCAA TCGCCGCGCC
1051 GGAGGTTTCG GGTTCGGTAA CGCCTAAACC GCCGCCCTCG CCTTTGAAAA
1101 CCATGTCCAA ACCCTGTGCG ATTTGCGCTT CATCGCCGAA CTCTTGCACT
1151 GGCTGCAACA CCAGCGCGCC TTCGATGCCG GTACGCAGCG TAACGGGCAC
1201 GCCGTAATGC CCCGCAATCC G

```

This corresponds to the amino acid sequence <SEQ ID 2062; ORF 642.a>:

```

a642.pep Length: 407
1 ACRRICPLSA ISAVQYVFAD VVQEGCGVF VFRLYEDKES GDDFADKDFL
51 QGAGIGQGVF LQEAADVFGQ SVVAGDGGKA GIGLQAVEQG LVFVQLHACF
101 FFFGGGADKL VVNFGIKHIV RAFKNREGAD VDSDIAGGVS AFKTLRAQEF
151 LQHLRGGVSV FRGEGFDDVR LHQLMGDGCN GRNGMADVAV KNLGNLMAAP
201 DFAAFVIDES DVVADVSFQV FKGVFHNAVR HADQLQAAAD KDVLERAQTG
251 SVALGEFHHG GCRHFGIDAV DGVTDGAQAF GCEGFAADVC FGDEQQVDDF
301 GEFVAVFALFG GNEEEVALRV ALPVFRGVDV NGLSVGIFVV RLHFSGNRRR
351 GGFGFGNA*T AALAFENHVQ TLCDLRFIAE LLQWLQHORA FDAGTQRNGH
401 AVMPRNP

```

m642/a642 95.8% identity in 407 aa overlap

m642.pep	10	20	30	40	50	60
a642	10	20	30	40	50	60
m642.pep	70	80	90	100	110	120
a642	70	80	90	100	110	120
m642.pep	130	140	150	160	170	180
a642	130	140	150	160	170	180
m642.pep	190	200	210	220	230	240
a642	190	200	210	220	230	240
m642.pep	250	260	270	280	290	300
a642	250	260	270	280	290	300
m642.pep	310	320	330	340	350	360
a642	310	320	330	340	350	360
m642.pep	370	380	390	400		
a642	370	380	390	400		

1021

370 380 390 400

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2063>:

```
g643.seq
  1 ATGGTGTTCG CTTGATGTT GTTGGCGACA ATCAGgTcgg CTACGCTGAc
  51 gttgtancGt TTGGcaATGt tGaaCAgggt gtcgccTTCT ACAACGCGGT
 101 GGATGCTGGC ATGGagcGGG GAGGTTTCGG CTTCGCCGTC GGCAGCTTTG
 151 GCTACGCGCG TTTCCAAACG TGCCCGCGT TtgCCGTCGG CGGCAACGGT
 201 ATGTTGCGGA GATGAGGAAA TGTTGTGTTT GGCAACTGTG TCAGGCGTGC
 251 CGATGACGGC GGagaTGGTT TCTTCAGCCT GCCGGCGCag gTTGTTTCGG
 301 GCAACAAGCT GCATGAGTTC GTCTGCCGCC TGCATGTCGT TTGGGGGGAt
 351 GACCTGCGCg aGTGtTCCGG TTGGGTTTC agacgGCATG GCAETCTGTT
 401 TTTcggTTTG a
```

This corresponds to the amino acid sequence <SEQ ID 2064; ORF 643>:

```
g643.pep
  1 MVLPLMLLAT IRSATLTLXR LAMLN RVSPS TTRWMLAWSG EVSASPSAAL
  51 ATRVSKRRRR LPSAA TVCCG DEEMLC SATV SGVPM TAEMV SSACRRRLFR
 101 ATSCMSSSAA CMSFGMTCA SVAVW VSDGM AVCFSV*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2065>:

```
m643.seq
  1 ATGGTGTTCG CTTGATGTT GTTGGCGACA ATCAGGTCGG CTACACTGAC
  51 GTTG TAGCGT TTGGCAATGT TGAACAGGGT GTCGCCTTCT ACAACGCGGT
 101 GGATGCTGGC ATGGAGCGGG GAGATTTCGG CTTCGCCGTC GGCAGCTTTG
 151 GCTACGCGCG TTTCCAAACG TACCCGGCGT TTGCCGTCGG CGGCAGCGGT
 201 ATGTTGCGGA GATGCGGAAA TTTGTGTTT GGCAACTGTG TCAGGCGTGC
 251 CGATGACGGC GGAGATGGTT TCTTCAGCCT GTCGGCGCAG GTTGTTCGG
 301 GCAACAAGCT GCATGAGTTC GTCTGCCGCC TGCATGTCGT TTTGGGGGAT
 351 GATCTGCGCG AGTGTTCGGG TTGGGTTTC AGACGGCATG GCGGTCTGTT
 401 TTTCCGTTTG A
```

This corresponds to the amino acid sequence <SEQ ID 2066; ORF 643>:

```
m643.pep
  1 MVLPLMLLAT IRSATLTL*R LAMLN RVSPS TTRWMLAWSG EISASPSAAL
  51 ATRVSKRRRR LPSAAAVCCG DAEILCSATV SGVPM TAEMV SSACRRRLFR
 101 ATSCMSSSAA CMSFWGMICA SVAVW VSDGM AVCFSV*
```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 643 shows 94.9% identity over a 136 aa overlap with a predicted ORF (ORF643.a) from *N. gonorrhoeae*:

m643/g643

	10	20	30	40	50	60
m643.pep	MVLPLMLLAT	IRSATLTLXRL	LAMLN RVSPS	TTRWMLAWSG	EISASPSAAL	ATRVSKRRR
g643	MVLPLMLLAT	IRSATLTLXRL	LAMLN RVSPS	TTRWMLAWSG	EVSASPSAAL	ATRVSKRRR
	10	20	30	40	50	60
	70	80	90	100	110	120
m643.pep	LPSAAAVCCG	DAEILCSATV	SGVPM TAEMV	SSACRRRLFR	ATSCMSSSAA	CMSFGMICA
g643	LPSAA TVCCG	DEEMLC SATV	SGVPM TAEMV	SSACRRRLFR	ATSCMSSSAA	CMSFGMTCA
	70	80	90	100	110	120
	130					
m643.pep	SVAVW VSDGM	AVCF SVX				
g643	SVAVW VSDGM	AVCF SVX				
	130					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2067>:

1022

a643.seq
 1 ATGGTGTTC CTTGATGTT GTTGGCGACA ATCAGGTCGG CTACACTGAC
 51 GTTGTAGCGT TTGGCAATGT TGAACAGGGT GTCGCCTTCT ACAACGCGGT
 101 GGATGCTGCG ATGGAGCGGG GAGATTTCGG CTTCGCCGTC GGCAGCTTTG
 151 GCTACGCGCG TTTCCAAACG TACCCGGCGT TTGCCGTCGG CGGCAACCGT
 201 ATGTTGCGGA GATGAGGAAA TGTGTGTTC GGCAACTGTG TCAGGCGTGC
 251 CGATGACGGC AGAGATGGTT TCTTCAGCCT GTCGGCGCAG GTTGTTCGG
 301 GCAACAAGCT GCATGAGTTC GTCTGCCGCC TGCATGTCGT TTTGGGGGAC
 351 GATCTGCGCG AGTGTTCGG TTTGGGTTTC AGACGGCATG GCGTCTGTT
 401 TTTGCGTTG A

This corresponds to the amino acid sequence <SEQ ID 2068; ORF 643.a>:

a643.pep
 1 MVLPLMLLAT IRSATLTL*L LAMLNRVSPS TTRWMLAWSG EISASPSAAL
 51 ATRVSKRTRR LPSAATVCCG DEEMLCSATV SGVPMTEMV SSACRRRLFR
 101 ATSCMSSSAA CMSFWGTICA SVAWVSDGM AVCFSV*

m643/a643 97.1% identity in 136 aa overlap

	10	20	30	40	50	60
m643.pep	MVLPLMLLATIRSATLTLXRLAMLNRVSPSTTRWMLAWSGEISASPSAALATRVSKRTRR					
a643	MVLPLMLLATIRSATLTLXRLAMLNRVSPSTTRWMLAWSGEISASPSAALATRVSKRTRR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m643.pep	LPSAAVCCGDAEILCSATVSGVPMTEMVSSACRRRLFRATSCMSSSACMSFWGMICA					
a643	LPSAATVCCGDEEMLCSATVSGVPMTEMVSSACRRRLFRATSCMSSSACMSFWGTICA					
	70	80	90	100	110	120
	130					
m643.pep	SVAWVSDGMVAVCFSVX					
a643	SVAWVSDGMVAVCFSVX					
	130					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2069>:

g644.seq
 1 ATGCCSTCTG AAAGGccgGC GGATTGTTGC CCGGTGCACT TTGTGGTAAA
 51 GTTTAGAAAA TTAACCTAA ACTGTGGCAG GCGGTTTGAC CGGCCGCCGA
 101 TTAATGGGAA CCGACAGAGG AAGCCGATGA TACACCCGA ACCGAGCGCG
 151 CAGCCGTCAG CCATGGACAC GGCTGCTTTT TTAAagcaca tgaatCCGC
 201 ATTCCCCCGC ATTTTTCAG ACGGCATCGA CCTGATGCGA TACCTGCCCG
 251 AAGACAAATG GCTTGCCTTG AAGCAGGCGG GTTTGCTGTT GCCCTTCCTC
 301 GACAAAAAAC ACGGCGGGCG CAAGGGCAGT CAGTTTGAAA TCCAAGAAGT
 351 CCTAAGGATT GCGGGGCATT ACGGCGTGCC CGTTACGCTG CGTACCGGCA
 401 TCGAAGGCGC GCTGGTGTG CAGCCTCTGC AAGagttcgg cggcgaagcG
 451 CAAGTCGCAC AAGGTTTGA CATGATTTTC AAaggcgaaa gccgcggttt
 501 gggcgTtacc gaaccggaAa cctccggcgc gGcgaTTGCA CGCGAAAtgc
 551 agtcctgcta cgaatatacc gacgaacaAA CCATTACGT caaCGCCGCG
 601 AAATACTGGC AGGGCAATTC GCAAAGCGAC TTCCTcctcg ttgccgccaa
 651 agagcgcaaa aacGGcaaac tcgccaaagt CATCGACCTG CTGCTCGTCC
 701 CCAAAACATA CATCCGCTGC GAAACCCCTG CATCCGAAGG CCTGCGCGCC
 751 GTCCGTTACG CCGTCAACCG CATCGATGCC GAAATGCCTG CAACCCCGCT
 801 GATGAACTC TCCCGGGCGC ACGCTGCCGG TTTGCGCGCG TTCCAAAACA
 851 TCTTTATCCG CAGCCGCTG CAACTGATCG GCATGACGCA CGGCATTATG
 901 GAATACATCC TTGACAACT GAACCGATAT GTCCGCAACG ATATCAGATT
 951 CGTCGATTAC GAACGCCGCG AAATCCAACG CCGCCATCAG GTTTCCGAAA
 1001 TCCTTTACCG CTACGCTGCG CATTCGCTTT CGcccgctgc GCccgTCGCC
 1051 CATCAATTGA TGGAGGCGAA catcgTCAAA AccctCGCCA CGGAATACAC
 1101 TTAegcCGCC GCGCAATGT TGCAAAACT CTTGGGCGCG AAGGTTTGT
 1151 AACGCGGACA CCCAGCCGGC AATATCGCCA TCGATATCCG CCCCTTCACG
 1201 ATCTTTTGAAG GCCCGAACGA TATGCTTTAT CCGCAAAATT ACGACCAATT
 1251 CGTCCGCGCC ACCGCCGAAG AAAAAGAAGC AGGCATTAAG TTGGACAAAA
 1301 accaaaCCCT Gctcgagccc gtgCAAAccg atGTCcgctt tgCCGCGGTT
 1351 GCCcgGacT ACGCTTTGCC CGAAGACATC CGCAGTTCC TGCAGGAACA
 1401 CACCCTGACC GACGCTGCG CCCTGCAAAA AGTCTTCATC GGCAAAATCA

1023

1451 TCGCCCGACT TTTGTCTTC GTACAGGAGG AACACGAAGA CACCACAGCC
 1501 TTCTGTCTGA ACGACATCCG CAAAGATATA TTGGACTGCC GATATTGCGG
 1551 ATAG

This corresponds to the amino acid sequence <SEQ ID 2070; ORF 644.ng>:

g644.pep
 1 MPSPERPADCC PVHEFVKFRK LTLNCGRRFD RPPINGNRQR KPMIHTEPSA
 51 QPSTMDTAAF LKHIESAFPR IFSDGIDLMR YLPEDKWLAL KQAGLLLPFL
 101 DKKHGGGRKGS QFEIQEVLRI AGHYGVPVTL RTGIEGALVL QPLQEFGGEA
 151 QVAQGLDMIF KGESRRLGVT EPETSGAIA REMQSCYEY DEQTIYVNAA
 201 KYWQNSQSD FLLVAAKERK NGKLAKVIDL LLVPKTYIRC ETLASEGLRA
 251 VRYAVNRIDA EMPATAVMKL SRGDAAGLRA FQNIIFIRSRL QLIGMTHGIM
 301 EYILDNLNRY VRNDIREVDY ERREIQRHQ VSEILYRYVC HSVSPVAPVA
 351 HQLMEANIVK TLATEYTYAA AQMLQKLLGA KGFERGHPAG NIAIDIRPFT
 401 IFEGPNOMLY AEIYDQFVRA TAEKEAGIK LDKNQTL LDA VQTDVRF AAV
 451 ARDYALPEDI RSFLQEHILT DACALQKVF GKIIARLFVF VQEHEDTTA
 501 FLLNDIRKDI LDCRYCG*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2071>:

m644.seq
 1 ATGCCGCTCTG AAAGGTCGGC GGATTGTTGC CCGGCGCACT TTGTGGTAAA
 51 GTTTAGAAAA TCAACTCTAA ACTGTGGCAG CGGGTTTGAC CGGCCGCCGA
 101 TTAATGGGAA CCGACAGAGG AAGCCGATGA TACACACCGA ACCGAGCGCG
 151 CAGCCGTCAA CTATGGACAC GGCTGCTTTT TTAAAGCACA TCGAATCCGC
 201 ATTCCGCGCG ATTTTTCAG ACGGTATCGA CCTGATGCGA TACCTGCCCG
 251 AAGACAAATG GCTTGCCCTG AAGCAGCGCG GTTTGCTGTT GCCCTTCCTC
 301 GACAAAAAAT ACGGCGGGCG CAAGGGCAGC CAGTTTGAAA TCCAAGAAAT
 351 CcTGCGGATT GCGGGGCATT ACGGCGTGCC CGTTACGCTG CGTACCGGCA
 401 TCGAAGGCGC GCTGGTGTG CAGCCACTGC AAGAGTTCGG CGATGAAGCG
 451 CAAGTCGCGC AAGTTTGA GAATGATTTT AAAGGCGAGG GCGGCGGTTT
 501 GGGTGTACC GAACCCGAAA CCTCCGGCGC GCGGATTGCA CGCGAAATGC
 551 AGTCCTACTA CGAATATATC GACGGACAAA CCATTTACGT CAACGCCGCG
 601 AATACTGGC AGGGCAACTC GCAAAGCGAC TTCTCTCTCG TTGCCGCCAA
 651 AGAGCGCAAA AACGGCAAAC TCGCCAAAGT CATCGACCTG CTGCTCGTCC
 701 CCCAAACATA CATCCGCTGC GAAACCTCG CATCCGAAGG CTGCGCGCG
 751 STCCGTACG CCGTCAACCG CATCGATGCC GAAATGCTG CAACCGCGCT
 801 EATGAAACTC TCCCAGAGCG ACCTGCGCG TTTGCGCGCG TTCCAAAACA
 851 TCTTTATCCG CAGCCGCGCT CAACTGATCG GCATGACGCA CGGCATTATG
 901 GAATACATCC TTGAAAATCT GGAACGATAC GTCCGCAACG ACATCAAATT
 951 CTCGATTAC GAACGCCGCG AATCCGCGC CGGCATCAG GTTCCGAGA
 1001 TTCTTTACCG CTACGCTGCG CATTCGGTTT CGCCTGTTGC CCCCCTCGCC
 1051 CATCAGCTGA TGGAGGCGAA CATCGTCAA ACCCTCGCCA CGGAATACAC
 1101 TTACGCCGCC GCGCAATGT TGCAAAACCT CTGGGTGCG AAGGGTTTTC
 1151 AACCGCGACA CACCGCCGCG AATATCGCTA TCGACATCCG CCCCTTCACG
 1201 ATTTTGAAG GCCCGAACGA TATGCTTTAT GCCGAAATTT ACGACCAGTT
 1251 TGTCGCCGCC ACCGCCGAAG AAAAAAGAGC AGGCATGAAG TTGGACAAAA
 1301 ACCAAACCTT GCTCGACCGC CTGCAAAACG ATGCCCGCTT TGCCGCCGCTC
 1351 GCCCGGCACT ACACCTTGCC TGAAGACATC CGCAGCTTCC TGCAGGAACA
 1401 CACCTGACG GATGCTGCG CCCTGCAAAA AGTCTTTAT GGCAAAATCA
 1451 TCGCCCGACT CTTGTCTTC GTACAGGCGA AACACGAAGA CACCGCAGCC
 1501 TTCTGTCTGA ACGACATCCG CAAAGATATA TTGGACTGCC GATATTGCGG
 1551 STAG

This corresponds to the amino acid sequence <SEQ ID 2072; ORF 644>:

m644.pep
 1 MPSPERSADCC PAHEFVKFRK STLNCGRRFD RPPINGNRQR KPMIHTEPSA
 51 QPSTMDTAAF LKHIESAFRR IFSDGIDLMR YLPEDKWLAL KQAGLLLPFL
 101 DKKYGGGRKGS QFEIQEVLRI AGHYGVPVTL RTGIEGALVL QPLQEFGDEA
 151 QVAQGLEMIF KEGGGGLGVT EPETSGAIA REMQSYEYI DGOTIYVNAA
 201 KYWQNSQSD FLLVAAKERK NGKLAKVIDL LLVPKTYIRC ETLASEGLRA
 251 VRYAVNRIDA EMPATAVMKL SQSDAAGLRA FQNIIFIRSRL QLIGMTHGIM
 301 EYILENLERY VRNDIKFVDY ERREIRRHQ VSEILYRYVC HSVSPVAPVA
 351 HQLMEANIVK TLATEYTYAA AQMLQKLLGA KGFERGHTAG NIAIDIRPFT
 401 IFEGPNOMLY AEIYDQFVRA TAEKEAGMK LDKNQTLDR LQTDARFAAV
 451 ARDYTLPEDI RSFLOEHLT DACALQKVF GKIIARLFVF VQAKHEDTAA
 501 FLLNDIRKDI LDCRYCG*

m644/g644 94.6% identity in 517 aa overlap

	10	20	30	40	50	60
m644.pep	MPSPERSADCCPAHEFVKFRKSTLNCGRRFDRPPINGNRQRKPMIHTEPSAQFSTMDTAAF					
g644	MPSPERPADCCPVHEFVKFRKLTNCGRRFDRPPINGNRQRKPMIHTEPSAQFSTMDTAAF					

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	10	20	30	40	50	60
m644 . pep	70	80	90	100	110	120
g644	LKHIESAFRRIFSDGIDLRYLPEDKWLALKQAGLLPFLDKKYGGRKGSQFEIQEVLRI					
	70	80	90	100	110	120
m644 . pep	130	140	150	160	170	180
g644	ACHYGVPTLRTGIEGALVLQPLQEFQDEAQAQGLEMIKFGEGGGLGVTEPETSGAAIA					
	130	140	150	160	170	180
m644 . pep	190	200	210	220	230	240
g644	REMQSYEYIDGQTIYVNAAKYWQNSQSDFLVAAKERKNGKLAKVIDLLVPKTYIRC					
	190	200	210	220	230	240
m644 . pep	250	260	270	280	290	300
g644	ETLASEGLRAVRYAVNRIDAEMPATAVMKLSQSDAAGLRAFQNI F I R S R L Q L I G M T H G I M					
	250	260	270	280	290	300
m644 . pep	310	320	330	340	350	360
g644	EYILENLERYVRNDIKFVDYERREIRRRHQVSEILYRYVCHSVSPVAPVAHQLMANIVK					
	310	320	330	340	350	360
m644 . pep	370	380	390	400	410	420
g644	TLATEYTYAAAQMLQKLLGAKGFERGHGTAGNIAIDIRPFTIFEGPNDMLYAEIYDQFVRA					
	370	380	390	400	410	420
m644 . pep	430	440	450	460	470	480
g644	TAEKEAGMKLDKNQTLDLRLQTDARFAAVARDYTLPEDIRSFLOEHTLTDACALQKVFI					
	430	440	450	460	470	480
m644 . pep	490	500	510			
g644	GKIIARLFVVFQAKHEDTAAFLNDIRKDLDCRYCGX					
	490	500	510			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2073>:

```

a644 . seq
1  ATGCCGTC TG AAAGGTCGGC GGATTGTTGC CCGGCGCACT TTGTGGTAAA
51  GTTTAGAAAA TCAACTCTAA ACTGTGGCAG GCGGTTTGAC CGGCCGCCGA
101 TTAATGGGAA CCGACAGAGG AAGCCGATGA TACACACCGA ACCGAGCGCG
151 CAGCCGTCAA CTATGGACAC GGCTGCTTTT TTAAAGCACA TCGAATCCGC
201 ATTCCGCCGC ATTTTTCGAG ACGGTATCGA CCTGATGCGA TACCTGCCCG
251 AAGACAAATG GCTTGCCCTTG AAGCAGGCGG GTTTGCTGTT GCCCTTCCTC
301 GACAAAAAAT ACGGCCGGCG CAAGGCAGC CAGTTTGAAA TTCAGGAAGT
351 CTGCGGATT GCGGGGCATT ACGGCGTGCC CGTTANNNNN NNNNNNNNNN
401 NNGAAGGCGC GCTGGTGTTG CAGCCACTGC AAGAGTTCGG CGATGAAGCG
451 CAAATCGCAC AGGGTTTGGA CATGGTTTTC AAAGGCGAGG GCGGCGGTTT
501 AGCGGTTACC GAACCCGAAA CCTCCGCGC GCGGATTGCC CGAGAAATGC
551 AGTCTTACTA CGAATATACC GACGGACAAA CCATTACGT CAACGCCGCG
601 AAATACTGGC AGGGCAACTC GCAAAGCGAC TTCCTCTCG TTGCCGCCAA
651 AGAGCGCAAA AACGGCAAA TCGCCAAAGT CATCGACCTG CTGCTCGTCC
701 CCAAAACATA CATCCGCTGC GAAACCTCG CATCCGAAGG CTTGCGCGCC
751 GTCCGTTACG CCGTCAACCG CATCGATGCC GAAATGCCTG CAACCGCCGT
801 GATGAACTC TCCAGAGCG ACGTGCCGG TTTGCGCGC TTCCAAAACA

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851 TCTTTATCCG CAGCCGCTG CAACTGATCG GCATGACGCA CGGCATTATG
901 GAATACACCC TTGAAAACCT GGAACGATAC GTCCGCAACG ACATCAGATT
951 CGTCGATTAC GAACGCGCGG AAATCCGCGC CCGCCATCAG GTTCCGAGA
1001 TTCTTTACCG CTACGTCTGC CATTCGGTTT CGCCCGTTGC ACCCGTCGCC
1051 CATCAACTGA TGGAGGCGAA CATCGTCAA ACCCTCGCCA CGGAATACAC
1101 TTACGCGGCC GCGCAAATGT TGCAAAACT CTGGGCGCG AAGGGTTTGT
1151 AACGCGGACA CACCGCCGGC AATATCGCTA TCGACATCCG CCCCTTCACG
1201 ATTTTGAAG GCCGAACGA TATGCTTAT GCCGAAATT ACGACCAGTT
1251 TGTCCGCGCC ACCGCGAAG AAAAAGAAG AGGCATGAAG TTGGACAAAA
1301 ACCAAACCT GCTCGACCG CTGCAAACG ATGCCCGCTT TGCCGCCGTC
1351 GCGCCGACT ACACTTGCC CGAAGACATC CGCAGCTTCC TGCAGGAACA
1401 CACCTGACC GATGCCTGCG CCCTGCAAAA AGTCTTTATC GGCAAAATCA
1451 TCGCCGACT CTTTGTCTTC GTACAGGCG AACACGAAGA CACCGCAGCC
1501 TTCCTGCTGA ACGACATCCG CAAAGACATA TTGGACTGCC GATATTGCGG
1551 ATAG

```

This corresponds to the amino acid sequence <SEQ ID 2074; ORF 644.a>:

```

a644.pep
1  MPSERSADCC PAHFVVKFRK STLNCGRRED RPPINGNRQR KPMIHTEPSA
51  QPSTMDTAAF LKHIESAFRR IFADGIDLMR YLPEDKWLAL KQAGLLLPFL
101 DKKYGGKGS QFEIQEVLRI AGHYGVPVXX XXXXEGALVL QPLQEFGEA
151 QIAQGLDMVF KEGGGLGVT EPETSGAIA REMQSYEYTG DGQTIYVNA
201 KYWQNSQSD FLLVAAKERK NGKLAKVIDL LLVPKTYIRC ETLASEGLRA
251 VRYAVNRIDA EMPATAVMKL SQSDAAGLRA FQNI FIRSRL QLIGMTHGIM
301 EYTLENLERY VRNDIRFVDY ERREIRRRHQ VSEILYRYVC HSVSPVAPVA
351 HQLMEANIVK TLATEYTYAA AQMLQKLLGA KGFERGHAG NIAIDIRPFT
401 IFEGPNDMLY AEIYDQFVRA TAEKEAGMK LDKNQTLDR LQTDARFAAV
451 ARDYTLPEDI RSFLQEHILT DACALQKVEI GKIIARLFVF VQAEHEDTAA
501 FLLNDIRKDI LDCRYCG*

```

m644/a644 97.3% identity in 517 aa overlap

	10	20	30	40	50	60
m644.pep	MPSERSADCCPAHFVVKFRKSTLNCGRREDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF					
a644	MPSERSADCCPAHFVVKFRKSTLNCGRREDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF					
	10	20	30	40	50	60
m644.pep	LKHIESAFRRIFSDGIDLMRYLPEDKWLALKQAGLLLPFLDKKYGGKGSQFEIQEVLRI					
a644	LKHIESAFRRIFADGIDLMRYLPEDKWLALKQAGLLLPFLDKKYGGKGSQFEIQEVLRI					
	70	80	90	100	110	120
m644.pep	LKHIESAFRRIFSDGIDLMRYLPEDKWLALKQAGLLLPFLDKKYGGKGSQFEIQEVLRI					
a644	LKHIESAFRRIFADGIDLMRYLPEDKWLALKQAGLLLPFLDKKYGGKGSQFEIQEVLRI					
	70	80	90	100	110	120
m644.pep	AGHYGVPVTLRTGIEGALVLQPLQEFGEAQVAQGLEMIFKGGGGLGVTEPETSGAIA					
a644	AGHYGVPVXXXXXEGALVLQPLQEFGEAQIAQGLDMVFKGGGGLGVTEPETSGAIA					
	130	140	150	160	170	180
m644.pep	AGHYGVPVTLRTGIEGALVLQPLQEFGEAQVAQGLEMIFKGGGGLGVTEPETSGAIA					
a644	AGHYGVPVXXXXXEGALVLQPLQEFGEAQIAQGLDMVFKGGGGLGVTEPETSGAIA					
	130	140	150	160	170	180
m644.pep	REMQSYEYIDGQTIYVNAKYWQNSQSDFLLVAAKERKNGKLAKVIDLLVPKTYIRC					
a644	REMQSYEYTDGQTIYVNAKYWQNSQSDFLLVAAKERKNGKLAKVIDLLVPKTYIRC					
	190	200	210	220	230	240
m644.pep	REMQSYEYIDGQTIYVNAKYWQNSQSDFLLVAAKERKNGKLAKVIDLLVPKTYIRC					
a644	REMQSYEYTDGQTIYVNAKYWQNSQSDFLLVAAKERKNGKLAKVIDLLVPKTYIRC					
	190	200	210	220	230	240
m644.pep	ETLASEGLRAVRYAVNRIDAEMPATAVMKLSQSDAAGLRAFQNI FIRSRLQLIGMTHGIM					
a644	ETLASEGLRAVRYAVNRIDAEMPATAVMKLSQSDAAGLRAFQNI FIRSRLQLICMTHGIM					
	250	260	270	280	290	300
m644.pep	ETLASEGLRAVRYAVNRIDAEMPATAVMKLSQSDAAGLRAFQNI FIRSRLQLIGMTHGIM					
a644	ETLASEGLRAVRYAVNRIDAEMPATAVMKLSQSDAAGLRAFQNI FIRSRLQLICMTHGIM					
	250	260	270	280	290	300
m644.pep	EYILENLERIVRNDIKFVDYERREIRRRHQVSEILYRYVCHSVSPVAPVAHQLMEANIVK					
a644	EYILENLERIVRNDIRFVDYERREIRRRHQVSEILYRYVCHSVSPVAPVAHQLMEANIVK					

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	310	320	330	340	350	360
	370	380	390	400	410	420
m644 . pep	TLATEYTYAAAQMLQKLLGAKGFERGHTAGNIAIDIRPFTIFEGPNDMLYAEIYDQFVRA					
a644	TLATEYTYAAAQMLQKLLGAKGFERGHTAGNIAIDIRPFTIFEGPNDMLYAEIYDQFVRA					
	370	380	390	400	410	420
	430	440	450	460	470	480
m644 . pep	TAEKEAGMKLDKNQTLDRQLQTDARFAAVARDYTLPEDIRSFLEHTLTDACALQKVFI					
a644	TAEKEAGMKLDKNQTLDRQLQTDARFAAVARDYTLPEDIRSFLEHTLTDACALQKVFI					
	430	440	450	460	470	480
	490	500	510			
m644 . pep	GKIIARLFVQAKHEDTAAFLNDIRKDILDCRYCGX					
a644	GKIIARLFVQAEHEDTAAFLNDIRKDILDCRYCGX					
	490	500	510			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2075>:

```

g645 . seq
1  ATGATGATGG TGTGGCGT GGGGATGTCG ATGCCGGTTT CGATGATGGT
51  GGAACAGAGC AACACATGA ATCTTTGCTG CAAAAGTCG CGCATGACTT
101 GTTCCAGCTC GCGCTCAGC AGTTSTCCG? GCGCCACGCC GATACGGGCT
151 TCGGGCAGCA GGGTTTCCAG CCGCTCGCGC ATATTCTCAA TCGTATCTAC
201 TTCATTGTGC AGGAAAAaTa cCTGTCTCC GCGTTTGAGT TCGCGCAACA
251 CCGCTTCGCG CACGCTGCCT TCGCTGAACG GTTGACAAA GGTTCACG
301 GCGAGGCGGC GGCTCGGTGC AGTGGTAATC AGCGAGAAGT CGCGCAGACC
351 TTCGAGCGCC ATGCTGAGGG TCGCGGGAAT CGCGTGGCG GTCATGGTTA
401 GGATGTCGAC ATTGGCGCGC AGGCGTTTGA GCTGCTCTT CTGTCGCACG
451 CCGAAGCGGT GTTCTTCATC GATAATCAAT AAACCTAAGT TTTTGAATTT
501 TATGTCGTCC TGCACCAATT TGTGCGTACC GATAACGATA TCGACAGTAC
551 CSTCCGCCAT GCCTTCGAGC GTGGCTTTGG TGGCTTTGCT GTTGTGAAA
601 CCGGAAAGGC TGGCGACTTT CACGGGGAAA TCGGCGAAAC GGTGCGCGAA
651 GTTTTGC GCGTGTCTCGA CCAGAAGCGT GGTGCGGCGC AGTACGGCGA
701 CCTGTTTGCC GCCCATCACC GCCACAACG CCGCGCGAAG GCGGACTTCG
751 GTTTTGCCGA AACCAGATC GCCGCACACA AGTCGGTCCA TCGGCTTCGC
801 CTGCGTCAA TCTTTAATCA CGGcgcgat ggcgcgcgcc TGGTCTTCGG
851 TTTCTCTGTA G

```

This corresponds to the amino acid sequence <SEQ ID 2076; ORF 645.ng>:

```

g645 . pep
1  MMMVLALGMS MPVSMMEQ S NTLNLCKKS RMTCSSRSR SCPCATPIRA
51  SGRSVSSRSR IFSIVSTSLC RNTCPPLRS SRNTASRTLP SLNGLTKVFT
101 ARRLGAVVI SEKSRPSSA MLRVRGIVA VMVRMSTLAR RRLSCSFCRT
151 EKRCSSSIIN KPKFLNFMSS CTNLCVPITI STVPSAMPSS VALVALLLLK
201 RERLATFTGK SAKRSKAFCA CCSTRSVVGA STATCLPPIT ATNAARRATS
251 VLPKPTSPHT SRSIGFACVK SLITAAMAAA WSSVSS*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2077>:

```

m645 . seq
1  ATGATGATGG TGTGGCGT GGGGATATCG ATACCGGTTT CGATGATGGT
51  GGAACAGAGC AACACGTTAA ATCGTTGCTG CAAAAGTCG CGCATGACTT
101 GTTCCAGCTC GCGCTCAGCG AGTTGTCCGT GCGCCACGCC GATGCGGGCT
151 TCGGGCAGCA GGGTTTCCAG CCGCTCGCGC ATATTTTCAA TCGTATCTAC
201 TTCATTGTGC AGGAAAAATA CCGTCTCTCC GCGTTTGAGT TCGCGCAACA
251 CCGCTTCGCG CACGCTGCCT TCGCTAAAGG GTTGACAAA GGTTCGACG
301 GCGAGGCGGC GGCTGGGCGC GGTGGTAATC AGCGAGAAGT CGCGCAGTCC
351 TCCCAACGCC ATACTTAAAG TACGCGGAAT CGCGTGGCG GTCATGGTTA
401 GGATATCAAC ATTGGCGCGC AGGCGTTTGA GCTGCTCTT CTGACGCACG
451 CCGAAGCGGT GTTCTTCGTC GATAATCACT AAACCTAAGT TTTTGAATTT
501 GATGTCGTCC TGCACCAATT TGTGCGTACC GATAACAATA TCGACCGTGC
551 CGTCTGCCAT GCCTTCAGC GCGCTTTGG TGGCTTTGCT GTTGTGAAA
601 CCGGAAAGGC TGGCGACTTT CACGGGGAAA TCGGCGAAAC GGTGCGCGAA
651 GTTTTGC GCGTGTCTCGA CCAAAGCGT GGTGCGGAGCA AGTACGGCGA
701 CCTGTTTGCC GCCCATCACC GCCACAACG CCGCGCGCAG GCGGACTTCG
751 GTTTTGCCGA AGCCGACATC GCCGCACACA AGCGATCCA TCGGCTTCGC
801 TTGCGTCAA TCTTTAATCA CGGCGGCGAT GCGGCGGCC TGGTCTTCGG

```

851 TTTCCTCGTA G

This corresponds to the amino acid sequence <SEQ ID 2078; ORF 645>:

m645.pep
 1 MMNVLALGIS IPVSM~~MM~~VEQS NTLNRCCKKS RMTCS~~SS~~SR SR SCPCATPMRA
 51 SG~~SR~~VSSRSR IFSIVSTSLC RKNTCP~~PR~~LS SRNTASRTLP SLKGLTKVLT
 101 AR~~RR~~LGAVVI SEKSRSPSNA ILKVRGIGVA VMVRISTLAR RRLSCSF*RT
 151 PKRCS~~SS~~IIIT KPKFLNLMSS CTS~~LC~~VPITI STVPSAMP~~SS~~ AALVALLLLK
 201 RERLATFTCK SAKRS~~AK~~FCA CCSTKSVVGA STATCLPPIT ATNAARRATS
 251 VLPKPTSPHT RRSIGFACVK SLITA~~AM~~AAA WSSVSS*

m645/g645 93.7% identity in 286 aa overlap

	10	20	30	40	50	60
m645.pep	MMNVLALGISIPVSM	VEQSN	TLNRCCKKS	RMTCS	SSRSR	SCPCATPMRASGSRVSSRSR
g645	MMNVLALGMSIPVSM	VEQSN	TLNRCCKKS	RMTCS	SSRSR	SCPCATPMRASGSRVSSRSR
	70	80	90	100	110	120
m645.pep	IFSIVSTSLCRKNTCP	PRLS	SRNTASRTLP	SLKGLTKVLT	ARRRLGAVVISEKSRSPSNA	
g645	IFSIVSTSLCRKNTCP	PRLS	SRNTASRTLP	SLKGLTKVLT	ARRRLGAVVISEKSRSPSNA	
	130	140	150	160	170	180
m645.pep	ILKVRGIGVAVMVRIS	TARRRLSCSFXRTP	PKRCS	SIITKPKFLNLMSS	SCTSLCVPITI	
g645	MLRVGIGVAVMVRIS	TARRRLSCSFXRTP	PKRCS	SIITKPKFLNLMSS	SCTSLCVPITI	
	190	200	210	220	230	240
m645.pep	STVPSAMPSSAALVALL	LLKRERLATFTGKS	SAKRS	AKFCACCSTKSVVGA	STATCLPPIT	
g645	STVPSAMPSSAALVALL	LLKRERLATFTGKS	SAKRS	AKFCACCSTKSVVGA	STATCLPPIT	
	250	260	270	280		
m645.pep	ATNAARRATSVLPKPT	SPHTRRSIGFACVK	SLITA	AMAAWSSVSSX		
g645	ATNAARRATSVLPKPT	SPHTRRSIGFACVK	SLITA	AMAAWSSVSSX		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2079>:

a645.seq
 1 ATGATGATGG TGTGGCGTT GGAATGTCG ATACCGGTTT CGATGATGGT
 51 GGAACAGAGC AACACGTTAA ATCGTTGCTG CAAAAAGTCG CGCATGACTT
 101 GTTCCAGCTC GCGCTCGCGC AGTTGTCCGT GCGCCACGCC GATGCGGGCT
 151 TCGGGCAGCA GGGTTTCCAG CCGCTCAGC ATGTTTTCGA TGGTATCCAC
 201 TTCATTGTGC AGGAAAAATA CTGCCC GCCGTTTGAGT TCGCGCAATA
 251 CGGCTTCGCG CACGCTGCCT TCGCTGAACG GTTTGACAAA GGTTTTGACG
 301 GCGAGGCGCG GGCTGGGCGC AGTGGTAATC AGCGAGAAGT CGCGCAGTCC
 351 TTCCAGCGCC ATACTTAAAG TACGCGGAAT CGGCGTAGCG GTCATGGTAA
 401 GGATGTCGAC ATTGGCGCGC AGGCGTTTGA GCTGCTCTTT CTGACGCACG
 451 CCGAAGCGGT GTTCTTCGTC GATAATCACT AAACCTACGT TTTTGAATTT
 501 TATGTCGTCC TGCACCAATT TGTGCGTACC GATAACAATA TCGACCGTGC
 551 CGTCCGCCAT GCCTTCCAGC GCGGCTTTGG TGGCTTTGCT GTTGTGAAA
 601 CGCGAAAGGC TGGCGACTTT CACGGGGAAA TCGCGCAAGC GGTGCGCAAA
 651 ATTTTGCGCG TGCTGCTCGA CCAGAAGCGT GGTGCGTGCG AGTACGGCAA
 701 CTTGTTTGCC ACCATTACC GCCACAAACG CGGCGCGCAG GCGGACTTCG
 751 GTTTTGCCGA AACCGACATC GCCGCACACG AGGCGGTCCA TCGGCTTCGC
 801 CTGCGTCAA TCTTTAATCA CGGCGCGGAT GCGGCGTGCC TGGTCTTCGG
 851 TTTCTTCGTA G

This corresponds to the amino acid sequence <SEQ ID 2080; ORF 645.a>:

a645.pep
 1 MMNVLALGMS IPVSM~~MM~~VEQS NTLNRCCKKS RMTCS~~SS~~SR SR SCPCATPMRA

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```

51  SGRVSSRSR MFSMVSTSLC RKNTCPPLRS SRNTASRTL P SLNGLTKVLT
101 ARRRLGAVVI SEKSRSPSSA ILKVRGIGVA VMVRMSTLAE RRLSCSF*RT
151 PKRCSSSIIT KPTFLNFMSS CTSLCVPITI STVPSAMPSS AALVALLLLK
201 RERLATFTGK SAKRSAKFCA CCSTRSVVGA STATCLPPIT ATNAARRATS
251 VLPKPTSPHT RRSIGFACVK SLITAAMAAA WSSVSS*

```

m645/a645 96.9% identity in 286 aa overlap

```

m645.pep      10      20      30      40      50      60
              MMMVLALGISIPVSMVEQSNTLNRCCKKSRMTCSSSRSRSCPCATPMRASGSRVSSRSR
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a645          10      20      30      40      50      60
              MMMVLALGMSIPVSMVEQSNTLNRCCKKSRMTCSSSRSRSCPCATPMRASGSRVSSRSR

m645.pep      70      80      90      100     110     120
              IFSIVSTSLCRKNICPPRLSSRNTASRTLPSLKGKLTAVLTARRRLGAVVISEKSRSPSNA
              :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
a645          70      80      90      100     110     120
              MFSMVSTSLCRKNICPPRLSSRNTASRTLPSLKGKLTAVLTARRRLGAVVISEKSRSPSSA

m645.pep      130     140     150     160     170     180
              ILKVRGIGVAVMVRISTLARRRLSCSEFXRTPKRCSSSIITKPKFLNLMSSCTSLCVPITI
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a645          130     140     150     160     170     180
              ILKVRGIGVAVMVRMSTLARRRLSCSEFXRTPKRCSSSIITKPTFLNFMSSCTSLCVPITI

m645.pep      190     200     210     220     230     240
              STVPSAMPSSAALVALLLLKRERLATFTGKSAKRSAKFCAACCSTKSVVGASTATCLPPIT
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a645          190     200     210     220     230     240
              STVPSAMPSSAALVALLLLKRERLATFTGKSAKRSAKFCAACCSTRSVVGASTATCLPPIT

m645.pep      250     260     270     280
              ATNAARRATSVLPKPTSPHTRRSIGFACVKSLITAAMAAWSSVSSX
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a645          250     260     270     280
              ATNAARRATSVLPKPTSPHTRRSIGFACVKSLITAAMAAWSSVSSX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2081>:

```

g647.seq
1  ATGCAAAGGC TCGCCGCAGA CGGCATCCAA ATCTTTTTTG TAGGTGTCGA
51 TGGGCAGTTT GCCTTGCGAA TAAACGGTTT GGTAAAGAG CGTGCACGCT
101 CCGTATTCTT TGGCAAGGTT TGCCGATGCT TTGAGCAGGT AATACTGTAT
151 GGCTTCAAAG GTACGGTGGG TCAGACCGAG CGCGGAACCG TCGCTGTAGC
201 GGACACCGTT TTTCGCCAGA TAGTAGGCGT AGTTGATGAC ACCGATGCCG
251 AGCGAACGGC GGTCCATAGT AGAGGTACGC GCGGCTTCTA CCGGATATCC
301 CTGATAATCT AA

```

This corresponds to the amino acid sequence <SEQ ID 2082; ORF 647.ng>:

```

g647.pep
1  MQRLAADGIQ IFFVGVGDQF ALRINGLVKE RARSVFFGKV CRCFEQVILY
51 GFKGTVGQTE RGTVAVADTV FRQIVGVVDD TDAERTAVHS RGTRGFYRIS
101 LII*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2083>:

```

m647.seq
1  ATGCAAAGGC TCGCCGCAGA CGGCATCCAA ATCTTTTTTG TAAGTGTGCA
51 TGGGCAGTTT GCCTTGCGAA TAAACGGTTT GGTAAAGAG CGTGCACGCA
101 CCGTATTCTT TGGCAAGGTT TGCCGATGCT TTGAGCAGGT AATACTGTAT
151 GGCTTCAAAG GTACGGTGGG TCAGACCGAG CGCGGAACCG TCGCTGTAGC
201 GGACACCGTT TTTCGCCAGA TAATAAGCAT AGTTAATCAC GCCGATGCCG
251 AGCGAACGGC GGCCCATAGT AGAGGTACGC GCGGCTTCTA CCGGATATCC
301 CTGATAATCT AA

```

This corresponds to the amino acid sequence <SEQ ID 2084; ORF 647>:

```

m647.pep
1  MQRLAADGIQ IFFVSDGQF ALRINGLVKE RARTVFFGKV CRCFEQVILY

```

51 GFKGTVGQTE RGTVAVADTV FRQIISIVNH ADAERTAHS RGTRGFYRIS
101 LII*

	10	20	30	40	50	60
m647.pep	MQRLAADGIQIFFVSV	DGQFALRINGLVKER	ARTVFFGKVCRCFEQ	VILYGFKGTVGQTE		
g647	MQRLAADGIQIFFVSV	DGQFALRINGLVKER	ARSVFFGKVCRCFEQ	VILYGFKGTVGQTE		
	10	20	30	40	50	60
	70	80	90	100		
m647.pep	RGTVAVADTVFRQII	SVNHADAERTA	AAHSRGTRG	FYRISLIIX		
g647	RGTVAVADTVFRQIV	GVDDTDAERTAV	HSRGTRG	FYRISLIIX		
	70	80	90	100		

```
a547.seq
1 GTGCAAAGGC TCGTTACACA CAGCGTCCAA GTCTTTTTTG TAGGTGTCGA
51 TGGGCAGTTT GCCTTGCGAA TAAACGGTTT GGTTAAAGAG CGTGCACGCA
101 CCGTATTCTT TGGCAAGGTT TGCCGATGCT TTGAGCAGGT AATACTGTAT
151 GGCTTCAAAG GTACGGTGGG TCAGACCGAG CCGGAGCCG TCGCTGTAGC
201 GGACACCGTT TTTGCGCAA TAATACGCAT AGTTGATCAC GCCGATACCG
251 AGCGAACGGC GGCCATAGT GGAGGTACGC GCGGCTTCTA CCGGATATCC
301 CTGATAATCT AA
```

```
a647.pep
1  VQRLVTHSVQ VFFVGVDGQF ALRINGLVKE RARTVFFGKV CRCFEQVILY
51  GFKGTVGQTE RGAVAVADTV FRQIIRIVDH ADTERTAAHS GGTRGFYRIS
101 LII*
```

	10	20	30	40	50	60
m647.pep	MQRLAADGIQIFFVSVDGQFALRINGLVKERARTVF	FFGKVCRCFEQVILYGFKGTVGGTE				
a647	VQRLVTHSVQVFFVGVDGQFALRINGLVKERARTVF	FFGKVCRCFEQVILYGFKGTVGGTE				
	10	20	30	40	50	60
	70	80	90	100		
π647.pep	RGTVAVADTVFERQIISIVNHADAERTAASRGTRGFYRISLIIX					
a647	RGAVAVADTVFERQIRIVDHADTERTAAHSGGTRGFYRISLIIX					
	70	80	90	100		

```

g648.seq
1  ATGAACACAGGC  GCAACGCGCG  GATCGAACGG  GCTGTGCGTA  TTGCAGTGTAT
51  CGACGCTTTTG  AATGTAGATG  CGCCCGGTCC  CGGCACGCTC  CTGCATCAGC
101  GTGAAAACAA  GATCGGCAGC  CGGAATGATA  CGCTTGCGTA  TGTTCGGGTC
151  TTGCTCGTAT  TTCGTATAGA  GCCGCTCAAA  TTCGTCTTGG  TCGGCAAAAA
201  ACGCTTCGTA  CAACCCCGAA  ACCTCGTTGG  GCGAAACAGC  CGTAATGTTG
251  CGCGCCCTTAA  TCAGGCGGGT  GTACAGCAGG  CGGTTGATTT  GCACGCCATA
301  ATCAAGCTGG  CGGATACGGT  TGTCCTCCAC  GCCCGGTGTT  TTTTTCRAAC
351  CACAGAGGCT  TTTCGGCTCA  ATATGCCACA  AGGGGTAGAA  CAAGGTTGCC
401  GCGCGCGCGC  GCACGCCACC  TTGCGACAAA  GATTTGACCG  CCGGCTGAAA
451  CATCTTAAAG  AAGGGAATGC  AGCCGGTATG  CCGGGCTTCA  CCGCCCCGGA
501  TTTCGCTGTC  CAGCCCGCGG  ATACGCTCGG  CATTGATGCC  GATGCCCCCG
551  CGTTCGGGAA  CGTATTTCAC  AATCGCGCTG  GTAGTGGCAT  TGATGGAATC
601  CAAACTATCG  TCGCATTTCA  TCAGCACACA  GCTTGA

```

g648.pap

1030

```

1  MNRRNARIER AVRIAVIDVL NVDAFPGTGL LHQRGKQVGS RNDTLAYVRV
51  LLVFRIEPLK FVLVGKKRFV QPRNLVGRKQ RNVAAALNQAG VQQAVIDLHAI
101 IKLADTVVFH APVVFOHQQA FGFNMPQGV E QGCRAAAHAT LRTRFDRRLK
151 HKEGNAAGM PGFTAPDFAV QPADTSGIDA DARALGNVFH NRAGSGIDGI
201 QTIVAFNQHT A*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2089>:

```

m648.seq
1  ATGAACAGGC GCGACGCGCG GATCGAACGG GCTGTGCGTA TTGCAGTGAT
51  CGACGTTTTG AATGTAGATG CGCCCGGTTT CCGCACGCTC CTGCATCAGC
101 GTGGAAAACA GGTCCGCAGC CGAATGATG CGCTTCCGGA TATCAGGCTC
151 TTGCTCGTAT TTCGTATAGA GCCGCTCAAA TTCGTCTTGG TCGGCAAAAA
201 ACGCTTCGTA CAATCCCGGA ACCTCGTTGG GCGAAAACAG CGTAATGTTG
251 CCGCCCTTAA TCAGGCGGGT GTACAGCAGG CGGTTGATTG GCACGCCGTA
301 ATCAAGCTGA CGGATACGGT TGTCTTCCAC ACCGCGGTTG TTTTCAACA
351 CCAGCAGGCT TTCGGCTTCG ATATGCCACA AGGGGTAGAA CAAGGTTGCC
401 GCGCCGCCGC GCACGCCGCC TTGCGAACAG GATTGACCG CCGCCTGAAA
451 CATTTTAAAG AAGGGAATGC AGCCGGTATG CCGCGCTTCG CCGCCCGGA
501 TTTCGCTGTC CAAACCGCGG ATACGTCCGG CATTGATGCC GATGCCCGCA
551 CGCTGGGAAA CGTATTTCAC AATCGCGCTG GTAGTGGCAT TGATGGAATC
601 CAAACTATCG TCGCATTCAA TCAGCACACA GCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2090; ORF 648>:

```

m648.pep
1  MNRRDARIER AVRIAVIDVL NVDAFPGSGL LHQRGKQVGS RNDALADIRV
51  LLVFRIEPLK FVLVGKKRFV QSRNLVGRKQ RNVAAALNQAG VQQAVIDLHAV
101 IKLADTVVFH TAVVFOHQQA FGFDMPOGVE QGCRAAAHAA LRTRFDRRLK
151 HFKEGNAAGM PRFAAPDFAV QTADTSGIDA DARTLGNVFH NRAGSGIDGI
201 QTIVAFNQHT A*

```

m648/g648 91.5% identity in 211 aa overlap

	10	20	30	40	50	60
m648.pep	MNRRDARIERAVRIAVIDVLNVDAFPGSGLLHQRGKQVGSRNDALADIRVLLVFRIEPLK					
g648	MNRRNARIERAVRIAVIDVLNVDAFPGTLLHQRGKQVGSRNDTLAYVRVLLVFRIEPLK					
	10	20	30	40	50	60
	70	80	90	100	110	120
m648.pep	FVLVGKKRFVQSRNLVGRKQRNVAAALNQAGVQQAVIDLHAVIKLTDTVVFHTAVVFOHQQA					
g648	FVLVGKKRFVQPRNLVGRKQRNVAAALNQAGVQQAVIDLHAIKLDADTVVFHAPVVFOHQQA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m648.pep	FGFDMPOGVEQGCRAAAHAAALRTGFDRLKHFEKGNAGMPRFAAPDFAVQTADTSGIDA					
g648	FGFNMPQGVQGCRAAAHATLRTRFDRRLKHLKEGNAAGMPGFTAPDFAVQPADTSGIDA					
	130	140	150	160	170	180
	190	200	210			
m648.pep	DARTLGNVFHNRAAGSGIDGIQTIVAFNQHTAX					
g648	DARALGNVFHNRAAGSGIDGIQTIVAFNQHTAX					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2091>:

```

a648.seq
1  ATGAACAGGC GCAACGCGCG GATCGAACGG GCTGTGCGTA TTGCAGTGAT
51  CGACGTTTTG AATGTAGATG CGCCCGGTTT CCGCACGCTC CTGCATCAGC
101 GTGGAAAACA GGTCCGCAGC CGAATGATG CGCTTCCGGA TATCAGGCTC
151 TTGCTCGTAT TTCGTATAGA GCCGCTCAAA TTCGTCTTGG TCGGCAAAAA
201 ACGCTTCGTA CAATCCCGGA ACCTCGTTGG GCGAAAACAG CGTAATGTTG
251 CCGCCCTTAA TCAGGCGGGT GTACAGCAGG CGGTTGATTG GCACGCCGTA
301 ATCAAGCTGA CGGATACGGT TGTCTTCCAC GCCCGGTTG TTTTCAACA
351 CCAGCAGGCT TTCGGCTTCG ATATGCCACA AGGGGTAGAA CAAGGTTGCC
401 GCGCCGCCGC GCACGCCACC TTGCGAACAG GATTTGACTG CCGCCTGAAA
451 CATTTTAAAG AAGGGAATGC AGCCGGTATG CCGTGTCTTCG CCGCCCGGA

```

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```

501 TTTCGCTGTC CAGTCCGCGG ATACGTCGCG CATTGATGCC GATGCCCGCA
551 CGCTGGGAAA CGTATTTCAC AATCGCGCTG GTAGTGGCGT TGATGGAATC
601 CAGGCTGTCTG TCGCATTCTGA TCAATACGCA GCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2092; ORF 648.a>:

```

a648.pep
1  MNRRNARIER AVRIAVIDVL NVDAPGSGTL LHQRGKQVGS RNDALADIRV
51  LLVFRIEPLK FVLVGKKRFV QSRNLVGRKQ RNVAALNQAG VQQAVIDLHAV
101 IKLTDTVVFH APVVFQHQQA FGFDMPQGV EGCRAAAHAT LRTGDCRLK
151 HFKEGNAAGM PCFAAPDFAV QSADTSGIDA DARTLGNVFH NRAGSGVDGI
201 QAVVAFDQYA A*

```

m648/a648 93.8% identity in 211 aa overlap

	10	20	30	40	50	60
m648.pep	MNRRDARIERAVRIAVIDVLNVDAPGSGTLLHQRGKQVGS	RNDALADIRVLLVFRIEPLK				
a648	:					
	10	20	30	40	50	60
m648.pep	FVLVGKKRFVQSRNLVGRKQNRNVAALNQAGVQQAVIDLHAVIKLTDTVVFHTAVVFQHQQA					
a648	FVLVGKKRFVQSRNLVGRKQNRNVAALNQAGVQQAVIDLHAVIKLTDTVVFHAPVVFQHQQA					
	70	80	90	100	110	120
m648.pep	FGFDMPQGVQGCRAAAHAALRTGDRRLKHFK	EGNAAGMPRFAAPDFAVQTADTSGIDA				
a648	FGFDMPQGVQGCRAAAHATLRTGDCRLKHFK	EGNAAGMPCFAAPDFAVQSADTSGIDA				
	130	140	150	160	170	180
m648.pep	DARTLGNVFHN	NRAGSGIDGIQTI	VAFNQHTAX			
a648	DARTLGNVFHN	NRAGSGVDGIQAVVAFDQYAAX				
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2093>:

```

g649.seq
1  ATGCTTGCCA TACTGTTGTC TGCAATACTG GGACTGGTAT CAACAACTGC
51  CGCTGCCGGT ACGTCAGAAC CCGCCCACCG ACATACCAA CATATCAGCA
101 AGGCAAAACAA GCAGATGCTG CACCCCGAAT GCAGGAAATA TTTGGAACGC
151 CGTGCCCGCT GGTACCGATC GCAAGGCAAC GTGCAGGAAT TGC CGCGAAAA
201 CAAAAGGCG CGCAAAGCAT TCCGCTCCCT GCCTTATGCG GAACAGAAAA
251 TCCAATGCCG GCGGCTTAT GAGGCTTTCG ATGATTTCGA CGCGCGCAGG
301 TTCCGCCGTT AA

```

This corresponds to the amino acid sequence <SEQ ID 2094; ORF 649.ng>:

```

g649.pep
1  MLAILLSAIL GLVSTTAAAG TSEPAHRHTK HISKANKQML HPECKYLER
51  RAAWYRSQGN VQELRENKKA RKAFTLPYA EQKIQCAAAY EAFDDFDGGR
101 FRR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2095>:

```

m649.seq
1  ATGCTTGCCA TACTGTTGTC TGCAATATTG GGACTGGTAT CGACAACTGC
51  CGCTGCCGGT ACGTCAGAAC CCGCCCACCG CGATACCAA CATATCCGCA
101 AGGCAAAACAA GCAGATGCTG CACCCCGAAT GCAGGAAATA TTTGGAACGC
151 CGTGCCCGCT GGTACCGATC GCAAGGCAAC GTGCAGGAAT TGC CGCGAAAA
201 CAAAAGGCG CGCAAAGCAT TCCGCTCCCT GCCTTATGCG GAACAGAAAA
251 TCCAATGCCG GCGGCTTAT GAGGCTTTCG ATGATTTCGA CGCGCGCAGT
301 TTCCGCCGTT AA

```

This corresponds to the amino acid sequence <SEQ ID 2096; ORF 649>:

m649.pep

1032

```

1  MLAILLSAIL GLVSTTAAAG TSEPAHRDTK HIRKANKQML HPECRKYLER
51 RAAWYRSQGN VQELRENKKA RKAFRSLPYA EQTIQCRAAY EAFDDFDGGS
101 FRR*

```

m649/g649 96.1% identity in 103 aa overlap

```

              10      20      30      40      50      60
m649.pep    MLAILLSAILGLVSTTAAAGTSEPAHRDTKHIRKANKQMLHPECRKYLERAAWYRSQGN
              |||||
g649         MLAILLSAILGLVSTTAAAGTSEPAHRHTKHISKANKQMLHPECRKYLERAAWYRSQGN
              10      20      30      40      50      60

              70      80      90      100
m649.pep    VQELRENKARKAFRSLPYAEQKIQCRAAYEAFDDFDGGSFRRX
              |||||
g649         VQELRENKARKAFRTLPLYAEQKIQCRAAYEAFDDFDGGRFRRX
              70      80      90      100

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2097>:

```

a649.seq
1  ATGCTTGCCA TACTGTTGTC TGCAATATTG GGACTGGTAT CGACAACTGC
51 CGCTGCCGGT ACGTCAGAAC CCGCCCACCG CGATACCAAA CATATCCGCA
101 AGGCAAACAA GCAGATGCTG CACCCCGAAT GCAGGAAATA TTGGAACGC
151 CGTGCCGCGT GGTACCGATC GCAAGGCAAC GTGCAGGAAT TGC GCGAAAA
201 CAAAAGGCG CGCAAAGCAT TCCGCTCCCT GCCTTATAAG GAACAGAAAA
251 CCCAATGCCG GCGGCTTAT GAGGCTTTCG ATGATTTCGA CGGCAGCAGG
301 TTCCGCCGTT AA

```

This corresponds to the amino acid sequence <SEQ ID 2098; ORF 649.a>:

```

a649.pep
1  MLAILLSAIL GLVSTTAAAG TSEPAHRDTK HIRKANKQML HPECRKYLER
51 RAAWYRSQGN VQELRENKKA RKAFRSLPYK EQTQCRAAY EAFDDFDGSR
101 FRR*

```

m649/a649 96.1% identity in 103 aa overlap

```

              10      20      30      40      50      60
m649.pep    MLAILLSAILGLVSTTAAAGTSEPAHRDTKHIRKANKQMLHPECRKYLERAAWYRSQGN
              |||||
a649         MLAILLSAILGLVSTTAAAGTSEPAHRDTKHIRKANKQMLHPECRKYLERAAWYRSQGN
              10      20      30      40      50      60

              70      80      90      100
m649.pep    VQELRENKARKAFRSLPYAEQKIQCRAAYEAFDDFDGGSFRRX
              |||||
a649         VQELRENKARKAFRSLPYKEQKTCRAAYEAFDDFDGSRFRRX
              70      80      90      100

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2099>:

```

g650.seq
1  ATGTCCAAC TCAAAACCAT CGCCCTGACC GCATCAGGTC TGTCCGTTTG
51 TCCGGGTTTC CTATATGCCC AAAACACCTC ATCACACCAA GTCGGTTTAG
101 CGATTATGCG GTTAAACTCT TCAATACTCG ACCTGCCACC GACAAACAA
151 TATTCCAAT CCGGCAGCCT GTGGGACGAG CTGCGCCAAG GCTTCCGGAT
201 GGGCGAAGTC AATCCCGAAC TGGTACGCCG CCACGAAAGC AAATTCATCG
251 CAAGCCGCGC CTATTTCGAC AGGGTCGTCA ACCGGAGCCG ACCCTATATG
301 TACCATATCG CCAACGAAGT CAAAAACGC AATATGCCCG CCGAAGCCGC
351 CCGCTTCCC TTATCGAAA GCGGTTCTGT CACCAAAGCC AAATCACACG
401 TCGGCGCATC GGGCCTGTGG CAGTTCATGC CCGCTACCGG CAGGCATTAC
451 CGCTTGGAAA AAACaccgGT TTACGacgGc aggcacGacg TTtacgcaGc
501 taccgatgcc gcacTCAACT AtctGcAATA TCTCTatggA CTGTTCCGGC
551 ACTGGCCGCT CGCCTTTGCC GCCTACAAC TGGGTGAAGG CAACGTCGGA
601 CGCGCCCTCA ACCGCGCCCG CGACCAAGGG CTCGAACCGA CCTACGAAAA
651 CCGCGTATG CCCAACGAAA CGCGCAACTA TGTCCCAAG CTGCTCGCCG
701 TCGCAACAT TATTGCCACC CCCCAATCTT TCGGCATGAA TATCAGCGAC

```

1033

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751 ATAGACAACA AACCCATTTT TCAGGCAGTC GAACCGGGCC GTCCGCTCGA
801 caacGAagcC ATCGCCCGGC TTGCCGGCAT CACGCAAAAGC GAGCTGCTCG
851 CCTCGAATCC TGCATTCAAC GTCCCGCGt tcatCCCCAA AAACaaacgc
901 aaactGCTGC TTCCTGTGCG GTCCGTCCAA ACCTTccaaa gcaACTACCT
951 CAACGCCGCA CCCGACAGCC TGTTTTCATG GGAAGTCTAT ACGCCTGCCG
1001 CCAAAACAGC CCTGTCCGAC ATCTCGACGG CAACCGGCAT GAGCATTGCC
1051 GACATCAAAAC GCCTCAACAA CCTGAACGGC AACCTTGTCa ACGCAGGACG
1101 CAGCATCCTT GTCGCCAAGA ACGGCAAGAC CCTTCATACG GCATCGGAaT
1151 ccGTCGTTTC CATCGACATC GACAATACGC CcgacacCTa ccgttccaaT
1201 ATGcCgycag gcaCGGTGAA CGTCAGCATt gccCgaatcc aacCCgccgc
1251 cgcaCAGACA gcggacatta ccgtcgacc tttgccgcaa gaaaccgtcc
1301 gtacgggaac ccgatcccct tgtccgcaTt accgaaccgc cccTTCGCAC
1351 AGCCGACAGC CaacctCAAA ccgAAAAACA GACTGCCATG CcgtctGA

```

This corresponds to the amino acid sequence <SEQ ID 2100; ORF 650.ng>:

```

g650 .pep
1  MSKLKTIALT ASGLSVCPGF LYAQTSSHQ VGLAIMRLNS SILOLPPTKQ
51  YFQSGSLWGE LRQGRFMGEV NPFLVRRHES KFIASRSYFD RVVNRSRPYM
101 YHIANEVKKR NMPAEAALLP FIESAFVTKA KSHVGASGLW QFMPATGRHY
151 GLEKTPVYDG RHDVYAATDA ALNYLQYLYG LFGDWPLAFA AYNWGEENVG
201 RAVNFARDQG LEPTYENLRM PNETRNYVPK LLAVRNIIAT PQSFGMNISD
251 IDNKPFYQAV EPGRPLDNEA IARLAGITQS ELLALNPAPN VPAFIPKNKR
301 KLLLPPVASVQ TFQSNYLNAA PDSLFSWEVY TPAAKTSLSD ISTATGMSIA
351 DTKRLNNLNG NLVNAGRSIL VAKNGKTLHT ASESVVSI DI DNTPTYRSN
401 MPAGTVNVSI ARIQPAQAQT ADITVAPLPQ ETVRTGTRSP CPHYRTRPCD
451 SRSATSNRKT DCHAV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2101>:

```

m650 .seq
1  ATGTCCAAC TCAAACCAT CGCTCTGACC GCATCAGGTC TGTCCGTTTG
51  TCCGGGTTTC CTATACGCCC AAAACACCTC ATCACACCAA ATCGGTTTGG
101 CGATTATGCG CTAAACTCT TCAATACTCG ACCTGCCCCC GACAAAACAA
151 TATTTCCAAT CCGGCAGCCT GTGGGGCGAG CTGCGCCAAG GCTTCCGGAT
201 GGGCGAAGTC AATCCCGAAC TGGTACGCCG CCACGAAAGC AAATTCATCG
251 CAAGCCACAG CTATTCAAC AGGGTCATCA ACCGGAGTAG ACCCTATATG
301 TACCATATCG CCAACGAAGT CAAAAACGC AATATGCCCG CCGAAGCGCG
351 CCTGCTTCCC TTCATCGAAA GCGCGTTCGT CACCAAAGCC AAATCACACG
401 TCGGCGCATC AGGATTATGG CAGTTTATGC CCGCTACCGG CAGGCATTAC
451 GGCCTGGAAA AAACACCGGT TTACGACGGC AGGCACGACG TTTACGCCGC
501 CACCGATGCC GCACTCAACT ATCTGCAATA CCTCTATGGA CTGTTCCGGC
551 ACTGGCGCGT TGCTTTGCC GCCTACAAC TGGGTGAAGG CAACGTCGGA
601 CGCGCCATCA ACCCGGCCCG CGCCCAAGGG CTCGAACCGA CCTACGAAA
651 CTGCGCTATG CCAACGAAA CGCGCAACTA TGTCGCCAAG CTGCTCGCCG
701 TCGCGAACAT TATTGCCACT CCCAATCTT TCGGCATGAA TATCAGCGAC
751 ATAGACAACA AACCCATTTT TCAGGCAGTC GAACCGGATC GTCCGCTCGA
801 CAACGGAAGCC ATCGCCCGGC TTGCCGGCAT CACGCAAAAG GAGCTGCTCG
851 CCTAAACCC CGCATTCAAC GTCCCGCGGT TTATCCCAA AAGCAAACGC
901 AAACCTGCTG TTCCTGTGCG GTCCGTACAA ACCTTCCAAA GCACTACCT
951 CAACGCCGCA CCCGACAGCC TGTTTTCATG GGAAGTCTAT ACGCCTGCCG
1001 CCAAAACAGC CCTGTCCGAC ATCTCGACGG CAACCGGCAT GAGCATTGCC
1051 GACATCAAAAC GCCTCAACAA CCTGAACGGC AACCTTGTCa ACGCAGGACG
1101 CAGCATCCTT GTCGCCAAGA ACGGCAAAAC CCTTCAGACG GCATCGGAAT
1151 CGTCGTTTC CATCGACATC GACAATACGC CCGACACCTA CCGTTCCAAT
1201 ATGCCGGCAG GCACGGTGAA CGTCGGCATT GCCCGAATCC GACCCGCCGC
1251 CGCAGACACA GCGGACATTA CCGTCGCACC TTTGCCGCAG AAAACCGTCC
1301 GTACGG .AAC CCGATCCCCT TGTCCGTATT GCCGAACCTG CCCTTGCAGC
1351 AGCCGACAGC CAACCTCAAA CCGAAAAACA GACCGCATG CCGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2102; ORF 650>:

```

m650 .pep
1  MSKLKTIALT ASGLSVCPGF LYAQTSSHQ IGLAIMRLNS SILOLPPTKQ
51  YFQSGSLWGE LRQGRFMGEV NPFLVRRHES KFIASHSYFN RVINRSRPYM
101 YHIANEVKKR NMPAEAALLP FIESAFVTKA KSHVGASGLW QFMPATGRHY
151 GLEKTPVYDG RHDVYAATDA ALNYLQYLYG LFGDWPLAFA AYNWGEENVG
201 RAINRARAQG LEPTYENLRM PNETRNYVPK LLAVRNIIAT PQSFGMNISD
251 IDNKPFYQAV EPDRPLDNEA IARLAGITOS ELLALNPAPN VPAFIPKSKR
301 KLLLPPVASVQ TFQSNYLNAA PDSLFSWEVY TPAAKTSLSD ISTATGMSIA
351 DIKRLNNLNG NLVNAGRSIL VAKNGKTLQT ASESVVSI DI DNTPTYRSN
401 MPAGTVNVGI ARIRPAAQT ADITVAPLPQ KTVRTXTRSP CPYCRCTPCD
451 SRSATSNRKT DRHAV*

```

m650/g650 96.1% identity in 465 aa overlap

1034

	10	20	30	40	50	60
m650.pep	MSKLTIALTASGLSVCPGFLYAQNTSSHQIGLAIMRLNSSILDLPPTKQYFQSGSLWGE					
g650	MSKLTIALTASGLSVCPGFLYAQNTSSHQVGLAIMRLNSSILDLPPTKQYFQSGSLWDE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m650.pep	LRQGFMRGEVNPELVRRHESKFIAHSYFNVRVNRSPYMYHIANEVKKRNMPAEALLP					
g650	LRQGFMRGEVNPELVRRHESKFIAHSYFDRVNRSPYMYHIANEVKKRNMPAEALLP					
	70	80	90	100	110	120
	130	140	150	160	170	180
m650.pep	FIESAFVTKAKSHVGSGLWQFMPATGRHYGLEKTPVYDGRHDVYAATDAALNYLQYLYG					
g650	FIESAFVTKAKSHVGSGLWQFMPATGRHYGLEKTPVYDGRHDVYAATDAALNYLQYLYG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m650.pep	LFGDWPLAFAAYNWGEGNVGRA_NRRARQGLEPTYENLRMPNETRNYVPKLLAVRNIIAT					
g650	LFGDWPLAFAAYNWGEGNVGRAVNRARQGLEPTYENLRMPNETRNYVPKLLAVRNIIAT					
	190	200	210	220	230	240
	250	260	270	280	290	300
m650.pep	PQSFQGMNISDIDNKPYPQAVEPDRPLDNEAIARLAGITQSELLALNPAFNVPAFIPKSKR					
g650	PQSFQGMNISDIDNKPYPQAVEPGRPLDNEAIARLAGITQSELLALNPAFNVPAFIPKNKR					
	250	260	270	280	290	300
	310	320	330	340	350	360
m650.pep	KLLLPVASVQTFQSNYLNAA PDSLFSWEVYTPAAKTSLSDISTATGMSIADIKRLNNLNG					
g650	KLLLPVASVQTFQSNYLNAA PDSLFSWEVYTPAAKTSLSDISTATGMSIADIKRLNNLNG					
	310	320	330	340	350	360
	370	380	390	400	410	420
m650.pep	NLVNAGRSILVAKNGKTLQTASESVVSDIDNTPDYRSNMPAGTVNVGIARIRPAAAQT					
g650	NLVNAGRSILVAKNGKTLHTASESVVSDIDNTPDYRSNMPAGTVNVSIARIQAAAQT					
	370	380	390	400	410	420
	430	440	450	460		
m650.pep	ADITVAPLPQKTVRTXTRSPCPYCRTPCDSRSATSNRKTDHRAVX					
g650	ADITVAPLPQETVRTGTRSPCPHYRTPCDSRSATSNRKTDCHAVX					
	430	440	450	460		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2103>:

```

a650.seq
1  ATGTCCAAAC  TCAAAACCAI  CGCCCTGACC  GCGTCAGGTC  TGTCCGTTTG
51  TCCGGGTTTC  CTATACGCC  AAAACACCTC  ATCACACCAA  ATCGGTTTGG
101 CGATTATGCG  CTFAAACTCT  TCAATACTCG  ACCTGCCACC  GACAAAACAA
151 TATTTCCAAT  CCGGCAGCCT  GTGGAGCGAG  CTGCGCCAAG  GCTTCCGGAT
201 GGGCGAAGTC  AATCCGAAC  TGGTACGCCG  CCACGAAAGC  AAATTCATCG
251 CAAGCCACAG  CTATTCAAC  AGGGTCATCA  ACGGAGTAG  ACCCTATATG
301 TACCATATCG  CCAACGAAGT  CAAAAACGC  AATATGCCCG  CCGAAGCCGC
351 CCTGCTTCCC  TTCATCGAAA  GCGCGTTCGT  CACCAAAGCC  AAATCACACG
401 TCGGCGCATC  GGGCCTGTGG  CAGTTCATGC  CCGCTACCGG  CAGGCATTAC
451 GGCCTGGAAG  AAACACCGGT  TTACGACGGC  AGGCACGACA  TTACGCCGC
501 CACCGATGCC  GCACTCAACT  ATCTGCAATA  CCTCTATGGA  CTGTTCCGCG
551 ACTGGCCGCT  CGCCTTTGCC  GCCTACAAC  TGGGTGAAGG  CAACGTCGGA
601 CGCGCCATCA  ACCGCGCCCG  CGCCAAGGG  CTGAACCGA  CCTACGAAAA
651 CCTGCGTATG  CCCAACGAAA  CGCGCAACTA  TGTTCCTAAG  CTGCTCGCCG
701 TCGCAACAT  CATTGCCCGC  CCCAATCTT  TCGGCATGAA  TATCAGCGAC
751 ATAGACAACA  AACCGTATTT  TCAGGCAGTC  GAACCGGACC  GTCCGCTCGA
801 CAACGAAGCC  ATCGCCCGGC  TTGCCGGCAT  CACGCAAAGC  GAGCTGCTCG
851 CCCTAAACCC  CGCATTC AAC  GTCCCGCGT  TCATCCCCAA  AAGCAAACGC

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1035

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901  AAACTGCTGC TTCCTGTCGC GTCCGTACAA ACCTTCCAAA GCAACTACCT
951  CAACGCCGCA CCCGACAGCC TGTTCATG GGAAGTCTAT ACGCCTGCCG
1001 CCAAAACCAG CTTGTCCGAC ATCTCGACGG CAACCGGCAT GAGCATTGCC
1051 GACATCAAAC GCCTCAACAA CCTGAACGGC AACCTTGTC ACGCAGGACG
1101 CAGCATCCTT GTCGCCAAGA ACGGCAAAAC CCTTCAGACG GCATCGGAAT
1151 CCGTCGTTTC CATCGACATC GACAATACGC CCAACACCTA CCGTTCCAAT
1201 ATGCCGCGAG GCACGGTGAA CGTCGGCATT GCCCGAATCC GACCCGCCGC
1251 CGCACAGACA GCGGACATTA CCGTCGCACC TTTGCCGCAG AAAACCGTCC
1301 GTACGG AAC CCGATCCCCT TGTCCGTATT GCCGAACCTG CCCTTGCGAC
1351 AGCCGCAGCG CAACCTCAAA CCGAAAACA GACCGCCATG CCGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2104; ORF 650.a>:

```

a650.pep
  1  MSKLKTIALT ASGLSVCPGF LYAQTSSHQ IGLAIMRLNS SILDLPPTKQ
 51  YFQSGSLWSE LRQGFMRGEV NPELVRHES KFIASHSYFN RVINRSRPFY
101  YHIANEVKKR NMPAEALLP FIESAFVTKA KSHVGASGLW QFMPATGRHY
151  GLEKTPVYDG RHDYIYAATA ALNYLQYLYG LFGDWPLAFA AYNWGEENVG
201  RAINRARAQG LEPTYENLRM PNETRNYVPK LLAVRNIIAA PQSFGMNISD
251  IDNKPYFQAV EPDRPLDNEA IARLAGITQS ELLALNPAFN VPAFIPKSKR
301  KLLLPVASVQ TFQSNYLNAA PDSLFSWEVY TPAAKTSLSD ISTATGMSIA
351  DIKRLNNLNG NLVNAGRSIL VAKNGKTLQT ASESVVSIDI DNTPTYRSN
401  MPAGTVNVGI ARIRPAAQOT ADITVAPLPQ KTVRTXTRSP CPYCRTCPCD
451  SRSATSNRKT DRHAV*

m650/a650  99.1% identity in 465 aa overlap

      10      20      30      40      50      60
m650.pep  MSKLKTIALTASGLSVCPGF LYAQTSSHQ IGLAIMRLNSSILDLPPTKQYFQSGSLWGE
a650      MSKLKTIALTASGLSVCPGF LYAQTSSHQ IGLAIMRLNSSILDLPPTKQYFQSGSLWGE
      10      20      30      40      50      60

      70      80      90     100     110     120
m650.pep  LRQGFMRGEVNPELVRHESKFIASHSYFN RVINRSRPFYMYHIANEVKKRNMPAEALLP
a650      LRQGFMRGEVNPELVRHESKFIASHSYFN RVINRSRPFYMYHIANEVKKRNMPAEALLP
      70      80      90     100     110     120

      130     140     150     160     170     180
m650.pep  FIESAFVTKAKSHVGASGLWQFMPATGRHYGLEKTPVYDGRHDVYAATAALNYLQYLYG
a650      FIESAFVTKAKSHVGASGLWQFMPATGRHYGLEKTPVYDGRHDVYAATAALNYLQYLYG
      130     140     150     160     170     180

      190     200     210     220     230     240
m650.pep  LFGDWPLAFAAYNWGEENVGRAINRARAQGLEPTYENLRMPNETRNYVPKLLAVRNIIAT
a650      LFGDWPLAFAAYNWGEENVGRAINRARAQGLEPTYENLRMPNETRNYVPKLLAVRNIIAA
      190     200     210     220     230     240

      250     260     270     280     290     300
m650.pep  PQSFGMNISDIDNKPYFQAVEPDRPLDNEAIARLAGITQSELLALNPAFNVPFIPKSKR
a650      PQSFGMNISDIDNKPYFQAVEPDRPLDNEAIARLAGITQSELLALNPAFNVPFIPKSKR
      250     260     270     280     290     300

      310     320     330     340     350     360
m650.pep  KLLLPVASVQTFQSNYLNAA PDSLFSWEVYTPAAKTSLSDISTATGMSIADIKRLNNLNG
a650      KLLLPVASVQTFQSNYLNAA PDSLFSWEVYTPAAKTSLSDISTATGMSIADIKRLNNLNG
      310     320     330     340     350     360

      370     380     390     400     410     420
m650.pep  NLVNAGRSILVAKNGKTLQTASESVVSIDIDNTPDYRSNMPAGTVNVGIARIRPAAQOT
a650      NLVNAGRSILVAKNGKTLQTASESVVSIDIDNTPDYRSNMPAGTVNVGIARIRPAAQOT

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1036

	370	380	390	400	410	420
	430	440	450	460		
m650.pep	ADITVAPLPQKTVRTXTRSPCPYCRTCPCDSRSATSNRKTDRAVX					
a650	ADITVAPLPQKTVRTXTRSPCPYCRTCPCDSRSATSNRKTDRAVX					
	430	440	450	460		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2105>:

g652.seq

```

1 ATGATCGAAT TGGACGGTAC TGAAAACAAA GGCAATTGG GTGCGAATGC
51 GACTTTGGCG GTCTCTATGG CGGTTGCACG CGCCGCTGCC GAAGACTCAG
101 GCCTGCCGCT TTACCGCTAC TTGGGGGGCG CAGGTCGAT GTCCTGCCCG
151 GTACCGATGA TGAACGTCAT CAACGGCGGC GAACACGCCA ACAACAGCCT
201 GAACATCCAA GAGTTTATGA TTATGCCCGT CGGCGCAAAA TCTTTCCGCG
251 AAGCGTTGCG CTGCGGTGCG GAAATTTTCC ACGCCTGAA AAAACTGTGC
301 GACAGTAAAG GCTTCCCGAC CACAGTCGGC GACGAAGCG GTTTCGCCCC
351 CAACCTGAAC AGCCACAAAG AAGCCCTGCA ACTGATGGTC GAAGCGGCCG
401 AAGCCGCCGG CTACAAGGCG GCGAAGACG TATTATTCGC ATTGGACTGC
451 GCGTCCAGCG AGTTCTACAA AGACGGCAAA TACCACTGG AAGCCGAAGG
501 CCGCTCCTAC ACCAACGCGG AATTGGCCGA ATACTTGAA GGCTTGGTTA
551 ACGAATTCCT GATTATTTCC ATTGAAGACG GGATGGACGA AAACGACTGG
601 GAAGGCTGGA AACTGCTGAC CGAAAAATTG GGCAAAAAAG TTCAATTGGT
651 CGGCGACGAC TTGTTTCGTAA CCAATCCGAA AATTCTTGCC GAAGGCATCG
701 AAAAAGCGCT AGCAAAACGCA TTGCTGGTCA AAGTCAACCA AATCGGTACT
751 TTAAGCGAAA CCTGAAAGC cgtcgatctg gCAAAATGCA accgctacGc
801 cagCGTGATG AGCCACcgct ccggCGAAAC CGAAGACAGT Accattgccc
851 ACTTGGCAGT CGCCACCAAC TGTATGCAGA TTAATAccgG TTCTTTGAGC
901 cgTTCCGACC GCATGGCGAA ATACAACCAa ctGCTGCGTA TCGAGGAAGA
951 ATTGGCGGAA GCGcctACT ACCCGGGCAA AGCCGCATTC TACCAACTGG
1001 GCAATAA
```

This corresponds to the amino acid sequence <SEQ ID 2106; ORF 652.ng>:

g652.pep

```

1 MIELDGTENK GN LGANATLA VSM AVARAAA EDSGLPLYRY LGGAGPMSLP
51 VPMNVINGG EHANNSLNIQ EFMIMPVGAK SFREALRCGA EIFHALKKLC
101 ESKGFPTTVG DEGGFAPNLN SHKEALQLMV EAAEAAGYKA GEDVLFALDC
151 ASSEFYKDGK YHLEAEGRSY TNAEFAEYLE GLVNEFP IIS IEDGMDENDW
201 EGWKLLTEKL GKKVQLVGDD LFTVNP KILA EGIKGVANA LLVKVNQIGT
251 LSETLKAVDL AKCNRYASVM SHRSGETEDS TIADLAVATN CMQIKTGSLS
301 RSDRMAYNQ LLRIEELAE AAYYPGKAAF YQLGK*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2107>:

m652.seq

```

1 ATGATCGAAT TGGACGGTAC TGAAAACAAA GGCAATTGG GTGCGAATGC
51 GACTTTGGCG GTTCTATGG CGGTTGCACG CGCCGCTGCC GAAGACTCAG
101 GCCTGCCGCT TTACCGCTAC TTGGGGCGCG CAGGCCGAT GTCCTGCCCG
151 GTACCGATGA TGAACGTCAT CAACGGCGGC GAACACGCCA ACAACAGCCT
201 GAACATCCAA GAGTTTATGA TTATGCCCGT CGGCGCAAAA TCTTTCCGCG
251 AAGCGTTGCG CTGCGGTGCG GAAATTTTCC ACGCCTGAA AAAACTGTGC
301 GACAGCAAAAG GCTTCCCGAC CACAGTCGGC GACGAAGCG GTTTCGCCCC
351 CAACCTGAAC AGCCACAAAG AAGCCCTGCA ACTGATGGTC GAGGCGACCG
401 AAGCCGCCGG CTACAAGGCG GCGAAGACG TATTATTCGC ATTGGACTGC
451 GCCTCCAGCG AGTTCTACAA AGACGGCAAA TACCACTGG AAGCCGAAGG
501 CCGCTCCTAC ACCAACGCGG AATTGGCCGA ATATCTGGAA GGCCTGGTCA
551 ACGAGTTCCC CATCATCTCC ATCGAAGACG GCATGGATGA AAACGACTGG
601 GAAGGCTGGA AACTGCTGAC CGAAAAACTG GCGGCTAGAG TCAATTGGT
651 TGGCGACGAC TTGTTTCGTAA CCAATCCAAA AATCTTGCCC GAAGGCATCG
701 AAAAAGCGCT AGCAAAACGCA TTGCTGGTCA AAGTCAATCA AATCGGTACT
751 TTGAGCGAGA CCTGAAAGC CGTCGACTTA GCCAAACGCA ACCGCTACGC
801 CAGCGTAATG AGCCACCGCT CCGGCGAAAC CGAAGACAGC ACCATTGCCG
851 ACTTGGCAGT CGCCACCAAC TGTATGCAGA TCAAAACCGG TTCTTTGAGC
901 CGTTCCGACC GCATGGCGAA ATACAACCAa CTGCTGCGTA TCGAGGAAGA
951 ATTGGCGGAA GCGCGCGACT ACCCCAGCAA AGCCGCATTC TACCAACTGG
1001 GCAATAA
```

This corresponds to the amino acid sequence <SEQ ID 2108; ORF 652>:

m652.pep

```

1 MIELDGTENK GN LGANATLA VSM AVARAAA EDSGLPLYRY LGGAGPMSLP
51 VPMNVINGG EHANNSLNIQ EFMIMPVGAK SFREALRCGA EIFHALKKLC
```

1037

```

101 DSKGFPTTVG DEGGFAPNLN SHKEALQLMV EATEAAGYKA GEDVLFALDC
151 ASSEFYKDGK YHLEAEGRSY TNAEFAEYLE GLVNEFPIIS IEDGMDENDW
201 EGWKLLETKL GGRVQLVGDD LFVTNPKILA EGIEKGVANA LLVKVNQIGT
251 LSETLKAVDL AKRNRYASVM SHRSGETEDS TIADLAVATN CMQIKTGSLS
301 RSDRMAYNQ LLRIEELAE AADYPSKAAF YQLGK*

```

m652/g652 98.2% identity in 335 aa overlap

```

              10      20      30      40      50      60
m652.pep      MIELDCTENKGNLGNATLAVSMAVARAAEDSGLPLYRYLGGAGPMSLPVPMNVINGG
              |||||
g652          MIELDGTENKGNLGNATLAVSMAVARAAEDSGLPLYRYLGGAGPMSLPVPMNVINGG
              10      20      30      40      50      60

              70      80      90      100     110     120
m652.pep      EHANNSLNIQEFMIMPVGAKSFREALRCGAEIFHALKKLCDSKGFPTTVGDEGGFAPNLN
              |||||
g652          EHANNSLNIQEFMIMPVGAKSFREALRCGAEIFHALKKLCDSKGFPTTVGDEGGFAPNLN
              70      80      90      100     110     120

              130     140     150     160     170     180
m652.pep      SHKEALQLMVEATEAAGYKAGEDVLFALDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLE
              |||||
g652          SHKEALQLMVEATEAAGYKAGEDVLFALDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLE
              130     140     150     160     170     180

              190     200     210     220     230     240
m652.pep      GLVNEFPIISIEDGMDENDWEGWKLLEKLGGRVQLVGDDLFVTNPKILAEGIEKGVANA
              |||||
g652          GLVNEFPIISIEDGMDENDWEGWKLLEKLGKVKQLVGDDLFVTNPKILAEGIEKGVANA
              190     200     210     220     230     240

              250     260     270     280     290     300
m652.pep      LLVKVNQIGTLSETLKAVDLAKRNRYASVMSHRSGETEDSTIADLAVATNCMQIKTGSLS
              |||||
g652          LLVKVNQIGTLSETLKAVDLAKRNRYASVMSHRSGETEDSTIADLAVATNCMQIKTGSLS
              250     260     270     280     290     300

              310     320     330
m652.pep      RSDRMAYNQLLRIEELAEAAADYPSKAAFYQLGKX
              |||||
g652          RSDRMAYNQLLRIEELAEAAAYPGKAAFYQLGKX
              310     320     330

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2109>:

```

a652.seq
1  ATGATCGAAT TGGACGGTAC TGAAAACAAA GGCAATTGGG GTGCGAATGC
51  GACTTTGGCG GTTCTATGG CGGTTGCACG CGCCGCTGCC GAAGACTCAG
101 GCTTGCCGCT TTACCGCTAC TTGGGCGGCG CAGGCCCGAT GTCCCTGCCC
151 GTACCGATGA TGAACGTCAT CAACGGCGGC GAACACGCCA ACAACAGCCT
201 GAACATCCAA GAGTTTATGA TTATGCCCGT CGGCGCAAAA TCCTTCCGCG
251 AAGCGTTCCG CTCGGGTCCG GAAATTTTCC ACGCCTTGA AAAACTGTGC
301 GACAGCAAAG GCTTCCCGAC CACAGTCGGC GACGAAGGCG GTTTCGCCCC
351 CAACCTGAAC AGCCACAAAG AAGCCCTGCA ACTGATGGTC GAGGCGACCG
401 AAGCCGCGCG CTACAAAGCG GGCGAAGACG TATTATTCCG ATTGGACTGC
451 GCGTCCAGCG AGTTCTACAA AGACGGCAAA TACCCTTGG AAGCCGAAGG
501 CCGCTCTTAC ACCAACGCGG AATTGCGCGA ATATCTGGAA GGCCTGGTCA
551 ACGAGTTCCC CATCATCTCC ATCGAAGACG GGATGGATGA AAACGACTGG
601 GAAGGCTGGA AACTGCTGAC CGAAAACTG GCGCGCAAG TCCAACCTCGT
651 TGGCGACGAC CTCTTCGTTA CCAACCCGAA AATCCTTGCC GAAGGCATTG
701 AAAAAGGCGT GGCAACGCA CTATTGGTCA AAGTCAACCA AATCGGTACT
751 TTGAGTGAAG CCCTGAAAGC CGTCGACTTA GCCAAACGCA ACCGCTACGC
801 CAGCGTAATG AGCCACCGCT CCGGCGAAAC CGAAGACAGC ACCATTGCGG
851 ACTTGGCAGT CGCCACCAAC TGTATGCAGA TCAAAACCGG TTCTTTGAGC
901 CGTTCGACG GCATGGCGAA ATACAACCAA CTGTGCGGTA TCGAGGAAGA
951 ATTGGCGGAA GCGCGCGACT ACCCCAGCAA AGCCGCATTG TACCAACTGG
1001 GCAATATA

```

This corresponds to the amino acid sequence <SEQ ID 2110; ORF 652.a>:

```

a652.pep
1  MIELDGTENK GNLGNATLA VSMVARARA EDSGLPLYRY LGGAGPMSLP
51  VPMNVINGG EHANNSLNIQ EFMIMPVGRK SFREALRCGA EIFHALKKLC
101 DSKGFPTTVG DEGGFAPNLN SHKEALQLMV EATEAAGYKA GEDVLFALDC

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1038

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151 ASSEFYKD GK YHLEAEGRSY TNAEFAEYLE GLVNEFP IIS IEDGMDENDW
201 EGWKLLETKL GGVQLVGDD LFTVNP KILA EGIEKGVANA LLVKVNQIGT
251 LSETLKAVDL AKRNRYASVM SHRSGETEDS TIADLAVATN CMQIKTGSLS
301 RSDRMAYNQ LLRIEELAE AADYPSKAAF YQLGK*

m652/a652 99.7% identity in 335 aa overlap

      10      20      30      40      50      60
m652.pep MIELDGTENKGNLGNATLAVSMAVARAAAEDSGLPLYRYLGGAGPMSLPVPMNVINGG
          |||
a652      MIELDGTENKGNLGNATLAVSMAVARAAAEDSGLPLYRYLGGAGPMSLPVPMNVINGG
          |||
      70      80      90     100     110     120
m652.pep EHANNSLNIQEFMIMPVGAKSFREALRCGAEIFHALKKLCDSKGFPPTVGDEGGFAPNLN
          |||
a652      EHANNSLNIQEFMIMPVGAKSFREALRCGAEIFHALKKLCDSKGFPPTVGDEGGFAPNLN
          |||
      130     140     150     160     170     180
m652.pep SHKEALQLMVEATEAAGYKAGEDVLFALDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLE
          |||
a652      SHKEALQLMVEATEAAGYKAGEDVLFALDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLE
          |||
      190     200     210     220     230     240
m652.pep GLVNEFP IIS IEDGMDENDWEGWKLLEKLGGRVQLVGDDLFVTNPKILAEGIEKGVANA
          |||
a652      GLVNEFP IIS IEDGMDENDWEGWKLLEKLGGRVQLVGDDLFVTNPKILAEGIEKGVANA
          |||
      250     260     270     280     290     300
m652.pep LLVKVNQIGT LSETLKAVDLAKRNRYASVM SHRSGETEDSTIADLAVATNCMQIKTGSLS
          |||
a652      LLVKVNQIGT LSETLKAVDLAKRNRYASVM SHRSGETEDSTIADLAVATNCMQIKTGSLS
          |||
      310     320     330
m652.pep RSDRMAYNQ LLRIEELAE AADYPSKAAF YQLGKX
          |||
a652      RSDRMAYNQ LLRIEELAE AADYPSKAAF YQLGKX
          |||
      310     320     330

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2111>:

g652-1.seq

```

1  ATGAGCGCAA TCGTTGATAT TTTGCCCCG GAAATTTTGG ACTCAGCGCG
51  CAACCCACAC GTGAGAGTGTG ATGTATTGCT CGAATCCGGC GTAATGGGAC
101 GTGCGGCCGT ACCGAGCGGC GCATCCACCG GTCAGAAAGA AGCTTTGGAA
151 CTTGCGGACG GCGACAAATC CCGCTATTCC GGCAAGGCGG TATTGAAGGC
201 CGTCGAACAC GTCAACAACC AAATCGCCCA AGCCCTCATC GGTATCGATG
251 CCAACGAGCA ATCTTATATC GACCAATATC TGATCGAATT GGACGGTACT
301 GAAAAACAAAG GCAATTTGGG TCGGAATGCG ACTTTGGCGG TCTCTATGGC
351 GGTTCGACGC GCCGCTGCCG AAGACTCAGG CCTGCCGCTT TACCGCTACT
401 TGGGGGGCGC AGGTCCGATG TCCCTGCCCG TACCGATGAT GAACGTCATC
451 AACGGCGGCG AACACGCCAA CAACAGCCTG AACATCCAAG AGTTTATGAT
501 TATGCCCGTC GGCACAAAAT CTTTCCGCGA AGCGTTGCGC TCGCGTGCGG
551 AAATTTTCCA CGCCTTGAAA AACTGTGCG ACAGTAAAGG CTTCGCCACC
601 ACAGTCGGCG ACGAAGGCGG TTTCGCCCCC AACCTGAACA GCCACAAGA
651 AGCCCTGCAA CTGATGTCG AAGCGGCCGA AGCCGCCGCG TACAAGGCGG
701 GCGAAGACGT ATTATTGCGA TTGGACTGCG CGTCCAGCGA GTTCTACAAA
751 GACGGCAAAT ACCACTTGGA AGCCGAAGGC CGCTCCTACA CCAACGCGGA
801 ATTTGCCGAA TACTTGGAAG GCTTGGTAA CGAATTCCTG ATTATTCCA
851 TTGAAGACGG GATGGACGAA AACGACTGGG AAGGCTGGAA ACTGCTGACC
901 GAAAAAATTGG GCAAAAAAGT TCAATTGGTC GCGCAGCACT TGTTCGTAAC
951 CAATCCGAAA ATTCTTGCCG AAGGCATCGA AAAAGGCGTA GCAAAACGCAT
1001 TGCTGGTCAA AGTCAACCAA ATCGGTACTT TAAGCGAAAC CCTGAAAGCC
1051 GTCGATCTGG CAAAATGCAA CCGCTACGCG AGCGTGATGA GCCACCGCTC
1101 CGGCGAAACC GAAGACAGTA CCATTGCCSA CTTGGCAGTC GCCACCAACT
1151 GTATGCAGAT TAAAACCGGT TCTTTGAGCG GTTCCGACCG CATGGCGAAA
1201 TACAACCAAC TGCTGCGTAT CGAGGAAGAA TTGGCGGAAG CCGCCTACTA
1251 CCCCAGCAAA GCCGCATTCT ACCAAGTGGC CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2112; ORF 652-1.ng>:

1039

g652-1.pep

```

1  MSAIVDIFAR EILDSRGNPT VECDVLLESG VMGRAAVPSG ASTGQKEALE
51  LRDGDKSRYG GKGVLKAVEH VNNQIAQALI GIDANEQSYI DQIMIELDGT
101 ENKGNLGNANA TLAVSMAVAR AAAEDSGLPL YRYLGGAGPM SLPVPMNVI
151 NGGEHANNSL NIOEFMIMPV GAKSFREALR CGAEIFHALK KLCDSKGFPT
201 TVGDEGGFAP NLNSHKEALQ LMVEAREAAAG YKAGEDVLFA LDCASSEFYK
251 DGKYHLEAEG RSYTNAEFAR YLEGLVNEFP IISIEDGMDE NDWEGWKLIT
301 EKLGGKQVLV GDDLFTVNPV ILAEGIEKGV ANALLVKVNO IGTLSETLKA
351 VDLAKRNRYA SVMSHRSGET EDSTIADLAV ATNCMOIKTG SLRSRDRMAK
401 YNQLLRIEEE LAEAAAYPGK AAFYQLGK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2113>:

m652-1.seq

```

1  ATGAGCGCAA TCGTTGATAT TTTGCCCCGC GAAATTTTGG ACTCACGCGG
51  CAACCCACACA GTCGAGTGTG ATGTATTGCT CGAATCCGGC GTAATGGGAC
101 GCGCAGCCGT ACCGAGCGGC GCGTCCACCG GTCAAAAAGA GGCTTTGGAA
151 CTTGCGGACG GCGACAAATC CCGTTATTCG GCGAAGGCGG TATTGAAGGC
201 GGTGCAACAC GTCAACAACC AAATCGCCCA AGCCCTCATT GGTATCGATG
251 CCAACGAGCA ATCTTATATC GACCAATCA TGATCGAATT GGACGGTACT
301 GAAACAAAG GCAATTGGG TGCGAATGCG ACTTGGCGG TTTCTATGGC
351 GGTTCACGCG GCGGCTGCGG AAGACTCAGG CTTGCCGCTT TACCGCTACT
401 TGGGCGGCGC AGGCCGATG TCCCTGCCCG TACCGATGAT GAACGTCATC
451 AACGGCGGCG AACACGCCAA CAACAGCCTG AACATCCAAG AGTTTATGAT
501 TATGCCCGTC GCGCCAAAAT CTTTCCGCGA AGCGTTGCGC TSCGGTGGCG
551 AAATTTTCCA CGCCTTGAAA AAAGTGTCG ACAGCAAAGG CTTCCCGACC
601 ACAGTCGGCG ACGAAGGCGG TTTGCCCCC AACCTGAACA GCCACAAGA
651 AGCCCTGCAA CTGATGGTCG AGCGACCGCA AGCCGCCGCG TACAAAGCGG
701 GCGAAGACGT ATTATTCGCA TTGGACTGCG CCTCCAGCGA GTTCTACAAA
751 GACGGCAAAAT ACCACTTGA AGCCGAAGGC CGCTCCTACA CCAACGCGGA
801 ATTTGCCGAA TATCTGGAAG GCCTGGTCAA CGAGTTCCCG ATCATCTCCA
851 TCGAAGACGG CATGGATGAA AACGACTGGG AAGGCTGGAA ACTGCTGACC
901 GAAAAAAGTG GCGGTAGAGT TCAATTGGTT GCGGACGACT TGTTCGTAAC
951 CAATCCAAA ATCTTGGCGG AAGGCATCGA AAAAGGCGTA GCAAACGCAT
1001 TGCTGGTCAA AGTCAATCAA ATCGGTACTT TGAGCGAGAC CCTGAAAGCC
1051 GTCGACTTAG CCAAACGCAA CCGCTACGCC AGCGTAATGA GCCACCGCTC
1101 CGGCGAAACC GAAGACAGCA CCATTGCCGA CTTGGCAGTC GCCACCAACT
1151 GTATGCAGAT CAAAACCGGT TCTTTGAGCC GTTCCGACCG CATGGCGAAA
1201 TACAACCAAC TGCTGCGTAT CGAGGAAGAA TTGGCGGAAG CCGCCGACTA
1251 CCCCAGCAA GCCGCAATTCT ACCAACTGGG CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2114; ORF 652-1>:

m652-1.pep

```

1  MSAIVDIFAR EILDSRGNPT VECDVLLESG VMGRAAVPSG ASTGQKEALE
51  LRDGDKSRYG GKGVLKAVEH VNNQIAQALI GIDANEQSYI DQIMIELDGT
101 ENKGNLGNANA TLAVSMAVAR AAAEDSGLPL YRYLGGAGPM SLPVPMNVI
151 NGGEHANNSL NIOEFMIMPV GAKSFREALR CGAEIFHALK KLCDSKGFPT
201 TVGDEGGFAP NLNSHKEALQ LMVEAREAAAG YKAGEDVLFA LDCASSEFYK
251 DGKYHLEAEG RSYTNAEFAR YLEGLVNEFP IISIEDGMDE NDWEGWKLIT
301 EKLGGKQVLV GDDLFTVNPV ILAEGIEKGV ANALLVKVNO IGTLSETLKA
351 VDLAKRNRYA SVMSHRSGET EDSTIADLAV ATNCMOIKTG SLRSRDRMAK
401 YNQLLRIEEE LAEAAAYPSK AAFYQLGK*

```

m652-1/g652-1 98.6% identity in 428 aa overlap

	10	20	30	40	50	60
m652-1	MSAIVDIFAREILDSRGNPTVECDVLLESGVMGRAAVPSGASTGQKEALELRDGDKSRYG					
g652-1	MSAIVDIFAREILDSRGNPTVECDVLLESCVMGRAAVPSGASTGQKEALELRDGDKSRYG					
	10	20	30	40	50	60
m652-1	GKGVLKAVEHVNNQIAQALIGIDANEQSYIDQIMIELDGTENKGNLGNANATLAVSMAVAR					
g652-1	GKGVLKAVEHVNNQIAQALIGIDANEQSYIDQIMIELDGTENKGNLGNANATLAVSMAVAR					
	70	80	90	100	110	120
m652-1	GKGVLKAVEHVNNQIAQALIGIDANEQSYIDQIMIELDGTENKGNLGNANATLAVSMAVAR					
g652-1	GKGVLKAVEHVNNQIAQALIGIDANEQSYIDQIMIELDGTENKGNLGNANATLAVSMAVAR					
	70	80	90	100	110	120
m652-1	AAAEDSGLPLYRYLGGAGPMSLPVPMNINVINGGEHANNSLNIOEFMIMPVGAKSFREALR					
g652-1	AAAEDSGLPLYRYLGGAGPMSLPVPMNINVINGGEHANNSLNIOEFMIMPVGAKSFREALR					
	130	140	150	160	170	180
m652-1	AAAEDSGLPLYRYLGGAGPMSLPVPMNINVINGGEHANNSLNIOEFMIMPVGAKSFREALR					
g652-1	AAAEDSGLPLYRYLGGAGPMSLPVPMNINVINGGEHANNSLNIOEFMIMPVGAKSFREALR					
	130	140	150	160	170	180

1040

	190	200	210	220	230	240
m652-1	CGAEIFHALKKLCDSKGFPPTTVGDEGGFAPNLNSHKEALQLMVEATEAAGYKAGEDVLFA					
g652-1	CGAEIFHALKKLCDSKGFPPTTVGDEGGFAPNLNSHKEALQLMVEATEAAGYKAGEDVLFA					
	190	200	210	220	230	240
	250	260	270	280	290	300
m652-1	LDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLEGLVNEFPIISIEDGMDENDWEGWKLTT					
g652-1	LDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLEGLVNEFPIISIEDGMDENDWEGWKLTT					
	250	260	270	280	290	300
	310	320	330	340	350	360
m652-1	EKLGGRRVQLVGDDLFVTNPKILAEGIEKGVANALLVKVNQIGTLSETLKAVDLAKNRNYA					
g652-1	EKLGGRRVQLVGDDLFVTNPKILAEGIEKGVANALLVKVNQIGTLSETLKAVDLAKNRNYA					
	310	320	330	340	350	360
	370	380	390	400	410	420
m652-1	SVMSHRSGETEDSTIADLAVATNCMQIKTGSLSRSDRMAYNQLLRIEELAEADYPSK					
g652-1	SVMSHRSGETEDSTIADLAVATNCMQIKTGSLSRSDRMAYNQLLRIEELAEADYPSK					
	370	380	390	400	410	420
	429					
m652-1	AAFYQLGKX					
g652-1	AAFYQLGKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2115>:

a652-1.seq

```

1  ATGAGCGCAA TCGTTGATAT TTTGCCCCGC GAAATTTTGG ACTCAGCGGG
51  CAACCCACCA GTCGAGTGTG ATGTATTGCT CGAATCCGGC GTAATGGGAC
101 GCGCAGCCGT ACCGAGCGGC GCGTCCACCG GTCAAAAAGA GGCTTTGGAA
151 CTTCGCGACG GCGACAAATC CCGTTATTCT GGCAAGGGCG TATTGAAGGC
201 GGTGGAACAC GTCAACAACC AAATCGCCCA AGCCCTCATT GGTATCGATG
251 CCAACGAGCA ATCTTATATC GACCAATCA TGATCGAATT GGACGGTACT
301 GAAACAAAGC GCAATTGGG TGCGAATGCG ACTTTGGCGG TTTCTATGGC
351 GGTTCGACGC GCCGCTGCCG AAGACTCAGG CCGCGCGCTT TACCGTACT
401 TGGGCGGCGC AGGCCCGATG TCCCTGCCCG TACCGATGAT GAACGTCATC
451 AACGCGCGCG AACACGCCAA CAACAGCCTG AACATCCAAG AGTTTATGAT
501 TATGCCCCGC GCGCAAAAT CTTCCGCGA AGCGTTCGCG TCCGCTGCGG
551 AAATTTTCCA CGCCTGAAA AAACCTGTGC ACAGCAAAGG CTTCCCGACC
601 ACAGTCGGCG ACGAAGGCGG TTTCGCCGCC AACCTGAACA GCCACAAAGA
651 AGCCCTGCAA CTGATGCTCG AGGCGACCGA AGCCGCGCGC TACAAAGCGG
701 GCGAAGACGT ATTATTGCGA TTGGACTGCG CGTCCAGCGA GTTCTACAAA
751 GACGGAACAT ACCACTTGGA AGCCGAAGGC CGCTCCTACA CCAACGCGGA
801 ATTTGCCGAA TATCTGGAAG GCCTGGTCAA CGAGTTCCCC ATCATCTCCA
851 TCGAAGACGG GATGGATGAA AACGACTGGG AAGGCTGGAA ACTGCTGACC
901 GAAAACTGGG GCGGCAAACT CCAACTCGTT GCGCAGCACC TCTTCGTTAC
951 CAACCCGAAA ATCCTTGCCG AAGGCATTGA AAAAGCGGTG GCAAACGCAC
1001 TATTGGTCAA AGTCAACCAA ATCGGTACTT TGAGTGAAC CCTGAAAGCC
1051 GTCGACTTAG CCAAACGCAA CCGCTACGCC AGCGTAATGA GCCACCCTC
1101 CGGCGAARAC GAAGACAGCA CCATTGCCGA CTGGCAGTC GCCACCACT
1151 GTATGCAGAT CAAAACCGGT TCTTTGAGCC GTTCCGACCG CATGGCGAAA
1201 TACAACCAAC TGCTGCGTAT CGAGGAAGAA TTGGCGGAAG CCGCCGACTA
1251 CCCGAGCAA GCCGCATTCT ACCAACTGGG CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2116; ORF 652-1.a>:

a652-1.pep

```

1  MSAIVDIFAR EILDSRGNPT VECVLLLESG VMGRAAVPSG ASTGQKEALE
51  LRDGDKSRYS GKGVLKAVEH VNNQIAQALI GIDANEQSYI DQIMIELDGT
101 ENKGNLGNAN TLAVSMAVAR AAEDSGLP YRYLGAGPML SLVPVPMNVI
151 NGGEHANNSL NIQEFMIMPV GAKSFREALR CGAEIFHALK KLCDSKGFPT
201 TVGDEGGFAP NLNSHKEALQ LMVEATEAAG YKAGEDVLFA LDCASSEFYK
251 DGKYHLEAEG RSYTNAEFAE YLEGLVNEFP IISIEDGMDN DWEGWKLTT
301 EKLGGKVVQL VDDLFVTNPK ILAEGIEKGV ANALLVKVNQ IGTLSLTKA
351 VDLAKNRNYA SVMSHRSGET EDSTIADLAV ATNCMQIKTG SLRSRDRMAK
401 YNQLLRIEEE LAEADYPSK AAFYQLGK*

```

m652-1/a652-1 99.8% identity in 428 aa overlap

10 20 30 40 50 60

1041

```

m652-1      MSAIVDIFAREILDSRGNPTVECDVLESVMGRAAVPSGASTGQKEALELRDGDKSRY
a652-1      MSAIVDIFAREILDSRGNPTVECDVLESVMGRAAVPSGASTGQKEALELRDGDKSRY
              10      20      30      40      50      60

m652-1      GKGVLKAVEHVNNQIAQALIGIDANEQSYIDQIMIELDGTENKGNLGNATLAVSMAVAR
a652-1      GKGVLKAVEHVNNQIAQALIGIDANEQSYIDQIMIELDGTENKGNLGNATLAVSMAVAR
              70      80      90      100     110     120

m652-1      AAAEDSGLPLYRYLGGAGPMSLPVPMNVINGGEHANNSLNIQEFMIMPVGAKSFREALR
a652-1      AAAEDSGLPLYRYLGGAGPMSLPVPMNVINGGEHANNSLNIQEFMIMPVGAKSFREALR
              130     140     150     160     170     180

m652-1      CGAEIFHALKKLDCSKGFPTTVGDEGGFAPNLSHKEALQLMVEATEAAGYKAGEDVLFA
a652-1      CGAEIFHALKKLDCSKGFPTTVGDEGGFAPNLSHKEALQLMVEATEAAGYKAGEDVLFA
              190     200     210     220     230     240

m652-1      LDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLEGLVNEFPIISIEDGMDENDWEGWKLLT
a652-1      LDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLEGLVNEFPIISIEDGMDENDWEGWKLLT
              250     260     270     280     290     300

m652-1      EKLGGRVQLVGDDLFVTNPKILAEGIEKGVANALLVKVNQIGTSETLKAVDLAKRNRYA
a652-1      EKLGGRVQLVGDDLFVTNPKILAEGIEKGVANALLVKVNQIGTSETLKAVDLAKRNRYA
              310     320     330     340     350     360

m652-1      SVMSHRSGETEDSTIADLAVATNCMQIKTGSLSRSDRMAYNQLLRIEELAEAAADYPSK
a652-1      SVMSHRSGETEDSTIADLAVATNCMQIKTGSLSRSDRMAYNQLLRIEELAEAAADYPSK
              370     380     390     400     410     420

m652-1      AAFYQLGKX
a652-1      AAFYQLGKX
              429

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2117>:

```

g653.seq
1  ATGGCGGcgg aaccgatgcg gAtgccggag gtaAcgtaCG GTTTTCCGG
51  ATCGTTCGGG ATGGCGTTTT TGTtgacggt GATGTGCGCt ttgcccAAG
101 CGGCTtcggc ggcctttgcCg gtgATTTTCA TCGGTTCGAG GtcgacgaGG
151 AAaacgTGGC TTTCGGTGCG GCCGGAaacy atgCGCaaac cgCGTttaac
201 caactcttcc gccATGACGG CAGCATTGAT TTTCATTGT TTTGCGTATT
251 GTTTGAactC GGGTTGcaac gcttctTTAA acgctACGGC TttgCGCGCG
301 ATAACGTgca tcaACGGAcc gCCTTGcAGG CTTGGGAAGA TGGAAGAGTT
351 CAGCGCTTTT TCGTGGGTAT TGTCACGGCA CAAATCACA CCGCCGCGAG
401 GCGCGCGTAG GGTTTTGTTG GTGGTAGTGg ttACgaaGtc GCAGaAtggc
451 ACGGGgttag gatattcgcc gccGCGCAACC AgtccgGCAT Ag

```

This corresponds to the amino acid sequence <SEQ ID 2118; ORF 653.ng>:

```

g653.pep
1  MAAEPMRMPE VTYGFSGSFG MAFLLTVMCA LPKAASAALP VIPIGCRSTR
51  RTWLSVRPET MRKPRLTNSS AMTAAALIFTC FAYCLNSGCN ASLNATALAA
101 ITCINGPPCR LGKMEEFSAF SWVLSRHKIT PPRGPRRVW VVVVTKSQNG
151 TGLGYSPPAT SPA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2119>:

```

m653.seq
1  ATGGCAGCGG AGCCGATGCG GATGCCGGAG GTAACGAAGG GTTTTCCGG
51  ATCGTTCGGA ATGGCGTTTT TGTGACGGT GATGTGCGCT TTGCCCAAG
101 CGGCTTCGGC GGCTTGCCG GTAATTTTCA TCGGTTCGAG GTCAACGAGG

```

1042

```

151 AAAACGTGGC TTTCGGTGCG GCCGGAACG ATGCGCAAAC CGCGTTTAAC
201 CAACTCTTCC GCCATGGCGG CTGCATTGAT TTTCATTGT TTTGCGTATT
251 GTTTGAACCT GGGTTGCAAT GCTTCTTTAA ACGCCACGGC TTTGGCGGCG
301 ATAACGTGCA TCAGCGGACC GCCTTGCAAG CTTGGGAAGA TGGAAAGAGT
351 CAACGCTTTT TCGTGGGTAT TGTGCGGCA CAAAATTACG CCGCCGCGAG
401 GACCGCGCAG GCTTTTGTGC CTGCTGGTGG TCACCAACTC GCAGAACGGC
451 ACCGGGTGG GATATTCGCC GCCGGCAACC AGACCGGCAT AG

```

This corresponds to the amino acid sequence <SEQ ID 2120; ORF 653>:

```

m653.pep
1  MAAEPMRMPE VTKGFSGSFG MAFLLTVMCA LPKAASAALP VIFIGCRSTR
51  KTWLSVRPET MRKPRLTNSS AMAAALIFTC FAYCLNSGCN ASLNATALAA
101 ITCISGPPCR LGKMEEFNAF SWVLSRHKIT PPRGPRRLW VVVVTKSONG
151 TGLGYSPPAT RPA*

```

m653/g653 96.9% identity in 163 aa overlap

	10	20	30	40	50	60
m653.pep	MAAEPMRMPEVTGKFSGSFGMAFLLTVMCALPKAASAALPVIFIGCRSTRKTWLSVRPET					
g653	MAAEPMRMPEVTGKFSGSFGMAFLLTVMCALPKAASAALPVIFIGCRSTRKTWLSVRPET					
	10	20	30	40	50	60
	70	80	90	100	110	120
m653.pep	MRKPRLTNSSAMAAALIFTCFAYCLNSGCNASLNATALAAITCISGPPCRLGKMEEFNAF					
g653	MRKPRLTNSSAMTAALIFTCFAYCLNSGCNASLNATALAAITCINGPPCRLGKMEEFSAF					
	70	80	90	100	110	120
	130	140	150	160		
m653.pep	SWVLSRHKITPPRGPRRLWVVVVTKSQNGTGLGYSPPATRPAX					
g653	SWVLSRHKITPPRGPRRLWVVVVTKSQNGTGLGYSPPATSPAX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2121>:

```

a653.seq
1  ATGCGCGCGG AACCGATGCG GATGCCGGAG GTAACGAAGS GTTTTCCCG
51  ATCATTCCGG ATGGCGTTT TGTGACAGT GATGTGCGCT TTGCCCAAAG
101 CAGCTTCGGC GGCTTTGCCG GTAATTTTCA TCGGTTGCAG GTCACGAGG
151 AAAACGTGGC TTTCGGTGCG GCCGGAACG ATGCGCAAAC CGCGTTTAAC
201 CAACTCTTCC GCCATGGCGG CTGCATTGAT TTTCATTGT TTTGCGTATT
251 GTTTGAACCT GGGTTGCAAT GCTTCTTTAA ACGCCACGGC TTTGGCGGCG
301 ATAACGTGCA TCAGCGGCC ACCTTGCAAG CTTGGGAAGA TGGAAAGAGT
351 CAACGCTTTT TCGTGGGTAT TGTGCGGCA CAAAATTACG CCGCCGCGAG
401 GACCGCGCAG GCTTTTGTGG GTGCTGGTGG TAACGAAGTC GCAGAACGGC
451 ACGGATTGG GATATTCGCC GCCGGCAACC AGACCGGCAT AG

```

This corresponds to the amino acid sequence <SEQ ID 2122; ORF 653.a>:

```

a653.pep
1  MAAEPMRMPE VTKGFSGSFG MAFLLTVMCA LPKAASAALP VIFIGCRSTR
51  KTWLSVRPET MRKPRLTNSS AMAAALIFTC FAYCLNSGCN ASLNATALAA
101 ITCISGPPCR LGKMEEFNAF SWVLSRHKIT PPRGPRRLW VVVVTKSQNG
151 TGLGYSPPAT RPA*

```

m653/a653 100.0% identity in 163 aa overlap

	10	20	30	40	50	60
m653.pep	MAAEPMRMPEVTGKFSGSFGMAFLLTVMCALPKAASAALPVIFIGCRSTRKTWLSVRPET					
a653	MAAEPMRMPEVTGKFSGSFGMAFLLTVMCALPKAASAALPVIFIGCRSTRKTWLSVRPET					
	10	20	30	40	50	60
	70	80	90	100	110	120
m653.pep	MRKPRLTNSSAMAAALIFTCFAYCLNSGCNASLNATALAAITCISGPPCRLGKMEEFNAF					
a653	MRKPRLTNSSAMAAALIFTCFAYCLNSGCNASLNATALAAITCISGPPCRLGKMEEFNAF					
	70	80	90	100	110	120
	130	140	150	160		
m653.pep	SWVLSRHKITPPRGPRRLWVVVVTKSQNGTGLGYSPPATRPAX					
a653	SWVLSRHKITPPRGPRRLWVVVVTKSQNGTGLGYSPPATRPAX					

1044

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2127>:

```
a656.seq
1  ATGCCGCGTT TGCTCGGTTT GACTTCTTCG ATGATTTCCA TGCGCGGGAC
51  TTTGGGTGCG CCGGAGAGTG TGCCGGCAGG GAAGGTAGCG GCGAGGATGT
101 CCATGTTGGT CATGCCGTCT TTCAGACGGC CTTCCGACGT GGAACGATG
151 TGCATTACAT GGGAGTATTT TTCAATCACC ATTTTGTCGG TAACTTTGAC
201 TTCGCCGGTT TTA CTGATGCG GGCCGACGTC GTTGCGTCCT AAGTCAATCA
251 ACATGACGTG TTCGGCGATT TCTTTGGCAT CGCTTAACAA ATCTTGTTCTG
301 TTGGCAAGGT CITCGGCGGG GGTTTTGGCG CGCAGGCGCG TGCCGGCGAT
351 GGGCGGACG ATGACATCGT CGCGTTTCGG GCGGACGAGG ATTTCGGGCG
401 AGGAGCCGAC GATGTGGAAA TCGCCGAAAT CGTAG
```

This corresponds to the amino acid sequence <SEQ ID 2128; ORF 656.a>:

```
a656.pep
1  MPRLLGSTSS MISMARTLGA PESVPAGKVA ARMSMLVMPs FRRPSTLETM
51  CITWEYFSIT ILSVTLTSPV LLMRPTSLRP KSINMTCSAI SLASLNKSCS
101 LARSSAGVLP RRRVPAMGRT MTSSRSRRTR ISGEEPTMWK SPKS*

m656/a656 98.6% identity in 144 aa overlap

      10      20      30      40      50      60
m656.pep MPRLLGSTSSMISMARTLGA PESVPAGKVA ARMSMLVMPs FRRPSTLETM CITWEYFSIT
a656.     MPRLLGSTSSMISMARTLGA PESVPAGKVA ARMSMLVMPs FRRPSTLETM CITWEYFSIT
      10      20      30      40      50      60

      70      80      90     100     110     120
m656.pep ILSVTLTSPV LLMRPTSLRP KSINMTCSAI SLASLNKSCS LARSSAGVLP RRRVPAMGRT
a656     ILSVTLTSPV LLMRPTSLRP KSINMTCSAI SLASLNKSCS LARSSAGVLP RRRVPAMGRT
      70      80      90     100     110     120

      130     140
m656.pep ITSLSRSRRTRISGEEPTMWKSPKSX
a656     MTSSRSRRTRISGEEPTMWKSPKSX
      130     140
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2129>:

```
g657.seq
1  ATGAACACAC CCCCCATCCT TCCTCCCGCC ATGCTCGGCA TCCTCGGCGG
51  CGGACAATTa ggcagAATGT TTGCCGTTGC CGCTAAACC ATGGGCTACA
101 AAGTAACCGT TCTCGATCCC GACCCGAATG CGCCGGCGGC GGAATTTGCC
151 GACCGCCATT TGTGCGCGCC GTTTGACGAC CGGGCCGCGT TGGACGAATT
201 GGC AAAATGC GCGGCGGTta cgACCGAATT TGA AAAacgtc aaTGCCGACG
251 CGATGCGCTC TCTGGCAAAG CATAACCAACG TTTCCCCCAG CGGCGACTGC
301 GTGTCCATTG CACAAAACCG CATT CAGGAA AAAGCGTGGA TACGCAAAGC
351 AGGCTTGCAA ACCGCGCCGT ATCAGGCGGT TTGCAAGGCC GAAGACATTA
401 CTGAAGCAAG CGCGCAATTT TTGCCCGGCA TCCTGAAAAC GGCTACGTTG
451 GGCTACGACG GCAAAGGTCA AATCCGCGTC AAAACGTTGG ACGAACTCAA
501 AGCCGCGTTT GCCGAACACG GCGGCGTGGA TTGCGTTTTG GAAAAAATGG
551 TGGACTTGCG CGGCGAGATT TCCGTGATCG TATGCCGTCT GAACGATGAA
601 AACGTGCAAA CCTTCGACCC CGCCGAAAAC ATCCACGAAA ACGGCATCTT
651 GGCTTatteC ATCGTCcccg CGCGGCTGAG TGCCGACGTG CAGCAACAGG
701 CGCGGCAGAC GCGCAACgc tTGGCGGACG AATTGGATTA TGTGCGCgta
751 TTGGCGGTAG AAATGTTTGT TGTGCGGCAC ACACATGAAT TGCTCGTCAA
801 TGA AACCGCC CCGCGCACGC ACAATTCGG CCACCATACG ATAGATGCCT
851 GCGCCGCAGA CCAGTTCCAA CAGCAGGTAC GCATTATGTG CAACctGCCG
901 cccGccgACA CCAAATTATT aTCCCcttgC TGTATGGCGA ATATTTTGGg
951 CGACGTTTGG CAGGAAGATG GCGGCGAACC GGATTGGCTG CCGTGCAGAA
1001 GCCGGCCGAA TGCACACCTG CACCTATACG GAAAAAAAC CGCACAGAAA
1051 GATTCGGAAA TGGGCACTT TaccgTTTTG ACCACCGGAT CCGACaccgC
1101 ATTTCAAGAA GCAAAAAAAC TGCATCAGTC CCTATAA
```

This corresponds to the amino acid sequence <SEQ ID 2130; ORF 657.ng>:

1045

g657.pap

1	MNTPPILPPA	MLGILGGGQL	GRMFAVAAKT	MGYKVIVLDP	DPNAPAAEFA
51	DRHLCAPFDD	RAALDELAKC	AAVTTEFENV	NADAMRSLAK	HTNVSPSGDC
101	VSIAQNRIQE	KAWIRKAGLQ	TAPYQAVCKA	EDITEASAQF	LPGILKTATL
151	GYDGKGQIRV	CTLDELKAAF	AEHGGVDCVL	EKMVDLRGEI	SVIVCRLNDE
201	NVQTFDPAEN	IHENGILAYS	IVPARLSADV	QQQARQTAQR	LADEL DYVGV

1046

251 LAVEMFVVD THELLVNETA PRTHNSGHHT IDACAADQFQ QQVRIMCNLP
 301 PADTKLLSPC CMANILGDVW QEDGGE PDWL PLQSRPNAHL HLYGKKTAKQ
 351 GRKMGHFTVL TTDSDTAFQE AKKLHQSL*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2131>:

m657.seq
 1 ATGAAAAACA TATCTCTTTC TCCGCCCGCC ATGCTTGCCA TCCTCGGCGG
 51 CGGACAATTA GGCAGAAATG TTACCGTTGC CGCCAAAACC ATGGGCTACA
 101 AAGTAACCGT TCTCGACCCC GATCCGACG CGCCGGCAGC AGAATTGACC
 151 GACCGCCATT TGTGCGCGCC GTTTAACGAC CAAGCTGCTT TGGACGAATT
 201 GGCAAAATGC GCGCGGTGA CCACTGAATT TGAAAACGTC AATGCCGATG
 251 CGATGCGCTT TTTGGCAAAA CATACCAATG TTTCCCTAG CGGCGATTGT
 301 AGGCGGATTG CACAAAACCG CATTACAGAA AAGGCATGGA TACGCAAGC
 351 GGGATTGCAA ACCGCGCCGT ATCAAGTGGT TTGTAAGGCT GAAGACATCA
 401 CTGAAGCAAG CGCGCAATTT TTGCCCGCA TCCTGAAAAC GGCTACGTTG
 451 GGCTACGACG GCAAAGGTCA AATCCGCGTA AAAACATTGG ATGAACCTCAA
 501 AGCGCGCTTT GCCGAACACG GCGGCGTGA TTGCGTTTGG GAAAAAATGG
 551 TGGATTTGCG CAGTGAAAT TCCGTAATCG TATGCCGTTT GAACAATGAC
 601 AACGTGCAAA CTTTCGACCC TGCCGAAAAC ATCCACGAAA ACGGCATCTT
 651 GGGTTATGCC ATCGTCCCG CGCGACTGAG TGCCGACGTG CAGCAACAGG
 701 CGCGGCAGAT GCGCAACGC TTGGCGGACG AATTGGATTA TGTCCGCGTA
 751 TTGGCGGTAG AAATGTTTGT TGTCCGTGAC ACGCATGAAT TGGTCGTCAA
 801 CGAAATCGCC CCGCGCCCGC ACAATTCCGG ACACCATACG ATAGATGCCT
 851 GCGCAGCAGA CCAGTTCCAG CAGCAGGTAC GCATTATGTG CAACCTGCCG
 901 CCTGCCGATA CCAAATTACT GAGTTCCTGC TGTATGGCAA ATATTTTGGG
 951 CGACGTTTGG CAGGAAGACG GCGGCGAACC GGATTGGCTG CCCTTGCAAA
 1001 GCCATCCGAA TGCACACCTG CACCTTTACG GCAAAAAAAC CGCGCACAAA
 1051 GGGCGGAAAA TGGGACACTT TACCGTTTAA ACCACCGATT CGGACACCGC
 1101 ATTTCAAGAA GCAAAAAAAC TGCATCAGTC CCTATAA

This corresponds to the amino acid sequence <SEQ ID 2132; ORF 657>:

m657.pep
 1 MKNISLSPPA MLGILGGGQL GRMFTVAAKT MGKVTVLDP DPAPAAEFA
 51 DRHLCAPFND QAALDELAKC AAVTTEFENV NADAMRFLAK HTNVSPSGDC
 101 VAIAQNRIQE KAWIRKAGLQ TAPYQVCKA EDITEASQF LPGILKTATL
 151 GYDGKGQIRV KTLDELKAAF AEHGGVDCVL EKMVDLRSEI SVIVCRLLND
 201 NVQTFDPAEN IHENGILAYS IVPARLSADV QOARQMAQR LADELQYVGV
 251 LAVEMFVVD THELVVNEIA PRPHNSGHHT IDACAADQFQ QQVRIMCNLP
 301 PADTKLLSSC CMANILGDVW QEDGGE PDWL PLQSRPNAHL HLYGKKTAKH
 351 GRKMGHFTVL TTDSDTAFQE AKKLHQSL*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m657/g657 93.9% identity in 378 aa overlap

	10	20	30	40	50	60
m657.pep	MKNISLSPPA	MLGILGGGQL	GRMFTVAAKT	MGYKVTVLDP	DPAPAAEFA	DRHLCAPFND
g657	MNTPLP	PAMLGILGGGQL	GRMFAVA	AKTMGYKVTVLDP	DPNAPAAEFA	DRHLCAPFND
	70	80	90	100	110	120
m657.pep	QAALDELAKC	AAVTTEFENV	NADAMRFLAK	HTNVSPSGDC	VAIAQNRIQE	KAWIRKAGLQ
g657	RAALDELAKC	AAVTTEFENV	NADAMRSLAK	HTNVSPSGDC	VSIAQNRIQE	KAWIRKAGLQ
	130	140	150	160	170	180
m657.pep	TAPYQVCKA	EDITEASQFL	PGILKTATL	GYDGKGQIRV	KTLDELKAAF	AEHGGVDCVL
g657	TAPYQAVCKA	EDITEASQFL	PGILKTATL	GYDGKGQIRV	KTLDELKAAF	AEHGGVDCVL
	130	140	150	160	170	180

1047

	190	200	210	220	230	240
m657.pep	EKMVDLRSEISVIVCRLNNDNVQTFDPAENIHENGILAYSIVPARLSADVQQQARQMAQR					
g657	EKMVDLRGEISVIVCRLNDENVQTFDPAENIHENGILAYSIVPARLSADVQQQARQTAQR					
	190	200	210	220	230	240
	250	260	270	280	290	300
m657.pep	LADEL DYVGV LAVEMFVVGDTHEL VVNEIAPRPHNSGHHTIDACAADQFQQQVRIMCNLP					
g657	LADEL DYVGV LAVEMFVVGDTHELLVNETAPRTHNSGHHTIDACAADQFQQQVRIMCNLP					
	250	260	270	280	290	300
	310	320	330	340	350	360
m657.pep	PADTKLLSSCCMANILGDVWQEDGGE PDWLP LQSHPN AHLHLYGKKT AHKGRKMGHFTVL					
g657	PADTKLLSPCCMANILGDVWQEDGGE PDWLP LQSRPN AHLHLYGKKT AQKGRKMGHFTVL					
	310	320	330	340	350	360
	370	379				
m657.pep	TTDSDTAFQEAKKLHQS LX					
g657	TTDSDTAFQEAKKLHQS LX					
	370					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2133>:

```

a657.seq
1  ATGAAAAACA TATCTCTTTC TCCGCCCGCC ATGCTCGGCA TTCTTGGCGG
51  CGGACAATTA GGCAGAAATG TTA CTGTTGCG TGC CCAAAACC ATGGGGCTACA
101 AAGTAACCGT ACTCGATCCC AACCCGAATG CGCCGGCAGC GGAATTTGCC
151 GACCGCCATT TGTGTGCGCC GTTTGACAAC CAAACCGCTT TGGAAGAATT
201 GGCAAAATGT GCGGCTGTTA CGACCGAGTT CGAAAACGTC AATGCCGATG
251 CGATGCGTTT TCTCGCCAAA CATACCAATG TTTCCCCAGC CGGCGACTGC
301 GTTGCCATCG CGCAAAACCG CATT CAGGAA AAGGCATGGA TACGCAAAGC
351 AGGCCTGCAA ACCGCGCCGT ATCAAGCAAT TTGCAAAGCC GAAGACATCA
401 CTGAAGAAAG CATACAATTT CTGCCCGGCA TCCTGAAAAC CGCTACATTG
451 GGTATGACG GCAAAGGCCA AATCCGCGTC AAAACGTTGG ATGAACTCAA
501 AGCCGCGTTT GCCGAACACC GCGGCGTGGA TTGCGTTTTG GAAAAAATGG
551 TGGACTTGCG CGCGGAAATT TCCGTTATCG TATGCCGTCT GAACAATGAC
601 AACGTGCAAA CTTCGATCC TGCCGAAAAC ATTCACGAAA ACGGTATCCT
651 CGCTACTCC ATCGTCCAG CCCGACTGAG TGCCGACATT CAGCAACAGG
701 CGCGACAAAT GGCGCAGCGT TTGGCCGATG AATTGAACTA CGTCGCGGTA
751 TTGGCGGTAG AAATGTTTGT TGTGCGCGAC ACGCATGAAT TGGTCGTCAA
801 CGAAATCGCG CGCGTCCGC ACAATTCCGG CCACCATACC GTCGACGCCT
851 GCGCGGCAGA CCAATTCAG CAACAGGTCC GCCTGATGTG CAACCTGCCA
901 CCTGCTGACA CCAAATTGCT GAGTTCTTGC TGTATGGCGA ATATTTTGGG
951 CGACGTTTGG CAGGAAGACG GCGGCGAACC GGATTGGTTT CCCCTGCAAA
1001 GCCGCGCCGA CGCGCACCTG CACCTTTACG GCAAAAAAAC CGCGCACAAA
1051 GGGCGGAAAA TGGGACACTT TACCATTTTA AGCACCGATT CGGACACCGC
1101 ATTTCAAGAA GCAAAAAAAC TGCATCAGTC CCTATAA

```

This corresponds to the amino acid sequence <SEQ ID 2134; ORF 657.a>:

```

a657.pep
1  MKNISLSPPA MLGILGGGQL GRMFTVAAKT MGYKVTVLDP NPNAPAAEFA
51  DRHLCAPFDN QTALEELAKC AAVTTEFENV NADAMRFLAK HTNVSPSGDC
101 VAIQNRIQE KAWIRKAGLQ TAPYQAICKA EDITEESIQF LPGILKTATL
151 GYDGKGQIRV KTVDELKAAF AEHRGVDCVL EKMVDLRGEI SVIVCRLNND
201 NVQTFDPAEN IHENGILAYS IVPARLSADI QQQARQMAQR LADELNYVGV
251 LAVEMFVVGDTHEL VVNEIAPRPHNSGHHT VDACAADQFQ QQVRLMCNLP
301 PADTKLLSSC CMANILGDVW QEDGGE PDWF PLQSRPDAHL HLYGKKTAKH
351 GRKMGHFTIL STDSDTAFQE AKKLHQS LX*

```

m657/a657 94.2% identity in 378 aa overlap

	10	20	30	40	50	60
m657.pep	MKNISLSPPA MLGILGGGQL GRMFTVAAKT MGYKVTVLDP DPDA PAAEFADRHL CAPFDN					

[illegible]

g658.seq

This corresponds to the amino acid sequence <SEO ID 2136; ORF 658.ng>:

q658.pcp

1 MVAGIVRARG GFIDEQFMCV ADNKHFYRQY ADIIQFVRQA LRRLPRLLLH
51 VGTQPRGDDG ISQDAVFVDV FGGVEGLHVF IVQTAYDHGN LAAOVHHFFQ

1049

```

101 NAIHAAVFGK RGFEFVQRFQ ADLTFVAVQA RSRFQDAGQK LRACFSNVFG
151 LANRLIRRGL QACFAYPRFF LNAVLCNGHA VAAGGNVGM LQRAHRVGLD
201 VFKFGRNRRR FCQFVQRGPV VKRRAQMAVG KFRRRRIRVG IENGYFVAHG
251 FSGNGKHSAX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2137>:

```

m658.seq
1  ATGGTGTCCG GAATTGTGCG GCGCGGGGCG GATTTCTGTTG ACGACCAATT
51  CATGCGTGTC ACCGACAACA AACATTTCTA CCGCCAATAC GCCGACATAA
101 TCCAATTCGT CCGCCAAGCG TTGCGCCATC TGCCGCGCCT GTTGCTGCAC
151 GTCGGCACTC AGTCGCGCGG GGACGATGGA ATAAGCCAAG ATGCCGTTT
201 CGTGGATGTT TTCGGCAGGG TCGAAAGTTT GCACGTTGTC ATTGTTCAAA
251 CGGCATACGA TTACGGAAAT TTTACTGCGC AAATCCACCA TTTTTCCTAA
301 AACGCAATCC ACGCCGCCGT GTTCGGCAAA CGCGGCTTTG AGTTCATCCA
351 ATGTTTATTAC GCGGATTTGA CCTTGCCGT CGTAGCCCAA CGTAGCCGT
401 TTCAGGATGC CGGGCAAAAA TTGCGCGCTT GCTTCAGTGA TGTCTTCAGC
451 CTTACAAACC ACTTGATACG GCGCGGTTTG CAATCCCGCT TTGCGTATCC
501 ATGCTTTTTC CTGAATGCGG TTTTGTGCAA TCGCCACACA ATCGCCGCTA
551 GGGGAAACAT TGGTATGTTT TGCCAAAAG CGCATCGCAT CGGCATTGAC
601 GTTTTCAAAT TCAGTGGTCA CCGCCGCGCA TTTTGCCAAAT TCGTCCAAAG
651 CAGCTTGGTC GTTAAACGGC GCGCACAAAT GCGGTCGCGC AAATTCTGCT
701 GCCGCGCGCT CCGGATCGGG GTCGAGAACG GTTACTTTGT AGCCCATGGT
751 TTTGCGGCA ACGGTAAACA TTTCGCCTAA

```

This corresponds to the amino acid sequence <SEQ ID 2138; ORF 658>:

```

m658.pep
1  MVSIVRARG DFVDDQFMRV TDNKHFYRQY ADIIQFVRQA LRHLPRLLH
51  VGTQSRGDDG ISQDAVFVDV FGRVESLHV IVQTAYDYG NFTAQIHFFQ
101 NAIHAAVFGK RGFEFIQCFY ADLTFVAVQA RSRFQDAGQK LRACFSNVFG
151 LTNHLIRRGL QSRFAYPCLF LNAVLCNRHT IAARGNIGMF CQKAHRIGID
201 VFKFSGHRRR FCQFVQSSLV VKRRAQMAVG KFCCRRVRIG VENGYFVAHG
251 FGGNGKHSAX

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m658/g658 82.2% identity in 259 aa overlap

	10	20	30	40	50	60
m658.pep	MVSIVRARGDFVDDQFMRVTDNKHFYRQYADIIQFVRQALRHLPRLLHLVGTQSRGDDG					
g658	MVAGIVRARGGFIDEQFMCVADNKHFYRQYADIIQFVRQALRRLPRLLHLVGTQPRGDDG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m658.pep	ISQDAVFVDVFGRVESLHVIVQTAYDYGNTAQIHFFQNAIHAAVFGKRGFEFIQCFY					
g658	ISQDAVFVDVFGGVEGLHVFIVQTAYDHGNLAAQVHHFFQNAIHAAVFGKRGFEFVQRFQ					
	70	80	90	100	110	120
	130	140	150	160	170	180
m658.pep	ADLTFVAVQAQRSRFQDAGQKLACFSDFSLTNHLIRRGLQSRFAYPCLFLNAVLCNRHT					
g658	ADLTFVAVQAQRSRFQDAGQKLACFSNVFGLANRLIRRGLQACFAYPRFFLNAVLCNGHA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m658.pep	IAARGNIGMFCQKAHRIGIDVFKFSGHRRRAFCQFVQSSLVVKRRAQMAVGKFCCRRVRIG					
g658	VAAGGNVGM LQRAHRVGLD VFKFGRNRRRAFCQFVQRGPVVKRRAQMAVGKFRRRRIRVG					
	190	200	210	220	230	240
	250	260				
m658.pep	VENGYFVAHGFGGNGKHSAX					

1050

```

          :|||||:|||||
g658      IENGYFVAHGFSNGKHSAX
          250      260

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2139>:

```

a658.seq
1   ATGGTGGCCG GAATTGTGCG GACGCGCGCG GATTCGTTG ACGACCAATT
51  CATGCGTGTC GCCGACAACA AACATTCTA CCGCCAATAC GCCGACGTAG
101 TTCAATTCAT CGGCCAAACG CTGCGCCATT TGTCGCGCCT GTTGCTGAAT
151 GTCGGCACTC AGTCGGGCTG GGACGATGGA GTAGGCGAGG ATACCGTTTT
201 CGTGAATGTT TTCGGCAGGA TCGAAAGTTT GCACGTTGTC ATTGTTCAGA
251 CGGCATACGA TAACGGAAAT TTCGCGCGCG AAGTCCACCA TTTTTCCTAA
301 AACGCAATCC ACGCCGCGGT GTTCGGCAAA CGCGGCTTTG AGTTCATCCA
351 CCGTTTGTAC GCGGATTTGG CCTTTGCCGT CATAGCCCAA TGTAGCGGTT
401 TTCAGGATGC CGGGCAGAAA TTGTATGCTT TCTTCAGTGA TGTCTTCGGC
451 TTTGCAAATT GCTTGATACG GCGCGGTTTG CAGGCCTGCT TTGCGTATCC
501 ATGCCTTTTC CTGAATGCGG TTTTGCGCGA TGGCAACGCA GTCGCCGCTG
551 GGGGAAACAT TGGTATGTTT GCGAGAAAA CGCATCGCAT CGGCATTGAC
601 GTTTTCGAAC TCGGTCGTAA CAGCCGCACA TTTTGCCAAT TCTTCCAAAG
651 CGGTTTGGTT GTCAAACGGC GCACACAAAT GCGGTCGGC AAATTCGCT
701 GCCGCGCAT TCGGTTGGG ATCGAGTACG GTTACTTTGT AGCCCATGGT
751 TTTGGCAGCA ACAGTAAACA TTCTGCCTAA

```

This corresponds to the amino acid sequence <SEQ ID 2140; ORF 658.a>:

```

a658.pep
1   MVAGIVRTRR DFVDDQFMRV ADNKHFYRQY ADVVQFIGQT LRHLSRLLLN
51  VGTQSGWDDG VGEDTVEFNV FGRIESLHV IVQTAYDNGN FAAQVHHFFQ
101 NAIHAAVFGK RGFEFIHRFD ADLAFAVIAQ CSGFQDAGQK LYAFFSDVFG
151 FANCLIRRLG QACFAYPCLF LNAVLRDNGA VAAGGNIGMF GEKTHRIGID
201 VFELGRNSRT FCQFFQSGLV VKRRTQMAVG KFCRRIRVIG IEYGYFVAHG
251 FGSNSKHSAS*

m658/a658      75.3% identity in 259 aa overlap

          10      20      30      40      50      60
m658.pep      MVSGIVRARGDFVDDQFMRVTDNKHFYRQYADIIQFVRQALRHLRLLLVGTQSRGDDG
a658           ||:||||:| |||||:|||||:|||||:|||||:||||:|: |||| ||||:|||| |||
          10      20      30      40      50      60
m658.pep      ISQDAVFVDVFGRVESLHVIVQTAYDYGNETAQIHFFQNAIHAAVFGKRGFEFIQCFY
a658           ::||:||||:|||||:|||||:|||||:|||||:|||||:|||||: |||
          70      80      90      100     110     120
m658.pep      VGEDTVEFNVFGRIESLHVIVQTAYDNGNFAAQVHHFFQNAIHAAVFGKRGFEFIHRFD
a658           70      80      90      100     110     120
          130     140     150     160     170     180
m658.pep      ADLTFVAVVAQRSRFODAGQKLACFSDFVSLTNHLIRRLQSRFAYPCLFLNAVLCNRHT
a658           |||:||||:| | ||||| | |||||:| | |||||: |||||: |||||: |||
          130     140     150     160     170     180
m658.pep      ADLAFAVIAQCSGFQDAGQKLYAFFSDVFGFANCLIRRLQACFAYPCLFLNAVLRDNGA
a658           130     140     150     160     170     180
          190     200     210     220     230     240
m658.pep      IAARGNIGMFQKAHRIGIDVFKFSGHRRAFQCFVQSSLVVKRRAQMAVGKFCRRVRIG
a658           :|| ||||| :||:|||||:|: : ||:|||| ||:|||||:||||| |||:|:|
          190     200     210     220     230     240
m658.pep      VAAGGNIGMFGEKTHRIGIDVFELGRNSRTFCQFFQSGLVVKRRTQMAVGKFCRRIRVIG
a658           190     200     210     220     230     240
          250     260
m658.pep      VENGYFVAHGFGGNGKHSAX
a658           :| |||||:|:|||||
          250     260
a658           IEYGYFVAHGFGSNGKHSAX
          250     260

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2141>:

1051

```

g661.seq
1  ATGCACATCG GCGGTATTAT TATCGACAAC CCCATCGCAC TTGCGCCGAT
51  GCGGGGCATT GCGGACAAAC CCTTCCGCCG CCTCTGTCGG GCGTTTGGCG
101 CAGGTTGGGC GGTGTGCGAA ATGCTGGCCA GCGATCCGAC GCTCAGGAAT
151 ACCGGA AAAA CCtgcaccg cagtgaTTTt gccgatgaag gCGGCATCGT
201 TGCCGTGCAG ATTGCCGGCA GCGACCCcga acaGATGGCG Gatgcggcgc
251 gttacAACGT CCGACTCGGG GCGCAGGTCA TCGACATcaa TATGGGCTGC
301 cccgccaaGA AAGTGTGCAA CGTCCAAGCC GGTAGCGCgc tGATGCAGGA
351 CGAGccgctg gttgcCgcca tTTtggaggc ggtggtcAAG GCGGCGGcg
401 TACCCGTTAC cctCAAAACc cgtTtgggtt ggcacgacga cgatcaaaac
451 ctgcCcgccg tcgccaaaat cgccgaagat tgcggcattg ccgccCttgc
501 cgtttcacgg gcgCGCgcgC ACGCAAATGT ACAAAGGCCG GCGcGTTAC
551 Gaactcatcg CCGAGACCAA AAGccgTCTG AACATCCCGG cctGggtCAA
601 CCGCGACATC actTCgcgcg AAAAAGCCGC CGccgTCCTC AAACAAACCG
651 CCGCCGACGG CATCATGATA GGGCGCGGCG CGCAAGGCAG GCCGTGGTTT
701 TTCCGCGATT TGAAGCATTG TGCCGAACAC GCGGTTTTAC CGCCTGCCTT
751 GAGTTTGGCA GAATGCAGAG CCGCCATTTT GAACACATC CGCGCCATGC
801 ACGCGTTTTA TGGTGAGACC GTCGGTGTGC GCATCGCACG CAAACACATA
851 GGCTGGTACA TCGCGGAAAT GCCCGACGGC GAACAGGCCG GCGTGA

```

This corresponds to the amino acid sequence <SEQ ID 2142; ORF 661.ng>:

```

g661.pep
1  MHIGGYFIDN PIALAPMAGI ADKPFRRLCR AFGAGWAVCE MLASDPTLRN
51  TGKTLHRSDF ADEGGIVAVQ IAGSDPEQMA DAARYNVGLG AQVIDINMGC
101 PAKKVCNVQA GSALMQDEPL VAAILEAVVK AAGVPVTLKT RLGWHDDQDN
151 LPVAKIAED CGIAALAVPR ARAHANVQRR GALRTHRRDQ KPSEHPGLGQ
201 RRHHFAAKSR RRPQTNRRRR HHDARRARQ AVVFPRFZAL CRTRRFTACL
251 EFGRMQSRHF EPHPRHARVL WXDRRCAHRT QTHRLVHRRN ARRTTGAA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2143>:

```

m661.seq
1  ATGCACATCG GCGGCTATTT TATCGACAAC CCCATCGCAC TTGCGCCGAT
51  GCGGGGCATT ACCGACAAAC CGTTCGCCCG ACTTTGCCGA GATTTTGGCG
101 CAGGTTGGGC GGTGTGCGAA ATGCTGACCA GCGACCCGAC GCTCAGAAAT
151 ACTAGAAAAA CCTTGACCG CAGCGATTTT GCCGATGAAG GCGGCATTGT
201 TGCCGTGCAG ATTGCCGGAA GCGATCCGCA GCAGATGGCG GATGCCGCGC
251 GTTACAACGT CAGCCTTGGG GCGCAGCTTA TCGACATCAA CATGGGCTGT
301 CCCGCTAAAA AAGTCTGCAA GTCCAAGCC GGTAGCGCGC TGATGCAGAA
351 CGAGCCGCTG GTTGCCGCCA TTTTGAAGC CGTCGTCCGT GCGGCAGGCG
401 TACCCGTTAC CCTCAAAACc CGTTTGGGTT GGCACGACGA CCATCAAAAC
451 CTGCCCCTCA TCGCCAAAAT CGCCGAAGAT TGCGGCATCG CCGCCCTTGC
501 CGTCC.AC GG ACGCACGCGT ACGCAAATGT ACAAAGGCCG A3CGCGTTAC
551 GAACTCATCG CCGAAACCAA ATGCCGTCTG AACATCCCGG TCTGGGTCAA
601 CGCGGACATT ACTTCGCCGC AAAAAGCCCA AGCCGTCCTC AAACAAACCG
651 CCGCCGACGG CATTATGATA GGGCGCGGCG CGCAAGGCAG GCCGTGGTTC
701 TTCCGCGATT TGAACATTA TGCCGAACAC GGTGTTTTGC CGCCTGCCTT
751 GAGTTTGGCA GAATGCGCGC CCGCTATTTT GAACACATC CGCGCCATAC
801 ACGCGTTTTA CGCGACACC GCGGTGTGC GCATCGCACG CAAACACATA
851 GGCTGGTACA TCGACGAAAT GCCCGACGGC GAACAGACAC GTCGTGA

```

This corresponds to the amino acid sequence <SEQ ID 2144; ORF 661>:

```

m661.pep
1  MHIGGYFIDN PIALAPMAGI TDKPFRRLCR DFGAGWAVCE MLTSDPTLRN
51  TRKTLHRSDF ADEGGIVAVQ IAGSDPQOMA DAARYNVSLG AQLIDINMGC
101 PAKKVCNVQA GSALMQNEPL VAAILEAVVR AAGVPVTLKT RLGWHDDHQN
151 LPVIAKIAED CGIAALAVXR THAYANVQRR SALRTHRRNQ MPSEHPGLGQ
201 RRHYFAAKSP SRPQTNRRRR HYDRARRARQ AVVLPREFEL CRTRCFAACL
251 EFGMRRRRYF EPHPRHTRVL RRHRRCAHRT QTHRLVHRRN ARRTDTS*

```

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

m661/g661 88.5% identity in 295 aa overlap

1052

	10	20	30	40	50	60
m661.pep	MHIGGYFIDNPIALAPMAGITDKPFRRLCRDFGAGWAVCEMLTSDPTLRNTRKTLHRSDF					
g661	MHIGGYFIDNPIALAPMAGIADKPFRRLCRAFGAGWAVCEMLASDPTLRNTGKTLHRSDF					
	10	20	30	40	50	60
m661.pep	70	80	90	100	110	120
	ADEGGIVAVQIAGSDPQQMADAARYNVSLGAQLIDINMGCPAKKVCNVQAGSALMQNEPL					
g661	ADEGGIVAVQIAGSDPEQMADAARYNVGLGAQVIDINMGCPAKKVCNVQAGSALMQDEPL					
	70	80	90	100	110	120
m661.pep	130	140	150	160	170	180
	VAAILEAVVRAAGVPVTLKTRLGWHDHQNLPVIAKIAEDCGIAALAVXRTHAYANVQRR					
g661	VAAILEAVVKAAGVPVTLKTRLGWHDHQNLPVAKIAEDCGIAALAVPRARAHANVQRR					
	130	140	150	160	170	180
m661.pep	190	200	210	220	230	240
	SALRTHRRNOMPSEHPGLGQRRHYFAAKSPSRPQTNRRRRHYDRARRARQAVVLPREFETL					
g661	GALRTHRRDQKPSHPGLGQRRHHFAAKSRRRPQTNRRRRHHDARRARQAVVFPREFEAL					
	190	200	210	220	230	240
m661.pep	250	260	270	280	290	299
	CRTRCFAACLEFGRMRRRYFEPHPRHTRVLRHRRCAHRTQTHRLVHRRNARRRTDTSX					
g661	CRTRRFTACLEFGRMQSRHFEPHPRHARVLWXDRCAHRTQTHRLVHRRNARRRTGAAX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2145>:

```

a661.seq
1  ATGCACATCG GCGGCTATTT TATCGACAAC CCCATCGCAC TTGCGCCGAT
51  GCGCGGCATT ACCGACAAAC CGTTCGCCCG ACTTTGCCGA GATTTTGCGG
101 CAGGTTGGGC GGTGTGCGAA ATGCTGACCA GCGACCCGAC GCTCAGAAAT
151 ACTAGAAAAA CCTGCGACCG CAGCGATTTT GCCGATGAAG GCGGCATTGT
201 TGCCGTGCAG ATTGCCGGAA GCGATCCGCA GCAGATGGCG GATGCCGCGC
251 GTTACAACGT CAGCCTTGGG GCGCAGCTTA TCGACATCAA CATGGGCTGT
301 CCGCTAAAAA AAGTCTGCAA TGTCCAAGCC GGTAGCGCGC TGATGCAGAA
351 CGAGCCGCTG GTTGCCGCCA TTTTGAGGCG GGTGGTCAA GCGGCGGGCG
401 TACCCGTAC CCTCAAAACC CGTTGGGTT GGCACGACGA CCATCAAAAC
451 CTGCCCGTCA TCGCCAAAAT CGCCGAAGAT TGCGGCATTG CCGCCCTTGC
501 CG.TCCACGG ACGCACGCGC ACGCAAATGT ACAAAGGCGA AGCGGCTTAC
551 GACCTGATTG CCGAAACCAA ATGCCGTCTG AACATCCCGG TCTGGGTCAA
601 CCGCGACATT ACCTCGCCGC AAAAAGCCCA AGCCGTCTC AAACAAACCG
651 CCGCAGACGG CATTATGATA GGGCGCGGCG CGCAAGGCAG ACCGTGTTTC
701 TTCCGCGATT TGAACATTA CGCCGAACAC GGTGTTTAC C3CCTGCCTT
751 GAGTTTGGA GAATGTACCG CCACTATTTT GAACCATATC CGAGCCATGC
801 ACGCGTTTTA CGCGCACACC GCCGGTGTGC GCATCGCACG CAAACACATA
851 GGCTGGTACA TCGACGAAAT GCCCACGGC GAACAGACAC GTCGTGA

```

This corresponds to the amino acid sequence <SEQ ID 2146; ORF 661.a>:

```

a661.pep
1  MHIGGYFIDN PIALAPMAGI TDKPFRRLCR DFGAGWAVCE MLTSDPTLRN
51  TRKTLHRSDF ADEGGIVAVQ IAGSDPQQMA DAARYNVSLG AQLIDINMG
101 PAKKVCNVQA GSALMQNEPL VAAILEAVVK AAGVPVTLKT RLGWHDHQN
151 LPVIAKIAED CGIAALAXPR THAHANVQRR SGLRPDCRNQ MPSEHPGLGQ
201 RRHYLAAKSP SRPQTNRRRR HYDRARRARQ TVVLPREFETL RTRRCFTACL
251 EFGMRMYRHYF EPHPSHARVL RRHRRCAHRT QTHRLVHRRN ARRRTDTS*

```

m661/a661 94.6% identity in 298 aa overlap

	10	20	30	40	50	60
m661.pep	MHIGGYFIDNPIALAPMAGITDKPFRRLCRDFGAGWAVCEMLTSDPTLRNTRKTLHRSDF					

1053

```

a661      MHIGGYFIDNPIALAPMAGITDKPFRRLCRDFGAGWAVCEMLTSDPTLRNTRKTLHRSDF
           10      20      30      40      50      60

           70      80      90      100     110     120
m661.pep  ADEGGIVAVQIAGSDPQQMADAARYNVSLGAQLIDINMGCPAKKVCNVQAGSALMQNEPL
           |||||
a661      ADEGGIVAVQIAGSDPQQMADAARYNVSLGAQLIDINMGCPAKKVCNVQAGSALMQNEPL
           70      80      90      100     110     120

           130     140     150     160     170     180
m661.pep  VAAILEAVVRAAGVPVTLKTRLGWHDHQNLPVIAKIAEDCGIAALAVXRTHAYANVQRR
           |||||
a661      VAAILEAVVKAAGVPVTLKTRLGWHDHQNLPVIAKIAEDCGIAALAXPRTHAHANVQRR
           130     140     150     160     170     180

           190     200     210     220     230     240
m661.pep  SALRTHRRNQMPSEHPGLGQRRHYFAAKSPSRPQTNRRRRHYDRARRARQAVVLPFRFETL
           |::|
a661      SGLRPDCRNQMPSEHPGLGQRRHYLAAKSPSRPQTNRRRRHYDRARRARQTVVLPFRFETL
           190     200     210     220     230     240

           250     260     270     280     290     299
m661.pep  CRTRCFAACLEFGRMRRRYFEPHPRHTRVLRHRHRCARHTQTHRLVHRRNARRRDTSTX
           |||||
a661      RRTRCFTACLEFGRMYRHYFEPHPSHARVLRHRHRCARHTQTHRLVHRRNARRRDTSTX
           250     260     270     280     290

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2147>:

```

g663.seq
1  ATGTGTACCG AGATGAAATT TATATTTTTT GTACTGTATG TTTTGCAGTT
51  TCTGCCGTTT GCGCTGCTGC ACAAGATTGC CGGCCTGATC GSTTCGCTTG
101 CCTACCTTCT GGTCAAACCG CGCCGCCGTA TCGGCGAAAT CAATTIGGCA
151 AAATGTTTTT CCGAATGGGA CGAAGAAAAG CGTAAAACCG TGTGAAACA
201 GCATTTCAA CACATGGCAA AACTGATGCT CGAATACGGC TTATATTGGT
251 ACGCGtctGC CAAATGCCTG AAATCGCTGG TGCCTACCG CAATAAGCAT
301 TATTTGGACG ACGCGCTGGC GCGGGGGGAA AAAGTCATCA TCCTGTACCC
351 GCACTTTACC GCGTTCGAGA TGGCGGTGTA CGCGCTTAAT CAGGATGTCC
401 CGCTGATCAG TATGTATTCC CACCAAAAAA ACAAGATATT GGACGAACAG
451 ATTTTGAAAg gccgcaACCG CTATCACAAC GTCTTCCTTA TCGGGCGCAC
501 CGAagggtcg cgCGCCctcg TCAAACAGTT CCGCAAAAGC AGTGCGCCGT
551 TCCTGTATCT GCCCGATCAG GATTTTCGAC GCAACAATTC GGTTTTGTG
601 GATTTTTTCG GCATtcagaC GGCAACGATT ACCGGCTTGA GCCGCATTGC
651 CCGCCTTGCA AATGCAAAAG TGATACCGC CATTCCGTC CGCGAGCGCG
701 ACAATACGGT TACATTGCAA TTCTATCCG CTTGGAAATC CTTCCGAGT
751 GAAGACGCGC AAGCCGACGC GCAACGTATG AACCGCTTGA TCGAAGAACG
801 CGTGCGCGAA CACCCGGAAC AATATTTCTG GCTGCACAAG CGTTTCAAAA
851 CCCGTCCGGA AGGCAGCCCC GATTTTTACT GA

```

This corresponds to the amino acid sequence <SEQ ID 2148; ORF 663.ng>:

```

g663.pep
1  MCTEMKFIFF VLYVLOFLPF ALLHKIAGLI GSLAYLLVKP RRRIGEINLA
51  KCFPEWDEEK RKTVLKQHFH HMAKLMLEYG LYWYASAKCL KSLVRYRNKH
101 YLDDALAGE KVILYPHFT AFEMAVYALN QDVPLISMYS HQKNKILDEQ
151 ILKGRNRYHN VELIGRTEGL RALVKQFRKS SAPFLYLPDQ DFRNNSVVF
201 DFFGIQTATI TGLSRIAALA NAKVIPAI PV READNTVTIQ FYPAWSFSP
251 EDAQADAQRM NRFIEERVRE HPEQYFWLHK RFKTRPEGSP DFY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2149>:

```

m663.seq
1  ATGTGTATCG AGATGAAATT TATATTTTTT GTACTGTATG TTTTGCAGTT
51  TCTGCCGTTT GCGCTGCTGC ACAAGATTGC CGACCTGACG GGTTCGCTTG
101 CCTACCTTCT GGTCAAACCG CGCCGCCGTA TCGGCGAAAT CAATTIGGCA
151 AAATGTTTTT CCGAATGGAG TGAGGAAAAG CGTAAAACCG TGTGAAACA

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1054

```

201 GCATTTCAAA CACATGGCGA AACTGATGTT GGAATACGGT TTATATTGGT
251 ACGCGCCTGC CGGACGTTTG AAATCGCTGG TGGCTACCG CAATAAGCAT
301 TATTTGACG ACGCGCTGGC GCGGGGGGAA AAAGTCATCA TCCTGTATCC
351 GCACTTCACC GCGTTCGAGA TGGCGGTGTA CGCGCTTAAT CAGGATATCC
401 CGCTGATCAG TATGTATTCC CATCAAAAAA ACAAGATATT GGACGAACAG
451 ATTTTGAAAG GCCGCAACCG CTATCACAAC GTCTTCCTTA TCGGGCGCAC
501 CGAAGGGCTG CGCGCCCTCG TCAAACAGTT CCGCAAAAGC AGCGCGCCGT
551 TTCTGTATCT GCCCGATCAG GATTTCGGAC GCAACGATTC GGTTTTGTG
601 GATTTTTTCG GTATTTCAGC GGCAACGATT ACCGGATTGA GCCGCATTGC
651 CGCGCTTGCA AATGCAAAAG TGATACCCGC CATTCCCGTC CGCGAGGCAG
701 ACAATACGGT TACATTGCAT TTCTACCCCTG CTGGGAAATC CTTCCGGGT
751 GAAGACGCGA AAGCCGACGC GCAGCGCATG AACCGTTTGA TCGAAGACAG
801 GGTGCGCGAA CATCCGGAAC AATATTTTGT GCTGCACAAG CGTTTAAAAA
851 CCCGTCCGGA AGGCAGCCCC GATTTTACT GA

```

This corresponds to the amino acid sequence <SEQ ID 2150; ORF 663>:

```

m663.pep
1  MCIEMKFIFF VLYVLQFLPF ALLHKIADLT GLLAYLLVKP RRRIGEINLA
51  KCFSEWSEK RKTVLKQHPK HMAKLMLEYG LYWYAPAGRL KSLVRYRNKH
101 YLDDALAAGE KVILYPHFT AFEMAVYALN QDIPLISMYS HQKNKILDEQ
151 ILKGRNRYHN VFLIGRTEGL RALVKQFRKS SAPFLYLPDQ DFGRNDSVFE
201 DFFGIQTATI TGLSRIAALA NAKVIPAI PVREADNTVT LH FYPAWSFPFG
251 EDAKADAQRM NRFIEDRVRE HPEQYFWLHK RFKTRPEGSP DFY*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m663/g663 94.9% identity in 293 aa overlap

m663.pep	10	20	30	40	50	60
	MCIEMKFIFFVLYVLQFLPFALLHKIADLTGLLAYLLVKPRRRIGEINLAKCFSEWSEK					
g663	10	20	30	40	50	60
	MCTEMKFIFFVLYVLQFLPFALLHKIAGLIGSLAYLLVKPRRRIGEINLAKCFPEWDEEK					
m663.pep	70	80	90	100	110	120
	RKTVLKQHPKHKMAKLMLEYGLYWYAPAGRLKSLVRYRNKHLYLDDALAAGEKVILYPHFT					
g663	70	80	90	100	110	120
	RKTVLKQHPKHKMAKLMLEYGLYWYASAKCLKSLVRYRNKHLYLDDALAAGEKVILYPHFT					
m663.pep	130	140	150	160	170	180
	AFEMAVYALNQDIPLISMYS HQKNKILDEQILKGRNRYHN VFLIGRTEGLRALVKQFRKS					
g663	130	140	150	160	170	180
	AFEMAVYALNQDVPLISMYS HQKNKILDEQILKGRNRYHN VFLIGRTEGLRALVKQFRKS					
m663.pep	190	200	210	220	230	240
	SAPFLYLPDQDFGRNDSVFEVDFFGIQTATITGLSRIAALANAKVIPAI PVREADNTVT LH					
g663	190	200	210	220	230	240
	SAPFLYLPDQDFGRNDSVFEVDFFGIQTATITGLSRIAALANAKVIPAI PVREADNTVT LQ					
m663.pep	250	260	270	280	290	
	FYPAWSFPFGEDAKADAQRMNRFIEDRVREHPEQYFWLHKRFKTRPEGSPDFYX					
g663	250	260	270	280	290	
	FYPAWSFPSEDAQADAQRMNRFIEERVREHPEQYFWLHKRFKTRPEGSPDFYX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2151>:

```

a663.seq
1  ATGTGTATCG AGATGAAATT TATATTTTTT GTACTGTATG TTTTGCACTT
51  TCTGCCGTTT GCGCTGCTGC ACAAACCTGC TGATCTGACA GGCTTGCTCG
101 CCTACCTTTT GGTCAAACCC CGCCGCCGTA TCGGCGAAAT CAATTGGCA

```

1055

```

151 AAATGCTTTC CCGAGTGGGA CGGAAAAAAG CGTAAACCG TGTGAAACA
201 GCATTTCAA CATATGGCGA AACTGATGTT SGAATACGGT TTATATTGGT
251 ACGCGCCCGC CGGGCGTTTG AAATCACTGG TCGGCTACCG CAACAAACAT
301 TATTTGGACG ACGCTCTGGC GGCAGGGGAA AAAGTCATCA TCCTGTATCC
351 GCAC TTCACC GCGTTCGAGA TGGCGGTGTA CGCGCTCAAT CAGGATGTTT
401 CGCTGATCAG TATGTATTCC CACCAAAAAA ACAAGATATT GGACGAACAG
451 ATTTTGAAAG GCGCAACCG CTATCACAAC GTTTTCCTTA TCGGGCGCAC
501 CGAAGGGCTG CGCGCCCTCG TCAACACAGT CCGCAAAAGC AGCGCGCCGT
551 TTCGTATCT GCCCGATCAG GATTTCGGAC GCAACGATTC GGTTTTTGTC
601 GATTTCCTCG GTATTCGGAC GGCAACGATT ACCGGCTTGA CCCGATTGTC
651 CGCGCTTGA AATGCAAAAG TGATACCCGC CATCCCTGTC CGCGAGGCGG
701 ACAATACGGT TACATTGCAT TTCTACCCTG CTGCGGAATC CTTTCCGAGT
751 GAAGATGCGC AGCGCGACGC GCAGCGCATG AACCCTTTTA TCGAGGAACG
801 CGTGC CGAA CATCCGAGC AGTATTTTGT GCTGCACAAG CGTTTCAAAA
851 CCCGTCCGA AGGCAGCCCC GATTTTACT GA

```

This corresponds to the amino acid sequence <SEQ ID 2152; ORF 663.a>:

```

a663.pep
1  MCIEMKFIFF VLYVLQFLPF ALLHKLADLT GLLAYLLVKP RRRIGEINLA
51  KCFPEWDGKK RRTVLKQHFH HMAKLMLEYG LYWYAPAGRL KSLVRYRNKH
101 YLDDALAAGE KVIIILYPHT AFEMAVYALN QDVPLISMYS HQKNKILDEQ
151 ILKGRNRYHN VFLIGRTEGL RALVKQFRKS SAPFLYLPDQ DFGNDSVFEV
201 DFFGIRTTAT TGLSRIAALA NAKVIPAIPV READNTVTLH FYPAWESFBS
251 EDAQADAQRM NRFIEERVRE HPEQYFWLHK RFKTRPEGSP DFY*

m663/a663 96.2% identity in 293 aa overlap

10 20 30 40 50 60
m663.pep MCIEMKFIFFVLYVLQFLPFALLHKLADLTGLLAYLLVKPRRRIGEINLAKCFSEWSEEK
a663 MCIEMKFIFFVLYVLQFLPFALLHKLADLTGLLAYLLVKPRRRIGEINLAKCFPEWDGKK
10 20 30 40 50 60

70 80 90 100 110 120
m663.pep RRTVLKQHFHMAKLMLEYGLYWYAPAGRLKSLVRYRNKHLYDDALAAGEKVIIILYPHT
a663 RRTVLKQHFHMAKLMLEYGLYWYAPAGRLKSLVRYRNKHLYDDALAAGEKVIIILYPHT
70 80 90 100 110 120

130 140 150 160 170 180
m663.pep AFEMAVYALNQDIPLISMYS HQKNKILDEQILKGRNRYHNVFLIGRTEGLRALVKQFRKS
a663 AFEMAVYALNQDVPLISMYS HQKNKILDEQILKGRNRYHNVFLIGRTEGLRALVKQFRKS
130 140 150 160 170 180

190 200 210 220 230 240
m663.pep SAPFLYLPDQDFGRNDSVFEVDFFGIQTATITGLSRIAALANAKVIPAIPVREADNTVTLH
a663 SAPFLYLPDQDFGRNDSVFEVDFFGIRTATITGLSRIAALANAKVIPAIPVREADNTVTLH
190 200 210 220 230 240

250 260 270 280 290
m663.pep FYPAWKSFPGEDAKADAQRMNRFIEDRVREHPEQYFWLHKRFKTRPEGSPDFYX
a663 FYPAWESFSEDAQADAQRMNRFIEERVREHPEQYFWLHKRFKTRPEGSPDFYX
250 260 270 280 290

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2153>:

```

g664.seq
1  ATGATACATC CGCACCACCT CCGCGCCTTT TTCATAAACG GTCATGGTGT
51  AGAAATGTGT CATCTCTCTCA TAGCTGACgg gCGCACCGG ATGGGCGGTC
101 GGGCCTGCGT CTTCCGGGGA CTGGTCTTGG CGCAGCAGGC GGATGTTCTC
151 GATCGGCGC ACGCGCGGC CGGCGCGGTC GCCGGAAAAC TCTTGGTCGC
201 GGAACACGGT CAGCCCTTCC TTCAGCGAAA GCTGGAACCA GTCGCGGCG
251 GTTACGCGGT TGCCCCCTCA GTTGTGAAA TATTCGTGTC CGACCACGGA
301 TTCAATGCCT TCGAAATCGG TATCGGTGGC GGTGCGGCTG TCGGCGAGGA
351 CGAACTTGGT GTTAAAAATG TTCAAACCTT GTTTTCCAT CGCGCCATA
401 TTGAAATCGC CTACGCGGAC GACCATGAaa atatccaagt cataTTCcaa
451 cCggaagcgc gtttcgtcCc acttcatcgC gTTTTTCAA cgaTTCCACG
501 GCAAAGCCGA CCTTGGGTTT GTCCGCTTCG GTGGTGTAaa ACTCGATTTT

```


1056

551 GA

This corresponds to the amino acid sequence <SEQ ID 2154; ORF 664.ng>:

g664.pep

```

1  MIHPHHFRAF FINGHGVEIV HLLIADGAHR MGRACVFGE LVLAQQADV
51  DAAHGAAGAV AGKLLVAEHG QPFLQRKLEP VAAGYAVARP VVEIFVSDHG
101 FNAFEIGIGG GAAVGEDELG VKNVQTLVFH RAHIEIAYGD DHENIQVIFQ
151 PEARFVPLHR VFSTIPRQSR PWVCPLRWCK TRF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2155>:

m664.seq

```

1  GTGATACATC CGCACTACTT CCGCGCCTTT TTCATAAACG GTCATGGTGT
51  AGAAATTGTT CATCTCCTCA TAGCTGGCGG GCGCACCAGG ATGGGCGGTC
101 GGGCCTGCGT CTTCGGGGAA CTGGTGCTGG CGCAGCAGGC GGATGTTTTC
151 GATGCGGCGC ACGGCGCGGC TGGCGCGGTC GCCGGAAAAT TCTTGGTCGC
201 GGAACACGGT CAGCCCTTCC TTCAGCGAAA GCTGGAACCA GTCGCGGCAG
251 GTTACGCGGT TGCCCGTCCA GTTGTGAAA TACTCGTGTC CGACCACGGA
301 TTCGATGCCT TCGAAATCGG TATCGGTGGC GGTGCGGCTG TCGGCAAGGA
351 CGAACTTGGT GTTAAAGATG TCAAAACCTT TGTTTTCCAT CGCGCCATA
401 TTGAAATCGC CCACGGCGAC GACCATGAAA ATATCCAAGT CGTATTCCAA
451 ACCGAAGCGC GTTTCGTCCC ATTTTCATGC GTTTTTT.CAA CGATTCCACG
501 GCAAAGCCGA CCTTGGGCTT GTCCGCTTCG GTGGTGTAAG ACTCGATTTT
551 GA

```

This corresponds to the amino acid sequence <SEQ ID 2156; ORF 664>:

m664.pep

```

1  VIHPHYFRAF FINGHGVEIV HLLIAGGAHR MGRACVFGE LVLAQQADV
51  DAAHGAAGAV AGKFLVAEHG QPFLQRKLEP VAAGYAVARP VVEILVSDHG
101 FDAFEIGIGG GAAVGKDELG VKDVQTLVFH RAHIEIAHGD DHENIQVVFQ
151 TEARFVFFHR VFXTIPRQSR PWACPLRWCK TRF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m664/g664 91.8% identity in 183 aa overlap

	10	20	30	40	50	60
m664 .pep	VIHPHYFRAFF	FINGHGVEIV	HLLIAGGAHR	MGRACVFGE	LVLAQQADV	FDAAHGAAGAV
	: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :
g664	MIHPHHFRAFF	FINGHGVEIV	HLLIADGAHR	MGRACVFGE	LVLAQQADV	LDAAHGAAGAV
	10	20	30	40	50	60
m664 .pep	70	80	90	100	110	120
	AGKFLVAEHG	QPFLQRKLE	FVAAGYAVAR	PVVEILVSDH	GDFAFEIGIG	GGAAGVKGDELG
	: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :
g664	AGKLLVAEHG	QPFLQRKLE	FVAAGYAVAR	PVVEIFVSDH	GFNAFEIGIG	GGAAGVGEDELG
	70	80	90	100	110	120
m664 .pep	130	140	150	160	170	180
	VKDVQTLVFH	RAHIEIAHG	DDHENIQVVF	QTEARFVPFH	RVFXTIPRQS	RPWACPLRWCK
	: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :
g664	VKNVQTLVFH	RAHIEIAYG	DDHENIQVIF	QPEARFVPLH	RVFSTIPRQS	RPWVCPLRWCK
	130	140	150	160	170	180
m664 .pep	TRFX					
	: : :					
g664	TRFX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2157>:

a664.seq

```

1  GTGATACATC CGCACCCTT CCGCGCCTTT TTCATAAACG GTCATGGTGT
51  AGAAATTGTT CATCTCCTCA TATCGGGCGG GCGCACCAGG ATGTGCGGTC
101 GGACCTGCGT CTTCGGGGAA CTGGTGCTGG CGCAGCAGGC GGATGTTTTC
151 GATACGGCGC ACGGCGCGGC TGGCGCGGTC GCCGGAAAAT TCTTGGTCGC

```

1057

```

201 GGAACACGGT CAACCCCTTCC TTCAGCGAAA GCTGGAACCA GTCCGCGGCAG
251 GTCACGCGGT TGCCCGTCCA GTTGTGGAAA TATTCGTGTC CGACCACGGA
301 TTCCGATGCTT TCAAAATCGG TATCGGTGGC GGTACGGCTG TCGGCAAGGA
351 CGAACTTGGT GTTAAAGATG TTCAAACCTT TGTTTCCAT CGCACCATA
401 TTGAAATCGC CCACGGCGAC GACCATGAAA ATATCCAAGT CGTATTCCAA
451 ACCGAAGCGC GTTTCGTCCC ACTTCATTGC GTTTTT.CAG CGATTCCACG
501 GCAAAGCCGA CCTTGGGCTT GTCCGCTTCG GTGGTGTAAA ACTCGATTTT
551 GA

```

This corresponds to the amino acid sequence <SEQ ID 2158; ORF 664.a>:

```

a664.pep
1  VIHPHHERAF FINGHGVEIV HLLISGGAHR MGRTCVFGE LVLAQQADVF
51  DTAHGAAGAV AGKFLVAEHG QPFLQRKLEP VAAGHAVARP VVEIFVSDHG
101 FDAFKIGIGG GTAVGKDELG VKDVQTLVFH RTHIEIAHGD DHENIQVVFQ
151 TEARFVPLHC VFXAIPRQSR PWACPLRWCK TRF*

```

m664/a664 92.9% identity in 183 aa overlap

```

          10      20      30      40      50      60
m664.pep  VIHPHYFRAFFINGHGVEIVHLLIAGGAHRMGRACVFGELVLAQQADVFDAHGAAGAV
          ||||:||||:||||:||||:||||: ||:||||:||||:||||:||||:
a664       VIHPHHERAFFINGHGVEIVHLLISGGAHRMGRTCVFGEVLVAQQADVFDTAHGAAGAV
          10      20      30      40      50      60

          70      80      90      100     110     120
m664.pep  AGKFLVAEHGQPFLQRKLEPVAAGYAVARPVVEILVSDHGFDAFEIGIGGGAAGVKDELG
          ||||:||||:||||:||||:||||: ||||:||||:||||:||||:
a664       AGKFLVAEHGQPFLQRKLEPVAAGHAVARPVVEIFVSDHGFDAFKIGIGGGTAVGKDELG
          70      80      90      100     110     120

          130     140     150     160     170     180
m664.pep  VKDVQTLVFHRAHIEIAHGDDHENIQVVFQTEARFVFPFHRVEXTIPRQSRPWACPLRWCK
          ||||:||||:||||:||||:||||: ||||:||||:||||:||||:
a664       VKDVQTLVFHRTHEIAHGDDHENIQVVFQTEARFVPLHCVFXAIPRQSRPWACPLRWCK
          130     140     150     160     170     180

m664.pep  TRFX
          ||||
a664       TRFX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2159>:

```

g665.seq
1  atgaagtGgG acgaaacgCG cttcgGgttg GAAatgact tggatatttt
51  CATGGTCGTC GCCGTAGGCG ATTTCAATAT GGGCGCGATG GAAAACAAGG
101 GTTTGAACAT TTTTAACACC AAGTTCGTCC TCGCCGACAG CCGCACCGCC
151 ACCGATACCG ATTTCGAAGG CATTGAATCC GTGGTCGGAC ACGAATATTT
201 CCACAACCTGG ACGGGCAACC GCGTAACCTG CCGCGACTGG TCCAGCTTT
251 CGCTGAAGGA AGGGCTGACC GTGTTCGCGG ACCAAGAGTT TCCGCGGAC
301 CGCGCCGGCC GCGCCGTGCG CCGCATCGAG AACATCGGCC TGCTGCGCCA
351 GAACCACTTC CCCGAAGACG CAGGCCGACG CGCCCATCCG GTGCGCcccc
401 TCAGCTATGA GGAGATGAAC AATTTCTACA CCATGACCGT TTATGAAAAA
451 GGCGCGGAAG TGGTGC GGAT GTATCATAACC CTGCTCGCGG AAGAGGGCTT
501 CCAAAAAGGC ATGAAGCTAT ATTTCCaacg CCACGACGGA CAGGCAGTGA
551 CCTGCGACGA TTTCCGCGCG GCGatggcgg ATGCGAACGG CATCAATCTC
601 GACCACTTCG CCTGTGGTA CAGCCAGGCG GGCACGCCCG TTTTGAAGC
651 CGAAGGCCGT CTGAAAAACA ATGTTTTCGA GTTAACCATT AAACAAACCG
701 TGCCGCCCAC GCCCGATATG GCGGACAAAC AGCCGATGAT GATTCCCGTC
751 AAAGTCGGGC TTCTGAACCG CAACGCGCAA GCGGTGGCAT TCGATTATCA
801 GGGCAAACGC GCAACCGAAG CCGTGTGCT GATGACCGAA GCCGAACagg
851 CCTTCCCGCT CGAAGGTGTA ACCGAAGCCG TCGTTCCCTC GCTGCTGCGC
901 GGGTTCAGCG CGCCAGTGTA TCTGAACTAT CCGTACAGCG ACGACGACCT
951 GCTGCTCCTG CTCGCCACG ACAGCGACGC TTTCACGTGC TGGGAAGCCG

```

```

1001 CCCAAACGCT CTACCGTCGC GCCGTGCGCG CCAACCTTGC CGCGCTTTCA
1051 GACGGCATCG GGTTGCCGAA ACACGAAAAA CTGCTTGCCG CCGTCGAAAA
1101 AGTCATTTCG GACGACCTCT TGGACAACGC CTTCAAAGCC CTGCTTTTGG
1151 GCGTGCCGTC CGAAGCCGAA ctGTGGGACG GCACGAAAAA CATcgaCCCG
1201 CTGCGCTACC ATCAGGCGCG CGAAGCCTTG TTGGATACGC TTGCCGtcCG
1251 CttcctgcCG AAATGGCAGC AATTGGaccg tcaggcggcg aagCAggaaa
1301 accaaagtTA CGAATACAGC CCCGAAACCG CCGACTGGCG CACGCTGCGC
1351 AACGCTTGCC GCGCCTtcgt cctGCGCGCC GACCCGCGC acatcgAAAC
1401 TGTGCGCGAA Aaatacggcg AAATGGCGCA AAACATGACC CACGAATGGG
1451 GCATCCTGTC CGCGCTCAAC GGCAACGAAA GCGATACGCG CAACTGCCTG
1501 CTGGCGCAGT TTGCCGcaa gTtttcAGAC GACGCGCTGG TGATGGACAA
1551 ATATTTCGCC CTTATCGGCT CAAGcgcgcg cagCGACACC CTGCAACAGG
1601 TTCAAACCGC CTTGCAGCAT CCGAAATTCA GTCTCGAAAA CCCCAACAAA
1651 GCCCGTTGCG TCATCGGCAG CTTAGCCCGC AACGTCCCGC ATTTTCACGC
1701 ACAAGACGGC AGCGGCTACC GCTTCATCGC CGACAAAGTC ATCGAAATCG
1751 ACCGCTTCAA cCCGCAggtc gccGCCCGC TGGTGCAGG GTTCAACCTC
1801 TGCAACAAGC TCGAGCCGCA CCGCAAAAC TTgGTGAAC AAGAATTGCA
1851 GTGCATTGCG GCGCAGGAAG GATTGTCGAA AGacGTGSGC CAaatcgtCG
1901 GCAAGATTTT GGGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2160; ORF 665.ng>:

g665.pep

```

1 MKWDETRFGL EYDLDFMVV AVGFENMGAM ENKGLNIFNT KFLVADSRTA
51 TDTFDEGLIES VVGHEYFHNW TGNRVTCRDW FQLSLKEGLT VFRDQEFSGD
101 RAGRAVRRIE NIRLLRQNF PEDAGPTAHP VRPVSYEEMN NFYTMTVYEK
151 GAEVVRMYHT LLGEEGFQKG MKLYFQRHDG QAVTCDDFRA AMADANGINL
201 DQFALWYSQA GTPVLEAAGR LKNNVFELTI KQTVPTPDM ADKQPMIPV
251 KVGLLNRRGE AVAFDYQGR ATEAVLLMTE AEQAFPLEGV TEAVVPSLLR
301 GFSAPVYINY PYSDDDLLL LAHDSDAFTC WEAAQTLYRR AVAANLAALS
351 DGIGLPHKEK LLAAVEKVIS DDLLDNAFKA LLLGVPSEAE LWDGTENIDP
401 LRYHQAREAL LDTLAVRFLP KWHELDROAA KQENQSYEYS PETADWRTL
451 NVCRAFLVLA DPAHIETVAE KYGEMAQNT HEWGILSAVN GNESDTRNCL
501 LAQFADKFSD DALVMDKYFA LIGSSRRSDT LQQVQTAQH PKFSLNPNK
551 ARSLIGFSR NVPHFHAQDG SGYRFIADKV IEIDRFNPQV AARLVQAFNL
601 CNKLEPHRKN LVKQELQ CIR AQEGLSKDVG EIVGKILG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2161>:

m665.seq

```

1 ATGAAATGGG ACGAAACGCG CTTGCGTTG GAATACGACT TSGATATTTT
51 CATGGTCGTC GCCGTGGGCG ATTTCAATAT GGGCGCGATG GAAAAACAAGG
101 GTTTGAACAT CTTTAACACC AAGTTCTGCC TTGCCGACAG CCGCACCGCC
151 ACCGATACCG ATTTCAAGG CATCGAATCC GTGGTCGGAC ACGAGTATTT
201 CCACAACCTG ACGGGCAACC GCGTAACCTG CCGCGACTGG TTCCAGCTTT
251 CGCTGAAGGA AGGGCTGACC GTGTTCCGCG ACCAAGAATT TTCCGGCGAC
301 CGCGCCAGCC GCGCCGTGCG CCGCATCGAA AACATCCGCC TGCTGCGCCA
351 GCACCAAGTC CCCGAAGACG CAGGCCUGAC CGCCCATCCG GTGCGCCCG
401 CCAGCTATGA GGAGATGAAC AATTCTACA CCATGACCGT TTATGAAAAA
451 GCGCGGAAG TAGTGCGGAT GTATCACACC CTGCTCGGCG AAGAGGGCTT
501 CCAGAAAGGC ATGAAGCTCT ATTTCAACG CCACGACGGA CAGGCCGTTA
551 CCTGCGACGA TTTCCGCGCG GCGATGGCGG ACGCGAACGG CATCAATCTC
601 GACCAAGTTC CTTGTGGTA CAGCCAGCGG GGCACGCCCG TTTTGGAAGC
651 GGAAGGTCGT CTGAAAAACA ATATTTTCGA GTTGACCGTC AAACAAACCG
701 TGCCGCCAC GCCGATATG ACGGATAAAC AGCCGATGAT GATTCCCGTC
751 AAGGTCGGGC TGCTGAACCG CAACGGCGAA GCGGTGGCAT TCGACTATCA
801 GGGCAACGCG GCGACCGAAG CCGTGTGCT GCTGACCGAA GCCGAACAGA
851 CCTTCCTGCT CGAAGGCGTA ACCGAAGCCG TCGTTCCTC GCTGCTGCGC
901 GGGTTCAGCG CGCCGGTGCA TCTGAACTAT CCGTACAGCG ACGACGACCT
951 GCTGCTCCTG CTCGCCATG ACAGCGACGC CTTACGCGC TGGGAAGCCG
1001 CCCAAACGCT CTACCGCCGC GCCGTGCGCG CCAACCTTGC CACGCTTTCA
1051 GACGGCGTTG AGCTGCCGAA ACACGAAAAA CTGCTTGCCG CCGTCGAAAA
1101 AGTCATTTCG GACGACCTCT TAGACAACGC CTTCAAAGCC CTGCTTTTGG
1151 GCGTGCCATC CGAAGCCGAG CTGTGGGACG GCGCAGAAAA CATCGACCCG
1201 CTGCGCTACC ATCAGGCGCG CGAAGCCTTG TTGGATACGC TTGCCGTCCA
1251 CTTCTGCGCG AAATGGCAGC AATTGAACCG TCAGGCGGCG AAGCAGGAAA
1301 ACCAAAGCTA CGAATACAGC CCCGAAGCCG CCGGCTGCGC CACGCTGCGC

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1351 AACGTCTGCC GCGCCTTTGT CCTGCGCGCC GACCCCGCGC ACATCGAAAC
1401 CGTTGCCGAA AAATACGGCG AAATGGCGCA AAACATGACC CACGAATGGG
1451 GCATCCTGTC CGCCGTCAAC GGCAACGAAA GCGATACGCG CAACCGCCTG
1501 CTGGCGCAGT TTGCCGACAA GTTTCAGAC GACGCGCTGG TGATGGACAA
1551 ATATTTTGCC CTCGTCGGCT CAAGCCGCCG CAGCGACACC CTGCAACAGG
1601 TTCGAACCGC CTTGCAGCAT CCGAAATTCA GCCTCGAAAA CCCCAACAAA
1651 GCCCGTTTCG TCATCGGCAG CTTAGCCGCG AACGTCCCGC ATTTCCACGC
1701 AGAAGACGGC AGCGGCTACC GCTTCATCGC CGACAAAGTC ATCGAAATCG
1751 ACCGCTTCAA CCCGAGGTC GCCGCCCGCT TAGTGCAGGC GTTCAACCTC
1801 TGCAACAAGC TCGAGCCGCA CCGCAAAAC TTGGTGAAAC AAGCATTGCA
1851 GCGCATTTCG GCGCAGGAAG GATTGTCGAA AGACGTGGGC GAAATCGTCG
1901 GCAAAATTTT GGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 2162; ORF 665>:

m665.pep

```

1 MKWDETRFGL EYDLDFMVV AVGDFNMGAM ENKGLNIENT KFLVADSRTA
51 TDTDFEGIES VVGHEYFHNW TGNRVTCRDW FQLSLKEGLT VFRDQEFSGD
101 RASRAVRRIE NIRLLRQHOF PEDAGPTAHP VRPASYEEMN NFYTMTVYEK
151 GAEVVRMYHT LLGEEGFQKG MKLYFORHDG QAVTCDDFRA AMADANGINL
201 DQFALWYSQA GTPVLEAAGR LKNNIFELTV KQTVPTPDM TDKQPMPIPV
251 KVGLLNRNGE AVAFDYQGRK ATEAVLLLTE AEQTFLLGV TEAVVPSLLR
301 GFSAPVHLNY PYSDDDLLL LAHDSDAFTR WEAQAQTLYR AVAANLATLS
351 DGVELPKHEK LLAAVEKVIS DDLDNAFKA LLGVPSAE LWDGAENIDP
401 LRYHQAREAL LDTLAVHFLP KWHELNQAA KQENQSYEYS PEAAGWRTL
451 NVCRAFLRA DPAHIETVAE KYGEMAQNT HEWGILSAVN GNESDTRNRL
501 LAQFADKFS DALVMDKYFA LVGSSRRSDT LQQVRTALQH PKFSLENPNK
551 ARSLIGFSR NVPHFAEDG SGYRFIADK IEIDRFNPQV AARLVQAFNL
601 CNKLEPHRKN LVKQALQIR AQEGLSKDVG EIVGKILD*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m665/g665 96.1% identity in 637 aa overlap

	10	20	30	40	50	60
m665.pep	MKWDETRFGL EYDLDFMVVAVGDFNMGAMENKGLNIENTKFLVADSRTATDTDFEGIES					
g665	MKWDETRFGL EYDLDFMVVAVGDFNMGAMENKGLNIENTKFLVADSRTATDTDFEGIES					
	10	20	30	40	50	60
	70	80	90	100	110	120
m665.pep	VVGHEYFHNW TGNRVTCRDW FQLSLKEGLTVFRDQEFSGDRASRAVRR IENIRLLRQHOF					
g665	VVGHEYFHNW TGNRVTCRDW FQLSLKEGLTVFRDQEFSGDRAGRAVRR IENIRLLRQNF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m665.pep	PEDAGPTAHPVRPASYEEMN NFYTMTVYEK GAEVVRMYHTLLGEEGFQGMKLYFORHDG					
g665	PEDAGPTAHPVRPVSYEEMN NFYTMTVYEK GAEVVRMYHTLLGEEGFQGMKLYFORHDG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m665.pep	QAVTCDDFRAAMADANGINLDQFALWYSQAGTPVLEAEGRLKNNIFELTVKQTVPTPDM					
g665	QAVTCDDFRAAMADANGINLDQFALWYSQAGTPVLEAEGRLKNNVFELTIKQTVPTPDM					
	190	200	210	220	230	240
	250	260	270	280	290	300
m665.pep	TDKQPMPIPVKVGLLNRNGEAVAFDYQGRKATEAVLLMTEAEQAFPLEGVTEAVVPSLLR					
g665	ADKQPMPIPVKVGLLNRNGEAVAFDYQGRKATEAVLLMTEAEQAFPLEGVTEAVVPSLLR					
	250	260	270	280	290	300

1060

	310	320	330	340	350	360
m665.pep	GFSAPVHLNYPYSDDDLLLLLAHSDAFTRWEEAAQTLYRRAVANLATLSDGVELPKHEK					
	: : : : :					
g665	GFSAPVYLNYPYSDDDLLLLLAHSDAFTCWEAAQTLYRRAVANLAALSDGIGLPKHEK					
	310	320	330	340	350	360
	370	380	390	400	410	420
m665.pep	LLAAVEKVISDDLLDNFAKALLLGVPSEAEELWDGAENIDPLRYHQAREALLDTLAVHFLP					
	: : : : :					
g665	LLAAVEKVISDDLLDNFAKALLLGVPSEAEELWDGTENIDPLRYHQAREALLDTLAVRFLP					
	370	380	390	400	410	420
	430	440	450	460	470	480
m665.pep	KWHELNROAAKQENQSYEYSPEAAGWRTLNRNVCRAFLVLRADPAHIETVAEKYGEMAQNMT					
	: : : : :					
g665	KWHELDROAAKQENQSYEYSPETADWRTLNRNVCRAFLVLRADPAHIETVAEKYGEMAQNMT					
	430	440	450	460	470	480
	490	500	510	520	530	540
m665.pep	HEWGILSAVNGNESDTRNRLLAQFADKFSDDALVMDKYFALVGSSRRSDTLQQVQTALQH					
	: : : : :					
g665	HEWGILSAVNGNESDTRNCLLAQFADKFSDDALVMDKYFALIGSSRRSDTLQQVQTALQH					
	490	500	510	520	530	540
	550	560	570	580	590	600
m665.pep	PKFSLENPNKARSLIGSFSRNVPHFHAEDGSGYRFIADKVIEIDRFNPQVAARLVQAFNL					
	: : : : :					
g665	PKFSLENPNKARSLIGSFSRNVPHFHAQDGSYRFIADKVIEIDRFNPQVAARLVQAFNL					
	550	560	570	580	590	600
	610	620	630	639		
m665.pep	CNKLEPHRKNLVKQALQIRAQEGLSKDVGIEIVGKILDX					
	: : : : :					
g665	CNKLEPHRKNLVKQELQCIRAQEGLSKDVGIEIVGKILGX					
	610	620	630			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2163>:

```

a665.seq
1  ATGAAGTGGG  ACGAAACGCG  CTTGCGTTTG  GAATACGACT  TGGATATTTT
51  CATGGTCGTC  GCCGTGGGCG  ATTTCAATAT  GGGTGCGATG  GAAAACAAGG
101  GTTTGAACAT  CTTTAACACC  AAGTTTCGTCC  TTGCCGACAG  CCGTACCGCC
151  ACCGATACCG  ATTTGAAGG  CATCGAATCC  GTGGTCGGAC  ACGAATATTT
201  CCACAACGCG  ACGGGCAACC  GCGTGACCTG  CCGCGACTGG  TTCCAGCTTT
251  CGCTGAAGGA  AGGGTTGACC  GTGTTCCGCG  ACCAAGAATT  TTCCGGCGAC
301  CGCGCCAGCC  GCGCCGTGCG  CCGTATCGAA  AACATCCGCC  TGCTGCGCCA
351  GCACCACTTC  CCCGAAGACG  CAGGTCCGAC  CGCACATCCG  GTGCGCCCCG
401  CCCGATATGA  GGAGATGAAC  AATTTCCTACA  CCATGACCGT  TTATGAAAAA
451  GCGCGGGAAG  TGGTGCGGAT  GTATCACACC  TTGCTCGGCG  AAGAGGGCTT
501  CCAAAAAGGT  ATGAAGCTCT  ATTTCCAACG  CCACGACGGA  CAGGCTGTTA
551  CCTGCGACGA  TTTCCGCGCG  GCGATGGTGG  ACGCGAACGG  CATCAACCTC
601  GACCAATTCT  CCTTGTGTA  CAGCCAAGCA  GGTACGCCGG  TTTTAGATGC
651  TCAAGGGCGT  CTGAAAAACA  ATGTGTTTGA  GTTAACCATC  AAACAAACCG
701  TGCGGCCAC  GCCGATATG  GCGGACAAAC  AGCCGATGAT  GATTCCCGTC
751  AAAATCGGGC  TGCTGAATG  CAACGGCGAA  GCGGTGGCAT  TTGATTATCA
801  GGGCAAACGC  GCGACCGAAG  CCGTGTGCT  GCTGACCGAA  GCCGAACAGA
851  CCTTCCAGTT  CGAAAGCGTA  ACCGAAGCCG  TCGTTCCCTC  GCTGCTSCGC
901  GGGTTCAGCG  CGCCGGTGCA  TCTGAATAT  CCGTACAGCG  ACGACGACCT
951  GCTGCTTCTG  CTCGCCCATG  ACAGCGACGC  CTTACGCGCG  TGGGAAGCCG
1001  CACAAACGCT  CTACGCCCGT  GCCGTCGCCG  CCAACCTTGC  CGCGCTTTCA
1051  GACGGCGTCG  AGTTGCCGAA  ACACGAAAAA  CTGCTTCCCG  CCGTCGAAAA
1101  AGTCATTTC  GACGACCTCT  TAGACAACGC  TTTCAAAGCC  CTGCTTTTGG
1151  GTGTGCCGTC  TGAAGCCGAG  CTGTGGGACG  GCGCGGAAAA  CATCGACCCG
1201  CTGCGCTACC  ATCAGGCGCG  CGAAGCCTTG  TTGGATATAC  TTGCCGTCCG
1251  CTTTCTGCCG  AAATGGCAGC  AATTGAACCG  TCAGGCGCG  AAGCAGGAAA
1301  ACCAAAGCTA  CGAGTACAGC  CCCGAAGCCG  CCGGTTGCGC  CACGCTGCGC
1351  AATGTCTGCC  GCGCCTTCGT  CTGCGCGCC  GATCCGCGCG  ACATCGAAAC

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1061

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1401 CGTTGCCGAG AAATACGCCG AAATGGCGCA AAACATGACC CACGAATGGG
1451 GCATCCTGTC CGCCGTCAAC GGCAACGAAA GCGATACGCG CAACCGCCTG
1501 CTGGCGCAGT TTGCCGACAA GTTTTCAGAC GACGCGCTGG TGATGGACAA
1551 ATATTTCCGCC CTCGTCGGCT CAAGCCGCCG CAGCGACACC CTGCAACAGG
1601 TTCAAACCGC CTTGCAGCAT CCGAAGTTCA GCCTCGAAAA TCCCAACAAA
1651 GCCCCGCTCGC TCATCGGCAG CTTCAGCCGC AACGTCCCGC ATTTCCACGC
1701 AGAAGACGGC AGCGGCTACC GCTTCATCGC CGACAAAGTC ATCGAAATCG
1751 ACCGCTTTAA CCCGCAGGTC GCCGCCCGCC TGGTGCAGGC GTTCAACCTC
1801 TCAACAAGC TCAGCCGCA CCGCAAAAC TTGGTGAAC AAGCATTGCA
1851 GCGCATTCGG GCGCAGGAAG GATTGTCGAA AGACGTGGGC GAAATCGTCG
1901 GCAAAATTTT GGATTGA
```

This corresponds to the amino acid sequence <SEQ ID 2164; ORF 665.a>:

```
a665.pep
  1 MKWDETRFGL EYDLDFMVV AVGDFNMGAM ENKGLNIFNT KFLVADSRTA
 51 TDTDFEGIES VVGHEYFHNW TGNRVTCRDW FQLSLKEGLT VFRDQEFSGD
101 RASRAVRRIE NIRLLRQHOF PEDAGPTAHP VRPARYEEMN NFYTMTVYEK
151 GAEVVRMYHT LLGEEGFQKG MKLYFQRHDG QAVTCDDFRA AMVDANGINL
201 DQFALWYSQA GTPVLDAQGR LKNNVFELTI KQTVPPPTDM ADKQPMMPV
251 KIGLLNCNGE AVAFDYQGR ATEAVLLLE AEQTFQFESV TEAVVPSLLR
301 GFSAPVHLNY PYSDDDLLL LAHDSDAFTR WEAQAQTLYRR AVAANLAALS
351 DGVELPKHEK LLAAVEKVIS DDLLDNAFKA LLLGVPSEAE LWDGAENIDP
401 LRYHQAREAL LDILAVRFLP KWHELNQAAA KOENQSYEYS PEAAGWRTLK
451 NVCRAFLVLA DPAHIETVAE KYAEMAQNMT HEWGILSAVN GNESDTRNRL
501 LAQFADKFS DALVMDKYFA LVGSSRRSDT LQQVQTALQH PKFSLENPNK
551 ARSLIGSFSS NVPHFAEDG SGYRFIADKV IEIDRFNPQV AARLVQAFNL
601 CNKLEPHRKN LVKQALQRIK AQEGLSKDVG EIVGKILD*
```

m665/a665 97.3% identity in 638 aa overlap

```

      10      20      30      40      50      60
m665.pep MKWDETRFGLEYDLDFMVVAVGDFNMGAMENKGLNIFNTKFLVADSRTATDTDFEGIES
      |||
a665      MKWDETRFGLEYDLDFMVVAVGDFNMGAMENKGLNIFNTKFLVADSRTATDTDFEGIES
      10      20      30      40      50      60

      70      80      90     100     110     120
m665.pep VVGHEYFHNWTGNRVTCRDWFQLSLKEGLTVFRDQEFSGDRASRAVRRIENIRLLRQHOF
      |||
a665      VVGHEYFHNWTGNRVTCRDWFQLSLKEGLTVFRDQEFSGDRASRAVRRIENIRLLRQHOF
      70      80      90     100     110     120

      130     140     150     160     170     180
m665.pep PEDAGPTAHPVRPASYEEMNMFYTMVYKGAEVVRMYHTLLGEEGFQKGMKLYFQRHDG
      |||
a665      PEDAGPTAHPVRPARYEEMNMFYTMVYKGAEVVRMYHTLLGEEGFQKGMKLYFQRHDG
      130     140     150     160     170     180

      190     200     210     220     230     240
m665.pep QAVTCDDFRAAMADANGINLDQFALWYSQAGTPVLEAEGRLKNNIFELTVKQTVPPPTDM
      |||
a665      QAVTCDDFRAAMVDANGINLDQFALWYSQAGTPVLDQGRKNNVFELTIKQTVPPPTDM
      190     200     210     220     230     240

      250     260     270     280     290     300
m665.pep TDKQPMMPVKVGLLNRNGEAVAFDYQGRATEAVLLLEAEQTFI.LEGVTEAVVPSLLR
      :|||
a665      ADKQPMMPVKIGLLNCNGEAVAFDYQGRATEAVLLLEAEQTFQFESVTEAVVPSLLR
      250     260     270     280     290     300

      310     320     330     340     350     360
m665.pep GFSAPVHLNYPYSDDDLLLHAHDSDAFTRWEAAQTLYRRAVAANLATLSDGVELPKHEK
      |||
a665      GFSAPVHLNYPYSDDDLLLHAHDSDAFTRWEAAQTLYRRAVAANLAALS.DGVELPKHEK
      310     320     330     340     350     360
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1062

	370	380	390	400	410	420
m665.pep	LLAAVEKVISDDLLDNAFKALLLGVPSAEELWDGAENIDPLRYHQAREALLDTLAVHFLP					
a665	LLAAVEKVISDDLLDNAFKALLLGVPSAEELWDGAENIDPLRYHQAREALLDILAVRFLP					
	370	380	390	400	410	420
	430	440	450	460	470	480
m665.pep	KWHELNRQAQKQENQSYEYSPEAAGWRTLNRNVCRAFLVLRADFAHIETVAEKYGEMAQNMT					
a665	KWHELNRQAQKQENQSYEYSPEAAGWRTLNRNVCRAFLVLRADFAHIETVAEKYAEMAQNMT					
	430	440	450	460	470	480
	490	500	510	520	530	540
m665.pep	HEWGILSAVNGNESDTRNRLLAQFADKFSDDALVMDKYFALVGSSRRSDTLQQVQTALQH					
a665	HEWGILSAVNGNESDTRNRLLAQFADKFSDDALVMDKYFALVGSSRRSDTLQQVQTALQH					
	490	500	510	520	530	540
	550	560	570	580	590	600
m665.pep	PKFSLENPNKARSLIGSFNRNVPFHAEADGSGYRFIADKVIEIDRFNPQVAARLVQAFNL					
a665	PKFSLENPNKARSLIGSFNRNVPFHAEADGSGYRFIADKVIEIDRFNPQVAARLVQAFNL					
	550	560	570	580	590	600
	610	620	630	639		
m665.pep	CNKLEPHRKNLVKQALQRIRAQEGLSKDVGEIVGKILD					
a665	CNKLEPHRKNLVKQALQRIRAQEGLSKDVGEIVGKILD					
	610	620	630			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2165>:

g665-1.seq

```

1  ATGAGCAAAA CCGTCCGTTA TCTGAAAGAT TACCAAAACGC CTGCCTACCG
51  CATTTCTGAA ACCGAACTGC ATTTTCGACAT TGCCGAACCG CAAACCGTCG
101 TGAAGTCGCG TTTGACGGTC GAGCCGCAGA GGGCGGGCGA GCCCTGGTG
151 TTGGACGGTT CGGCAAAACT CTTGTCCGTC AAAATCAACG GCGCGGCGGC
201 GGATTATGTG TTGGAAGGCG AGACGCTGAC GATTGCAGAC GTACCGTCCG
251 AACGCTTCAC CGTCGAAGTG GAAACCGAAA TCCTGCCGCG GGAACCAAAA
301 TCGCTGATGG GGCTGTATGC TTCCGGCGGC AATCTGTTTA CCCAGTGCGA
351 GCCGGAGGGC TTCCGCAAAA TCACGTTCTA CATCGACCGT CCGGATGTGA
401 TGTCCAAGTT CACGACCACC ATCGTCGCGG ACAAAAACG CTATCCCGTT
451 TTGCTTTCCA ACGGCAACAA AATCGACGGC GGCGAGTTT CAGACGGCCG
501 CCATTGGGTG AAATGGGAAG ACCCGTTTGC CAAACCGAGT TATCTGTTTG
551 CTTTGGTCGC GGGCGATTG GCGGTAACGG AAGACCGTTT CACCACCATG
601 AGCGGCAGAA ACGTCAAAAT CGAGTTTAC ACCACCGAAG CGGACAAACC
651 CAAGTCCGCG TTGCCCCTGG AATCGTTGAA AAACGCGATG AAGTGGGACG
701 AAACGCGCTT CGGTTTGAA TATGACTTGG ATATTTTCAT GGTCTGCGCC
751 GTAGGCGATT TCAATATGGG CCGATGGAA AACAGGGTT TGAACATTTT
801 TAACACCAAG TTCGTCCTCG CCGACAGCCG CACCGCCACC GATACCGATT
851 TCGAAGGCAT TGAATCCGTG GTCGGACACG AATATTTCCA CAACTGGACG
901 GGCAACCGCG TAACCTGCGG CGACTGGTTC CAGCTTTCGC TGAAGGAAGG
951 GCTGACCGTG TTCCGCGACC AAGAGTTTTC CGGCGACCGC GCCGGCCGCG
1001 CCGTCCGCGC CATCGAGAAC ATCCGCTGCG TGCGCCAGAA CCAGTTCCCC
1051 GAAGACGCGG GCCCGACCGC CCATCCGGTG CGCCCCGTCA GCTATGAGGA
1101 GATGAACAAT TTCTACACCA TGACCGTTTA TGAAAAAGGC GCGGAAGTGG
1151 TGCGGATGTA TCATACCTCG CTCGCGAAG AGGGCTTCCA AAAAGGCATG
1201 AAGCTATATT TCCAACGCCA CGACGGACAG CAGTGACCT GCGACGATTT
1251 CCGCGCGCGC ATGGCGGATG CGAACGGCAT CAATCTCGAC CAGTTCGCCT
1301 TGTGGTACAG CCAGCGGGC ACGCCCGTT TGGAAGCCGA AGGCCGTCTG
1351 AAAACAATG TTTTCGAGTT AACCATTAAA CAAACCGTGC CGCCACGCCC
1401 CGATATGGCG GACAAACAGC CGATGATGAT TCCCGTCAA GTCCGGCTTC
1451 TGAACCGCAA CGGCGAAGCG GTGGCATTGG ATTATCAGGG CAAACGCGCA
1501 ACCGAAGCCG TGTGCTGAT GACCGAAGCC GAACAGCCCT TCCCGCTCGA
1551 AGGTGTAAAC GAAGCCGTCG TTCCCTCGCT GCTGCGCGGG TTCAGCGCGC
1601 CAGTGATCTT GAACATCCG TACAGCGACG ACGACCTGCT GCTCCTGCTC
1651 GCCCACGACA GCGACGCTTT CACGTGCTGG GAAGCCGCC AAACGCTCTA
1701 CCGTCCGCGC GTCGCGGCCA ACCTTGCCGC GCTTTCAGAC GGCATCGGGT

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1751 TGCCGAAACA CGAAAACTG CTTGCCGCCG TCGAAAAAGT CATTTCAGAC
1801 GACCTCTTGG ACAACGCCCTT CAAAGCCCTG CTTTGGGCG TGCCGTCGCA
1851 AGCCGAACCTG TGGGACGGCA CGGAAACAT CGACCCGCTG CGCTACCATC
1901 AGGCGCGCGA AGCCTTGTGT GATACCCCTT CCGTCCGCTT CCTGCCGAAA
1951 TGGCAGCAAT TGGACCGTCA GCGCGCGAAG CAGGAAACCC AAAGTTACGA
2001 ATACAGCCCC GAAACCGCCG ACTGGCGCAC GCTGCGCAAC GTCTGCCGCG
2051 CCTTCGTCTT GCGCGCCGAC CCCGCGCACA TCGAAACTGT TGCCGAAAAA
2101 TACGGCGAAA TGGCGCAAAA CATGACCCAC GAATGGGGCA TCCTGTCCGC
2151 CGTCAACGGC AACGAAAGCG ATACGCGCAA CTGCTGTCTG GCGCAGTTTG
2201 CCGACAAGTT TTCAGACGAC GCGCTGGTGA TGGACAAATA TTTGCCCCCTT
2251 ATCGGCTCAA GCCGCCGAG CGACACCCCTG CAACAGGTTT AAACCGCCTT
2301 GCAGCATCCG AAATTCAGTC TCGAAAAACC CAACAAAGCC CGTTCGCTCA
2351 TCGGCAGCTT CAGCCGCAAC GTCCCGCATT TTCACGCACA AGACGGCAGC
2401 GGCTACCGCT TCATCGCCGA CAAAGTCATC GAAATCGACC GCTTCAACCC
2451 GCAGGTCGCG GCCCGCCTGG TGCAGGCGTT CAACCTCTGC AACAAGCTCG
2501 AGCCGCACCG CAAAAACTTG GTGAAACAG AATTGCAGTG CATTGCGGCG
2551 CAGGAAGGAT GTTCGAAAGA CGTGGCGCAA ATCGTCGGCA AGATTTTGGG
2601 TTGA

```

This corresponds to the amino acid sequence <SEQ ID 2166; ORF 665-1.ng>:

g665-1.pep

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1 MSKTVRYLKD YOTPAYRILE TELHFDIAEP QTVVKSRLTV EPQRAGEPLV
51 LDGSAKLLSV KINGAAADYV LEGETLTIAD VPSEFRTVEV ETEILPAENK
101 SLMLGLYASGG NLFTQCEPEG FRKITFYIDR PDVMSKFTTT IVADKKRYPV
151 LLSNGNKIDG GEFSNDRHWV KWEDPFAPKS YLFALVAGDL AVTEDRFMTM
201 SGRNVKIEFY TTEADKPKVG FAVESLKNAM KWDETRFGLE YDLDFMVVA
251 VGDFNMGAME NKGLNIFNTK FVLADSRAT DTDFEGIESV VGHEYFHNWT
301 GNRVTCRDWF QLSLKEGLTV FRDQEFSGDR AGRVVRRIEN IRLIRQNGFP
351 EDAGPTAHPV RPSVYEEMNN FYTMTVYEKG AEVVRMYHTL LGEEGFQKGM
401 KLYFQRHDGQ AVTCDDFRAA MADANGINLD QFALWYSQAG TPFVLEAEGRL
451 KNNVFELTIK QTVPPPTDMA DKQPMMPVK VGLLNRRNGEA VAFDYQCKRA
501 TEAVLLMTEA EQAFPLEGVT EAVVPSLLRG FSAFVYLNYP YSDDDLLLLL
551 AHSDAFTCW EAAQTLYRRA VAANLAALSD GIGLPKHEKL LAAVEKVIDS
601 DLLDNAFKAL LLGVPSAEAL WDGTEINIDPL RYHQAREALL DTLAVRFLPK
651 WHELDROAAK QENQSYEYSP ETADWRTLRLN VCRAFVLRAD PAHIETVAEK
701 YGEMAQNMTH EWGILSAVNG NESDTRNCLL AQFADKFSDD ALVMDKYFAL
751 IGSSRRSDTL QQVQTAHQHP KFSLENPNKA RSLIGSFERN VPHFHAQDGS
801 GYRFIADKVI EIDRENQOVA ARLVQA7NLC NKLEPHRKNL VKQELQCIRA
851 QEGLSKDVGE IVGKILG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2167>:

m665-1.seq

```

1 ATGAGCAAAA CCGTGCATTA TCTCAAAGAC TATCAAACGC CCGCCTACCA
51 TATTCTCAAA ACCGATTATC ATTTTGATAT TAATGAACCG CAAACCGTCG
101 TGAAGTCGCG TTTGACGGTT GAGCCGCGAG GGGTAGGGGA GCCGCTGGTG
151 TTGACGGGTT CGGCGAAACT CTTGTCCGTC AAAATCAACG GGGCGGCGGC
201 GGATTATGTG TTGGAAGGAG AGACGCTGAC GATTGCGGGC GTGCCGTCCG
251 AACGCTTCAC CGTCAAGTG GAAACCGAAA TCCTGCGCGC GAAAAACAAA
301 TCGCTGATGG GGCTGTATGC TTCCGGCGGC AATTGTGTTA CCCAGTGCGA
351 GCCGGAGGGC TTCCGCAAAA TCACATTTTA CATCGACCGT CCGGATGTGA
401 TGTCCTAAGT CACCACCACC ATCGTCGCGC ACAAACACG CTATCCCCTT
451 TTGCTTTCCA ACGGCAACAA AATCGACGGC GCGAGTTTTT CAGACGGCCG
501 CCATTGGGTG AAATGGGAAG ACCCGTTTTC CAAACCGAGC TATCTGTTTG
551 CTTTGGTTCG GGGCGATTTG GCGGTAACGG AAGACTATTT CACCACCATG
601 AGCGGCAGAA ACGTCAAAAT CGAGTTTATC ACCACCGAAG CGGACAAGCC
651 CAAGGTCGCG TTTGCCGTGG AATCGTTGAA AAACGCGATG AAATGGGACG
701 AAACGCGCTT CGGTTTGGAA TACGACTTGG ATATTTTCAT GGTCTGCGCC
751 GTGGCGGATT TCAATATGGG CGCGATGGAA AACAAAGGTT TGAACATCTT
801 TAACACCAAG TTCGTCTTGG CCGACAGCCG CACCGCCACC GATACCGATT
851 TCGAAGGCAT CGAATCCGTG GTCGGACACG AGTATTTCCA CAACTGGACG
901 GGCAACCGCG TAACCTGCCG CGACTGGTTC CAGCTTTCGC TGAAGGAAGG
951 GCTGACCGTG TTCCGCGACC AAGAATTTTC CGGCGACCGC GCCAGCCGCG
1001 CCGTGGCGCG CATCGAAAAC ATCCGCTTGC TGCGCCAGCA CCACTTCCCC
1051 GAAGACGCGC GCCCGACCGC CCATCCGGTG CGCCCCGCCA GCTATGAGGA
1101 GATGAACAAAT TTCTACACCA TGACCGTTTA TGAAAAAGGC GCGGAAGTAG
1151 TGGCGATGTA TCACACCTTG CTCGGCGAAG AGGCTTCCA GAAAGGCATG
1201 AAGCTCTATT TCCAACGCCA CGACGGACAG GCCGTTACCT GCGACGATTT
1251 CCGCGCGCGC ATGGCGGACG CGAACGGCAT CAATCTCGAC CAGTTCGCCT
1301 TGTGGTACAG CAGGCGGGC ACGCCCGTTT TGAAGCGGGA AGGTCGCTCTG
1351 AAAAAAATA TTTTCGAGTT GACCGTCAAA CAAACCGTGC CGCCACGCGC
1401 CGATATGACG GATAAACAGC CGATGATGAT TCCGCTCAAG GTCGGGCTGC
1451 TGAACCGCAA CGGCGAAGCG GTGGCATTCG ACTATCAGGG CAAACGCGCG

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1064

1501 ACCGAAGCCG TGTTGCTGCT GACCGAAGCC GAACAGACCT TCCTGCTCGA
 1551 AGGCGTAACC GAAGCCGTCG TTCCTTCGCT GCTGCGCGGG TTCAGCGCGC
 1601 CCGTGCATCT GAACATATCCG TACAGCGACG ACGACCTGCT GCTCCTGCTC
 1651 GCCCATGACA GCGACGCCCTT CACGCGCTGG GAAGCCGCCC AAACGCTCTA
 1701 CCGCCGCGCC GTCGCCGCCA ACCTTGCCAC GCTTTCAGAC GGCCTTGAGC
 1751 TGCCGAAACA CGAAAAACTG CTTGCCGCGG TCGAAAAAGT CATTTCAGAC
 1801 GACCTCTTAG ACAACGCCCTT CAAAGCCCTG CTTTGGGCG TGCCATCCGA
 1851 AGCCGAGCTG TGGGACGGCG CAGAAAAACAT CGACCCGCTG CGCTACCATC
 1901 AGGCGCGCGA AGCCTTGTTG GATACGCTTG CCGTCCACTT CCTGCCGAAA
 1951 TGGCAGCAAT TGAACCGTCA GCGCGCGAAG CAGGAAAACC AAAGCTACGA
 2001 ATACAGCCCC GAAGCCGCGG GCTGGCGCAC GCTGCGCAAC GTCTGCCGCG
 2051 CCTTTGTCTT GCGCGCGGAC CCCGCGCACA TCGAAACCGT TGCCGAAAAA
 2101 TACGCGGAAA TGGCGCAAAA CATGACCCAC GAATGGGGCA TCCTGTCCGC
 2151 CGTCAACGGC AACGAAAGCG ATACCGCGAA CCGCCTGCTG GCGCAGTTTG
 2201 CCGACAAGTT TTCAGACGAC GCGCTGGTGA TGGACAAATA TTTTGCCCTC
 2251 GTCGGCTCAA GCCCGCCGAG CGACACCCCTG CAACAGGTTT GAACCGCCTT
 2301 GCAGCATCCG AAATTCAGCC TCGAAAAACC CAACAAAGCC CGTTCGCTCA
 2351 TCGGCAGCTT CAGCCGCAAC GTCCCGCATT TCCACGCAGA AGACGGCAGC
 2401 GGCTACCGCT TCATCGCCGA CAAAGTCATC GAAATCGACC GCTTCAACCC
 2451 GCAGCTCGCC GCCCGCTTAG TGCAGGCGTT CAACCTCTGC AACAGCTCG
 2501 AGCCGCAACG CAAAAACTTG GTGAAACAAG CATTGCAGCG CATTGCGGCG
 2551 CAGGAAGGAT TGTGAAAGA CGTGGGCGAA ATCGTCGCGA AAATTTTGA
 2601 TTGA

This corresponds to the amino acid sequence <SEQ ID 2168; ORF 665-1>:

m665-1.pep

1 MSKTVHYLKD YQTPAYHILK TDLHFDINEP QTVVKSRLTV EPQRVGEPLV
 51 LDGSAKLLSV KINGAADYV LEGETLTIAG VPSEFTVEV ETEILPAENK
 101 SLMGLYASGG NLFTQCEPEG FRKITFYIDR PDVMSKFTTT IVADKKRYPV
 151 LLSNGNKIDG GEFSGGRHWV KWEDPFSKPS YLFALVAGDL AVTEDYFTTM
 201 SGRNVKIEFY TTEADKPKVG FAVESLKNAM KWDETRFGL EYLDIFMVVA
 251 VGFENMGAME NKGNIIFNTK FVLADSRAT DTFEGIESV VGHEYFHNWT
 301 GNRVTCRDWF QLSLKEGLTV FRDQEFSGDR ASRAVRRIEN IRLLRQHQP
 351 EDAGPTAHVP RPASYEEMNN FYTMTVYEKG AEVVRMYHTL LGEEGFQKGM
 401 KLYFQRHDGQ AVTCDDFRAA MADANGINLD OFALWYSQAG TPVLEAEGRL
 451 KNNIFELTVK QTVPTPDMT DKQPMIIPVK VGLNLRNGEA VAFDYQKRA
 501 TEAVLLLTEA EQTFLLGVT EAVVPSLLRG FSAPVHLNYP YSDDDLLLL
 551 AHDSDAFTRW EAAQTLYRRA VAANLATLSD GVLPKHEKL LAAVEKVISD
 601 DLLDNAFKAL LLGVPSAEAL WDGAENIDPL RYHQAREALL DTLAVHFLPK
 651 WHELNQAAK QENOSYEYSP EAAGWRTLNR VCRAFLVLRAD PAHIETVAEK
 701 YGEMAQNMTH EWGILSAVNG NESDTRNRL AOFADKFSDD ALVMDRYFAL
 751 VGSSRRSDTL QQVRTALQHP KFSLENPNKA RSLIGSFSRN VPHFHAEDGS
 801 GYRFIADKVI EIDRFNPQVA ARLVQAENLC NKLEPHRKNL VKQALQIRIA
 851 QEGLSKDVGE IVGKILD*

m665-1/g665-1 96.1% identity in 866 aa overlap

	10	20	30	40	50	60
m665-1.pep	MSKTVHYLKD	YQTPAYHILK	TDLHFDINEP	QTVVKSRLTV	EPQRVGEPLV	LDGSAKLLSV
g665-1	MSKTVRYLKD	YQTPAYRIE	TELHFDIAEP	QTVVKSRLTV	EPQRAEPLV	LDGSAKLLSV
	70	80	90	100	110	120
m665-1.pep	KINGAADYV	LEGETLTIAG	VPSEFTVEV	ETEILPAENK	SLMGLYASGG	NLFTQCEPEG
g665-1	KINGAADYV	LEGETLTIAD	VPSEFTVEV	ETEILPAENK	SLMGLYASGG	NLFTQCEPEG
	130	140	150	160	170	180
m665-1.pep	FRKITFYIDR	PDVMSKFTTT	IVADKKRYPV	LLSNGNKIDG	GEFSGGRHWV	KWEDPFSKPS
g665-1	FRKITFYIDR	PDVMSKFTTT	IVADKKRYPV	LLSNGNKIDG	GEFSGGRHWV	KWEDPFAKPS
	190	200	210	220	230	240
m665-1.pep	YLFALVAGDL	AVTEDYFTTM	SGRNVKIEFY	TTEADKPKVG	FAVESLKNAM	KWDETRFGL
g665-1	YLFALVAGDL	AVTEDRFTTM	SGRNVKIEFY	TTEADKPKVG	FAVESLKNAM	KWDETRFGL
	250	260	270	280	290	300
m665-1.pep	YLDIFMVVA	VGFENMGAME	NKGNIIFNTK	FVLADSRAT	DTDFEGIESV	VGHEYFHNWT
g665-1	YLDIFMVVA	VGFENMGAME	NKGNIIFNTK	FVLADSRAT	DTDFEGIESV	VGHEYFHNWT

	250	260	270	280	290	300
m665-1.pep	310	320	330	340	350	360
	GNRVTCRDWFQLSLKEGLTVFRDQEFSGDRASRAVRRIENIRLLRQHQPEDAGPTAHPV					
g665-1	GNRVTCRDWFQLSLKEGLTVFRDQEFSGDRAGRAVRRIENIRLLRQHQFPEDAGPTAHPV					
	310	320	330	340	350	360
m665-1.pep	370	380	390	400	410	420
	RPASYEEMNNFYMTVYEKGAEVVRMYHTLLGEEGFQKGMKLYFQRHDGQAVTCDDFRAA					
g665-1	RPVSYEEMNNFYMTVYEKGAEVVRMYHTLLGEEGFQKGMKLYFQRHDGQAVTCDDFRAA					
	370	380	390	400	410	420
m665-1.pep	430	440	450	460	470	480
	MADANGINLDQFALWYSQAGTPVLEAEGRLKNNIFELTVKQTPPTPDMTDKQPMPIPVK					
g665-1	MADANGINLDQFALWYSQAGTPVLEAEGRLKNNVFELTIKQTPPTPDMADKQPMPIPVK					
	430	440	450	460	470	480
m665-1.pep	490	500	510	520	530	540
	VGLLNRRNGEAVAFDYQGKRATEAVLLLTAEQTFLEGVTEAVVPSLLRGFSAPVHLNYP					
g665-1	VGLLNRRNGEAVAFDYQGKRATEAVLLMTEAQAPPLEGVTEAVVPSLLRGFSAPVYLNYP					
	490	500	510	520	530	540
m665-1.pep	550	560	570	580	590	600
	YSDDDLLLLLAHDSDAFTWEAAQTLRYRAVANLATLSGVELPKHEKLLAAVEKVISD					
g665-1	YSDDDLLLLLAHDSDAFTCWEAAQTLRYRAVANLAALSDGIGLPHKEKLLAAVEKVISD					
	550	560	570	580	590	600
m665-1.pep	610	620	630	640	650	660
	DLLDNAFKALLLGVPSAEALWDGAENIDPLRYHQAREALLDTLAVHFLPKWHELNQAAK					
g665-1	DLLDNAFKALLLGVPSAEALWDGTENIDPLRYHQAREALLDTLAVRFLPKWHELDQAAK					
	610	620	630	640	650	660
m665-1.pep	670	680	690	700	710	720
	QENQSYEYSPAAAGWRTLNRNVCRAFLRADPAHIETVAEKYGEMAQNMTHWEGILSAVNG					
g665-1	QENQSYEYSPETADWRTLNRNVCRAFLRADPAHIETVAEKYGEMAQNMTHWEGILSAVNG					
	670	680	690	700	710	720
m665-1.pep	730	740	750	760	770	780
	NESDTRNRLLAQFADKFSDDALVMDKYFALVGSSRRSDTLQQVRTALQHPKFSLENPNKA					
g665-1	NESDTRNCLLAQFADKFSDDALVMDKYFALIGSSRRSDTLQQVQTALQHPKFSLENPNKA					
	730	740	750	760	770	780
m665-1.pep	790	800	810	820	830	840
	RSLIGSFSSRNVPFHFAEDGSGYRFIADKVIIDRFNPQVAARLVQAFNLCNKLEPHRKNL					
g665-1	RSLIGSFSSRNVPFHFAQDGSYRFIADKVIIDRFNPQVAARLVQAFNLCNKLEPHRKNL					
	790	800	810	820	830	840
m665-1.pep	850	860				
	VKQALQIRAQEGLSKDVGEIVGKILDX					
g665-1	VKQELQCIRAQEGLSKDVGEIVGKILGX					
	850	860				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2169>:

a665-1.seq

```

1  ATGAGCAAAA CCGTGCATTA TCTCAAAGAC TATCAAACGC CCGCCTACCA
51  TATTCTCAA ACCGATTAC ATTTGATAT TAACGAACCG CAAACCATTTG
101 TGAAGTCGCG TTTGACGGTC GAGCCGAAGA GGGTGGGAGA GCCGCTGGTG
151 TTGGACGGTT CGGCGAAACT CTTGTCCGTC AAAATCAACG GCGTGGCGGC
201 GGATTATGTG TTGGAAGCGC AGACGCTGAC GATTGCGGAC GTGCCGTCGG
251 AACGCTTCAC CGTCGAAGTG GAAACCGAAA TCCTGCCGGC GGAAACACAA
301 TCGCTGATGG GGCTGTATGC GTCCGCCGGT AACCTGTTTA CCCAGTCCGA
351 GCCGGAGGGC TTCCGCAAAA TCACGTTCTA TATCGACCGT CCGGATGTCA
401 TGTCCAAGTT CACGACCACC ATCGTCGCGG ACAAAAAACG CTATCCCGTT
451 TTGCTCTCCA ACGGCAACAA AATCGACGGC GCGAGTATT CAGACGGCCG

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501 CCATTGGGTG AAATGGGAAG ACCCGTTTGC CAAACCGAGT TATCTGTTTG
551 CTTTGGTCGC GGGCGATTTC GCGGTACAGG AAGACTATTT CACCACCATG
601 AGCGGCAGAA ACGTCAAAAT CGAGTTTAC ACCACCGAAG CGGACAAGCC
651 CAASGTCGGC TTGCGCTGG AATCGCTGAA AAACGCAATG AAGTGGGACG
701 AAACGCGCTT CGGTTTGAA TACGACTTGG ATATTTTCAT GGTCGTCGCC
751 GTGGGCGATT TCAATATGGG TCGGATGGAA AACAAGGGTT TGAACATCTT
801 TAACACCAAG TTCGTCTTGG CCGACAGCCG TACCGCCACC GATACCGATT
851 TTGAAGGCAT CGAATCCGTG GTCGGACACG AATATTTCCA CAACTGGACG
901 GGCAACCGCG TGACCTGCCG CCACTGGTTC CAGCTTTCGC TGAAGGAAGG
951 GTTGACCGTG TTCCGCGACC AAGAATTTTC CGGCGACCGG GCCAGCCGCG
1001 CCGTGCGCCG TATCGAAAAC ATCCGCTTGC TCGCCAGCA CCAGTTCCCC
1051 GAAGACGCAG GTCCGACCGC ACATCCGGTG CGCCCCGCCG GATATGAGGA
1101 GATGAACAAT TTCTACACCA TGACCGTTTA TGA AAAAGGCG GCGGAAGTGG
1151 TCGCGATGTA TCACACCTTG CTCGGCGAAG AGGGCTTCCA AAAAGGTATG
1201 AAGCTCTATT TCCAACGCCA CGACGGACAG GCTGTACCT GCGACGATTG
1251 CCGCGCGGCG ATGGTGGACG CGAACGGCAT CAACCTCGAC CAATTCGCCT
1301 TGTGGTACAG CCAAGCAGGT ACGCCGGTTT TAGATGCTCA AGGGCGTCTG
1351 AAAACAATG GTTTCGAGT AACCATCAAA CAAACCGTGC CGCCACGCCG
1401 CGATATGGCG GACAAACAGC CGATGATGAT TCCCGTCAAA ATCGGGCTGC
1451 TGAAGTCAA CGGCGAAGCG GTGGCATTTC ATTATCAGGG CAAACGCGCG
1501 ACCGAAGCCG TGTTGCTGCT GACCGAAGCC GAACAGACCT TCCAGTTCGA
1551 AAGCGTAACC GAAGCCGTCG TTCCCTCGCT GCTGCGCGGG TTCAGCGCGC
1601 CGGTGCATCT GAACTATCCG TACAGCGACG ACGACCTGCT GCTTCTGCTC
1651 GCCCATGACA GCGACGCCCT CACGCGCTGG GAAGCCGCAC AAACGCTCTA
1701 CCGCGGTGCC GTCGCCGCCA ACCTTGCCGC GCTTTCAGAC GGGCTCGAGT
1751 TGCCGAAACA CGAAAAACTG CTTGCCGCGG TCGAAAAAGT CATTTCAGAC
1801 GACCTCTTAG ACAACGCTTT CAAAGCCCTG CTTTGGGTG TGCCGTCTGA
1851 AGCCGAGCTG TGGGACGGCG CGGAAAACAT CGACCCGCTG CGCTACCATC
1901 AGGCGCGCGA AGCCTTGTTG GATATACTTG CCGTCCGCTT TCTGCCGAAA
1951 TGGCAGCAAT TGAACCGTCA GCGCGCGAAG CAGGAAAACC AAAGCTACGA
2001 GTACAGCCCC GAAGCCGCCG GTTGGCGCAC GCTGCGCAAT GTCTGCCGCG
2051 CTTTCGCTCT GCGCGCCGAT CCCGCGCACA TCGAAACCGT TGCCGAGAAA
2101 TACGCCGAAA TGGCGCAAAA CATGACCCAC GAATGGGGCA TCCTGTCCGC
2151 CGTCAACGGC AACGAAAGCG ATACGCGCAA CCGCTGCTG GCGCAGTTTG
2201 CCGACAAGTT TTCAGACGAC GCGCTGCTGA TGGACAAATA TTTCCGCCCTC
2251 GTCGGCTCAA GCGCGCGCAG CGACACCTG CAACAGGTTT AAACCGCCTT
2301 GCAGCATCCG AAGTTCAGCC TCGAAAATCC CAACAAAGCC CCCTCGCTCA
2351 TCGGCAGCTT CAGCGCAAC GTCCCGCATT TCCACGCGA AGACGGCAGC
2401 GGCTACCGCT TCATCGCCGA CAAAGTCATC GAAATCGACC GCTTTAACCC
2451 GCAGGTCCGC GCCCGCCTGG TGCAGGCGTT CAACCTCTG AACAGCTCG
2501 AGCCGACCG CAAAACCTTG CTGAAACAAG CATTGCAGCG CATTGGGCG
2551 CAGGAAGGAT TGTCGAAAGA CGTGGCGGAA ATCGTCCGCA AAATTTTGGA
2601 TTGA

```

This corresponds to the amino acid sequence <SEQ ID 2170; ORF 665-1.a>:

a665-1.pep

```

1 MSKTVHYLKD YQTPAYHILK TDLHFDINEP QTIIVKSRLTV EPKRVGEPLV
51 LDGSAKLLSV KINGVAADYV LEGETLTID VPSEFTEVEV ETEILPAENK
101 SLMLYASAG NLFTQCEPEG FRKITFYIDR PDVMSKFTTT IVADKKRYPV
151 LLSNGNKIDG GEYS DGRHWV KWEDPFAKPS YLFALVAGDL AVTEDYFTTM
201 SGRNVKIEFY TTEADKPKVG FAVESLKNAM KWDETRFGL EYLDIFMVVA
251 VGDFNMGAME NKGLNIFNTK FVLADSRAT DTDFEGIESV VGHEYFHNWT
301 GNRVTCRDWF QLSLKEGLTV FRDQFESGDR ASRAVRRIEN IRLLRQHOF
351 EDAGPTAHVP RPARYEEMNN FYTMTVYERK AEVVRMYHTL LGEEGFQKGM
401 KLYFORHDGQ AVTCDDFRAA MVDANGINLD QFALWYSQAG TPVLDAQGRL
451 KNNVFELTIK QTVPTPDMA DKQPMIIPVK IGLLNCNGEA VAFDYQGKRA
501 TEAVLLLTEA EQTFQFESVT EAVVPSLLRG FSAPVHLNYP YSDDDLLLLL
551 AHDSDAFTRW EAAQTLYRRA VAANLAALSD GVELEPKHEKL LAAVEKVIDS
601 DLLDNAFKAL LLGVPSEAE LWDGAENIDPL RYHQAREALL DILAVRFLPK
651 WHELNRAQAK QENQSYEYSP EAAGWRTLNR VCRAFVLRAD PAHIETVAEK
701 YAEQAQNMTH EWGILSAVNG NESDTRNRL L AQFADKFSDD ALVMDKYFAL
751 VGSSRSRSDL QOVQALQHP KFSLENPNKA RSLIGSFSRN VPFHAEEDGS
801 GYRFIADKVI EIDRFNPQVA ARLVQAFNLC NKLEPHRKNL VKQALQRIRA
851 QEGLSKDVG EIVGKILD*

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a665-1/m665-1 97.2% identity in 867 aa overlap

	10	20	30	40	50	60
a665-1.pep	MSKTVHYLKD	YQTPAYHILK	TDLHFDINEP	QTIIVKSRLT	VEPKRVGEPL	VLDGSAKLLSV
m665-1	MSKTVHYLKD	YQTPAYHILK	TDLHFDINEP	CTIVKSRLT	VEPQRVGEPL	VLDGSAKLLSV
	10	20	30	40	50	60
	70	80	90	100	110	120

a665-1.pep	KINGVAADYVLEGETLTIADVPSEKFTVEVETEILPAENKSLMGLYASAGNLFTQCEPEG
m665-1	KINGAADYVLEGETLTIAGVPSEKFTVEVETEILPAENKSLMGLYASGGNLFTQCEPEG
	70 80 90 100 110 120
a665-1.pep	130 140 150 160 170 180
m665-1	FRKITFYIDRPDVMKFTTTIVADKKRYPVLLSNGNKIDGGEYS DGRHWVKWEDPFAKPS
	130 140 150 160 170 180
a665-1.pep	190 200 210 220 230 240
m665-1	YLFALVAGDLAVTEDYFTTMSGRNVKIEFYITTEADKPKVGF AVESLKNAMKWDETRFGLE
	190 200 210 220 230 240
a665-1.pep	250 260 270 280 290 300
m665-1	YLDIFMVVAVGDFNMGAMENKGLNIFNTKFLVADSRTATD TDFEGIESVVGHEYFHNWT
	250 260 270 280 290 300
a665-1.pep	310 320 330 340 350 360
m665-1	GNRVTCRDWFQLSLKEGLTVFRDQEFSGDRASRAVRRIENIRLLRQH QFPEDAGPTAHPV
	310 320 330 340 350 360
a665-1.pep	370 380 390 400 410 420
m665-1	RPARYEEMNNFYTMTVYEKGAEVVRMYHTLLGEEGFQKGMKLYFORH DGAQVTCDDFRAA
	370 380 390 400 410 420
a665-1.pep	430 440 450 460 470 480
m665-1	MVDANGINLDQFALWYSOAGTPVLDAQGRLENNVFELTIKQTVPPTPD MADKQPMIIPVK
	430 440 450 460 470 480
a665-1.pep	490 500 510 520 530 540
m665-1	IGLLNCGEAVAFDYQGKRATEAVLLTEAEQTFQFESVTEAVVPSLLRGFSAPVHLNYP
	490 500 510 520 530 540
a665-1.pep	550 560 570 580 590 600
m665-1	YSDDDLLLLLAHDSDAFTRWEEAQTLYRRAVAANLAALS DGVLPKHEKLLAAVEKVISD
	550 560 570 580 590 600
a665-1.pep	610 620 630 640 650 660
m665-1	DLLDNAFKALLLGVPSAEELWDGAENIDPLRYHQAREALLDILAVRFLPKWHELNROAAK
	610 620 630 640 650 660
a665-1.pep	670 680 690 700 710 720
m665-1	QENQSYEYSPEAAGWRTLNRVCFVLRADFAHIETVAEKYAEQAQNM THEWGILSAVNG
	670 680 690 700 710 720
a665-1.pep	730 740 750 760 770 780
m665-1	NESDTRNRLLAQFADKFSDDALVMDKYFALVGSSRRSDTLQQVQTALQHPKFSLENPNKA
	730 740 750 760 770 780
a665-1.pep	790 800 810 820 830 840
m665-1	RSLIGSFSRNVPHFAEDGSGYRFIADKVI EIDRFNPQVAARLVQAFNLCNKLEPHRKNL
	790 800 810 820 830 840

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	790	800	810	820	830	840
	850	860				
a665-1.pep	VKQALQIRIRAQEGLSKDVGEIVGKILDX					
m665-1	VKQALQIRIRAQEGLSKDVGEIVGKILDX					
	850	860				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2171>:

```

g666.seq
1  ATGCTTTGTA TGAATTATCA ATCAAACCTCA GGCGAAGGAG TGCTTGTAGC
51  TAAAACATAT TTATTGACTG CATTGATAAT GTCTATGGTA ATCTCCGGAT
101 GTCGAAGTCAT CCATGCCAAT CAAGGTAAGG TTAATACTAA TTCTGCTGTC
151 ATCGCAGGTG CAGACGCTCA CACGCCTGAA CATGTAACGG GACTGACCGA
201 ACAAAGCAG GTGATTGCAA GTGATTTTAT AGTAGCGTCA GCCAATCCAT
251 TAGCAACACA AGCTGGCTAT GATATCTTAA AGCAAGGCGG TAGCGCTGCA
301 GATGCGATGG TGGCGGTGCA GACGACACTA AGCTTGGTAG AGCCACAGTC
351 GTCAGGCTTG GCGCGTGGTG CATTCTGTT GTATTGGGAC AATACCGCCA
401 AACATTGAC CACATTGAT GGGCGTGAGA CGGCACCGAT GCGTGCACG
451 CCAGAATTAT TTTTGGATAA AGATGGTTAA CCATTGAAAT TTATGGAAGC
501 GGTGGTCGCT CGGTAGGTAC GCCTGCTATC CCTAAACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2172; ORF 666.ng>:

```

g666.pep
1  MLCMNYQSNS GEGVLVAKTY LLTALIMSMV ISGCQVIHAN QGKVNTHSAV
51  IAGADAHTPE HVTGLTEQKQ VIASDFIVAS ANPLATQAGY DILKQGGSA
101 DAMVAVQTTL SLVEPQSSGL GGGAFVLYWD NTAKTLTTFD GRETAPMRAT
151 PELFLDKDGX PLKFMEAVVA RXVRLLSLN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2173>:

```

m666.seq
1  ATGCCTTGTA TGAATCATCA ATCAAACCTCA GGCGAAGGAG TGCTTGTTGGC
51  TAAAACATAT TTATTGACTG CATTGATAAT GTCTATGACA ATCTCTGGAT
101 GTCGAAGTCAT CCATGCCAAT CAAGGTAAGG TTAATACTCA TTCTGCTGTC
151 ATCACAGGTG CAGACGCTCA CACGCCTGAA CATGCAACGG GACTGACCGA
201 ACAAAGCAG GTGATTGCAA GTGATTTTAT GGTAGCGTCA GCCAATCCAT
251 TAGCAACACA AGCTGGCTAT GATATCTTAA AGCAAGGCGG TAGCGCTGCA
301 GATGCGATGG TGGCGGTGCA GACGACACTA AGCTTGGTAG AGCCACAGTC
351 GTCAGGCTTG GCGCGTGGTG CATTGTGTT GTATTGGGAT AATACCGCCA
401 AACATTGAC CACATTGAT GGGCGTGAGA CGGCACCGAT GCGTGCACG
451 CCGGAATTAT TTTTGGATAA AGATGGTCAA CCATTGAAAT TTATGGAAGC
501 GGTGGTCGTG GTCGCTCGGT GGTACGCCT GCTATCCCTA AACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2174; ORF 666>:

```

m666.pep
1  MPCMNHQSNS GEGVLVAKTY LLTALIMSMT ISGCQVIHAN QGKVNTHSAV
51  ITGADAHTPE HATGLTEQKQ VIASDFIVAS ANPLATQAGY DILKQGGSA
101 DAMVAVQTTL SLVEPQSSGL GGGAFVLYWD NTAKTLTTFD GRETAPMRAT
151 PELFLDKDGQ PLKFMEAVV VARWVRLSL N*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m666/g666 93.9% identity in 181 aa overlap

	10	20	30	40	50	60
m666.pep	MPCMNHQSNSGEGVLVAKTYLLTALIMSMTISGCQVIHANQGKVNTHSAVITGADAHTPE					
g666	MLCMNYQSNSGEGVLVAKTYLLTALIMSMTISGCQVIHANQGKVNTHSAVITGADAHTPE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m666.pep	HATGLTEQKQVIASDFIVASANPLATQAGYDILKQGGSAADAMVAVQTTL					
	SLVEPQSSGL					

```

g666      |:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
HVTGLTEQKQVIASDFIVASANPLATQAGYDILKQGGSAAADAMVAVQTTLSLVEPOSSGL
              70              80              90              100             110             120

              130             140             150             160             170             180
m666.pep  GGGAFVLYWDNTAKTLTTFDGRETAPMRATPELFLDKDGQPLKFMEAVVVVARWVRLLSL
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g666      GGGAFVLYWDNTAKTLTTFDGRETAPMRATPELFLDKDGXPLKFMEAVV--ARXVRLLSL
              130             140             150             160             170

m666.pep  NX
           ||
g666      NX
           180

```

a666.seq

```
1 ATGCCTTGTA TGAATCATCA ATCAAACCTCA GGCGAAGGAG TGCTTGTTGGC
51 TAAAACATAT TTATTGACTG CATTGATAAT GTCTATGACA ATCTCTGGAT
101 GTC AAGTCAT CATGCCAAAT CAAGGTAAGG TTAATACTCA TTCTGCTGTC
151 ATCACAGGTG CAGACGCTCA CACGCCCTGAA CATGCAACGG GACTGACCGA
201 ACAAAGACAG GTGATTGCAA GTGATTTTAT GGTAGCGTCA GCCAATCCAT
251 TAGCAACACA AGCTGGCTAT GATATCTTAA AGCAAGGCGG TAGCGCTGCA
301 GATGCGATGG TGGCGGTGCA GACGACACTA AGCTTGGTAG AGCCACAGTC
351 GTCAGGCTTG GCGCGTGGTG CATTTGTGTT GTATTGGGAT AATACCGCCA
401 AAACATTGAC CACATTTGAT GGGCGTGAA AGATGGTCAA CCATTGAAAT TTATGGAAGC
451 CCGGAATTAT TTTTGGATAA GGGTACGCCT GCTATCCCTA AACTGA
501 GGTGGTCGTG GTCGCTCGGT
```

a666.pep

1	MPCMNHOSNS	GEGVLAKTY	<u>LLTALIMSMT</u>	ISGCOVIHAN	QGKVNTHSAV
51	ITGDAHTPE	HATGLTEQKQ	VIASDFMVAS	ANPLATQAGY	DILKQGGGSA
101	DAMVAVQTTL	SLVEPQSSGL	GGGAFVLYWD	NTAKTLTTFD	GRETAPMRAT
151	PELFLDKDGO	PLKFMEAVVV	VARVVRLLSL	N*	

		10	20	30	40	50	60
m666.pep		MPCMNHQNSGEGVLVAKTYLLTALIMSMTISGCQVIHANQGKVNTHSAVITGADAHTPE					
a666		MPCMNHQNSGEGVLVAKTYLLTALIMSMTISGCQVIHANQGKVNTHSAVITGADAHTPE					
		10	20	30	40	50	60
		70	80	90	100	110	120
m666.pep		HATGLTEQKQVIASDFMVASANPLATQAGYDILKQGGSAADAMVAVQTTLSLVEPQSSGL					
a666		HATGLTEQKQVIASDFMVASANPLATQAGYDILKQGGSAADAMVAVQTTLSLVEPQSSGL					
		70	80	90	100	110	120
		130	140	150	160	170	180
m666.pep		GGGAFVLYWDNTAKTLTTFDGREAPMRATPELFLDKDGQPLKFMEAVVVVARWVRLLSL					
a666		GGGAFVLYWDNTAKTLTTFDGREAPMRATPELFLDKDGQPLKFMEAVVVVARWVRLLSL					
		130	140	150	160	170	180
m666.pep		NX					
a666		NX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2177>:

```

g667.seq
1   atgcggtttg tcttctgttt gggcgGAGAG ATAGtttctg atccgtgtga
51  tttccAtttg gtattcgtcc gcgtcgaatc tgccgctgAc CAGAcagaaa
101 cgCAGataca tCaaatacgt attcacggca tcggtttcgc aatAAttgcg
151 GAtttccttc agcgtgcccg cgtgGAacgc tccccacact ttgtgccgt
201 ccataCCCAg ctTGCCCGGA AAGCCGCACA GTTTCgcCat atcgtccagC
251 GGCACATTcg ccctcggtG GTAAAGCGCG AGCAAATCCA TCAAATCGCA
301 GTGGCGTTGG TGATAACGGC TGATGTAGTT GTTCCActtg AAATCGCGGC
351 tgtcgccgAA ATCGccgTCG CCCGTATCCC AATAGCCGCG GCGGTTGATG
401 CCGTATATCA GGGAGCGGTA ATGCAGTACG GGCAGGTCGA AACCGCCGCC
451 GTTCCAGCTG ACCAGTTGCG GCGTATGTTT TTCAACCAAT TCGAAAAACT
501 TGGCAATCAC GACTTCTTCG CCATCGTCCA TCTCGCCGAT GGTGCCGACA
551 TGAACCTTGT CCTGCCCCCA GCGCATACAG CAGGAAACCG CCACAACCTG
601 ATGGAGGTGG TGCTGCATAA AATCGCCGCC GGTCTGTGCG CGGCGTTTCT
651 GCTGCGCGAA CAGCACCCTG TCGTCATCCG GCAGGGAAGA CGGCAAGTCA
701 TACACGTAC GGATACCCTG CACATCGGGT ACGGTTTCAA TATCGAAAGC
751 CAAAATCGTA TTCATGGCag tACCTTGCAT tcaAAAACAG ActTGCGCCT
801 ATTgTgtcaT TAA

```

This corresponds to the amino acid sequence <SEQ ID 2178; ORF 667.ng>:

```

g667.pep
1   MRFVFCLGGE IVSDPCDFHL VFVRVESAAD QTETQIHQIR IHGIGFAIIA
51  DFLQRRARVER FPHFAAVHTQ LARKAAQFRH IVQRHIRPRL VKREQIHQIA
101 VALVITADV VPLEIAAVAE IAVARIPIAR GVDVYQGAV MQYGQVETAA
151 VPADQLRRMF FNQFEKLG NH DFFAIVHLAD GADMNLVLP AHTAGNRHNL
201 MEVVLHKIAA GLCAAFLLRE QHHEVIRQGR RQVIQRTDTL EIGYGFNIES
251 QNRHGSTLH SKTDLRLLLCH *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2179>:

```

m667.seq (PARTIAL)
1   ATGCGGCTTT TCCCCGGCTT GTGCGGACAG GTAATTCCGC ATCGGTTTGA
51  TTTCATTTTC GTATTCTGTC GCATCCAGCC TGCCGCTGAC CAGACAGAAA
101 CGCAGGTACA TCAGATAAGT GTTGCCGCG TCGGTTTCGC AATAATTGCG
151 GATTTCCTTC AGCCTGCCCG TATGGAATGC CTCCCAAACC TTGCTGCCGT
201 CCATACCCAG CTTGCCCGGA AAACCGCACA GTTTCGCCAT ATCGTCCAGC
251 GGCACGTTTG CCCTCGGCTG GTAAAGCGCG AGCAAATCCA TCAATCGCA
301 GTGGCGTTGG TGATAACGGC TGATGTAGTT GTTCCACTTG AAATCGCGGC
351 TGTCGCCGAA ATCGCCGTCG CCCATATCCC AATAGCGCGC GCGGTTGATG
401 CCGTATATCA GGGAGCGGTA ATGCAGTACG GGCAGATCGA AACCGCCGCC
451 GTTCCAACCTG ACCAGTTGCG GCGTATGTTT TTCAATCAAT TCGAAAAATT
501 TAGCAATGAC CACTTCTCTG CCGTCATCCA TCTCGCCGAT GGTGCCGACA
551 TGTACTTTAT CCTGCCCCCA ACGCATGCAG CACGAAATCG CCACAACCTG
601 ATGAAGATGA TGCTGCATAA AATCGCCGCC CGTCTGAGCA CGGCGTTTGT
651 GCTGGGCAAT CAGCACCCT TG...

```

This corresponds to the amino acid sequence <SEQ ID 2180; ORF 667>:

```

m667.pep (partial)
1   MRLFPGLCGQ VIPHPDFHF VFVRIQPAAD QTETQVHQIS VCRVGFAIIA
51  DFLQPARMEC LPNLAHVHTQ LARKTAQFRH IVQRHVCPR L VKREQIHQIA
101 VALVITADV VPLEIAAVAE IAVAHIPIAR GVDVYQGAV MQYGQIETAA
151 VPTDQLRRMF FNQFEKFSND HFLAVIHLAD GADMYFILPP THAARNRHN L
201 MKMMLHKIAA RLSTAFVLGN QHHL...

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m667/g667 75.0% identity in 224 aa overlap

```

          10      20      30      40      50      60
m667.pep  MRLFPGLCGQVIPHPDFHFVFVRIQPAADQTETQVHQISVCRVGFAIIADFLQPARMEC
          ||:  | |:::  | |||:||||: |||||:| | : : ||||| ||:|

```

g667	MRFVFC	LGGEIV	SDPCDF	HLVFVR	VE	SAADOT	ETETQI	HQIRIH	GIGFAI	IADFLQ	RARVER	
	10	20	30	40	50	60						
m667.pep	70	80	90	100	110	120						
	LPNLA	AAVHTQ	LARKTA	QFRHIV	QRHVCP	RLVKRE	QIHQI	IAVALV	ITADVV	VVPLEI	AAVAE	
g667	:	:	:	:	:	:	:	:	:	:	:	
	70	80	90	100	110	120						
m667.pep	130	140	150	160	170	180						
	IAVAHI	PIARGV	DAVYQG	AVM	QYQGI	ETA	AAVPTD	QLRRM	FFNQ	FEKFS	NDHFL	AVIHLAD
g667	:	:	:	:	:	:	:	:	:	:	:	
	130	140	150	160	170	180						
m667.pep	190	200	210	220								
	GADMY	FILP	PTHAA	RNRH	NLMK	MLHK	IAARL	STAF	VLGN	QHHL		
g667	:	:	:	:	:	:	:	:	:	:		
	190	200	210	220	230	240						
m667.pep	GADMN	LVLPP	AHTAG	RNRH	NLM	EVVL	HKIA	AGLCA	AFLL	REQH	FVIR	QGRROV
g667	:	:	:	:	:	:	:	:	:	:	:	
	190	200	210	220	230	240						
m667.pep	HIGY	GFNI	ESQ	NRH	GSTL	HSK	TDL	RL	LL	CHX		
g667	:	:	:	:	:	:	:	:	:	:		
	250	260	270									

```

a667.seq
1 ATGCGGTTTG TCTTCTGTTT GGGCGGAGAG ATAGTTTCTG ATCCGCTTGA
51 TTCCATTTC GTATTGCTGT GCGTCGAATC TGCCGCTGAC CAGACAGAAA
101 CCGAGATACA TCAGATAGCT ATTTACCGCA TCGGTTTCGC AATAATTGCG
151 GATTTCCTTC AGCCTGCCCG CTTGGAAACG CTCCCACACC TTGCTGCCGT
201 CCATACCCAG CTTGCCCGGA AAACCGCACA GTTTCGCCAT ATCGTCCAAC
251 GGCACATTCC CCCTCGGCTG GTAAGACGCG AGCAAATCCA TCAAATCGCA
301 ATGACGTTGG TGGTAGCGCG TCGATGTAGT GTTCCACTTG AAATCGCGGC
351 TGTCGCCGAA ATCGCCGCTG CCATATCCCT AATAGCGCGC GGCCTTGTAT
401 CCGTGTAGCA GCGAACGETA ATGCAGAACG GGCAGGTGCA AACCGCGCCG
451 GTTCCAAC TGAGTTGCG GCGTATGTTT TTCAATCAAC TCGAAAAATT
501 TGGCGATAAC CACTTCCTCG CCGTCATCCA TCTCGCGGAT TGTACCGACA
551 TGGACTTTAT CCTGCCCCCA ACGCATGCAG CAGGAAATCG CCACAATCTG
601 ATGAAGATGA TGCTGCATAA AATCCCCACC CGTCTGAGCA CGGCGTTTT
651 GCTGGGCAAA CAGCACCAC TCATCGTCCG GCAGCGAGGA CGGCAAGTCA
701 TACAGCGTAC GGATACACTG CACATCGGGT ACGGTTTCAA TATCGAAAGC
751 CAAAATCGTG GTCATGACAG CACCTTGAT TTA AAAA.CAG ACTTGGCGCT
801 ATTGTGTCAT TAA

```

a667.pep

1	MRFVFCFLGGE	IVSDPLDFHF	VFVCVESAAD	QTETQIHQIG	IYRIGFAIIA
51	DFLQPARVER	LPHLAAVHTQ	LARKTAQFRH	IVQRHIRPRL	VKNRQIHQIA
101	MTLVVAADV	VPLEIAAVAE	IAVAHIPIAR	GVDVA*QRTV	MQRQVETAA
151	VPTDQLRRMF	FNQLEKFGDN	HFLAVIHLAD	CTDMDFILPP	THAARNRHNL
201	MKMMHLHKIPT	RLSTAFLLGK	QHHFIVGQRG	RQVIQRTDTL	HIGYGFNIES
251	ONRGHDSITLY	LKXDIRLLCH	*		

	10	20	30	40	50	60
m667.pep	MRLFPGLCGGVIPHFDHFVVR	QIPAAADQTETQVHQISV	CRVGF	AIADFLQ	PARMEC	
a667	MRFVFC	LGGEIVSDPLDFHFVFCVESAADQTETQIHQIGIYRIGF	AIADFLQ	PARVER		
	10	20	30	40	50	60
m667.pep	LPNLA	AVHTQLARKTAQFRHIVQRHVC	PRLVKREQIHQIA	VALVITADVVVPLEIA	AAVAE	
a667	LPHLA	AVHTQLARKTAQFRHIVQRHIRPRLVKREQIHQIAMTLVVAADVVVPLEIA	AAVAE			
	70	80	90	100	110	120

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	70	80	90	100	110	120
m667.pep	130	140	150	160	170	180
	I A V A H I P I A R G V D A V Y Q G A V M Q Y G Q I E T A A V P T D Q L R R M F F N Q F E K F S N D H F L A V I H L A D					
a667	130	140	150	160	170	180
	I A V A H I P I A R G V D A V X Q R T V M Q N R Q V E T A A V P T D Q L R R M F F N Q L E K F G D N H F L A V I H L A D					
m667.pep	190	200	210	220		
	G A D M Y F I L P P T H A A R N R H N L M K M M L H K I A A R L S T A F V L G N Q H H L					
a667	190	200	210	220	230	240
	C T D M D F I L P P T H A A R N R H N L M K M M L H K I P T R L S T A F L L G K Q H H F I V G Q R G R Q V I Q R T D T L					
a667	250	260	270			
	H I G Y G F N I E S Q N R G H D S T L Y L K X D L R L L C H X					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2183>:

```

g669.seq
1   ATGCGCGCA TCGTTAAAA ACACGAGCCC GTAAACGCGC CACATATCGT
51  TTTGGAATT CGGATAATGA AACTGCATCG CGCGTTTGTC TTCCTTGGGC
101 GGAAACGTCC CCATCATCAT GACCGCAGCC TTCGCGGCA ACACGGGATC
151 GAAGGGATGG GTTTCGATT CAAGCAGATT TTCAGACACG TTCAATCCTC
201 CAACAGGCAA AGCGGCAGAC AGCCGGTTTG CACCAAACCG CCAAACACGG
251 CAAGCCTTCA AACAGCATTA TCACGCCCTG CCGTTTTCGG TTACAATGCC
301 GACATCAAAC GGATACTGTA A

```

This corresponds to the amino acid sequence <SEQ ID 2184; ORF 669.ng>:

```

g669.pep
1   MRRIVKKHQP VNAPHIVLEI RIMKLHRAFV FLGRKRPHHH DRSLRRQHGI
51  EGMGFDFKQI FRHVQSSNRQ SGRQPVCTKP PNTASLQTAL SRPAVFGYNA
101 DIKRIL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2185>:

```

m669.seq
1   ATGCGCGCA TCATTAAAA ACACGAGCCC ATAAACGCGC CACATATCGT
51  TTTGGAATT CGGATAATGA AACTGCATCG CGCGTTTGTC TTCCTTGGGC
101 GGAAACGTCC CCATCATCAT GACAGCAGCC TTCGGCGGCA ACACGGGATC
151 GAAGGGATGG GTTTCGATT CAAGCAGATT TTCAGACACG TTCAATCCTC
201 CAACAGGCAA AACGGCAGAC AGCCGGTTTG CACCAAACCG CCAAACACGG
251 CAAGCCTTCA AACAGCATTA TCACGCCCTG CCGTTTTCGG TTACAATGCC
301 GACATCAAAC GGATACTGTA A

```

This corresponds to the amino acid sequence <SEQ ID 2186; ORF 669>:

```

m669.pep
1   MRRIIKKHQP INAPHIVLEI RIMKLHRAFV FLGRKRPHHH DSSLRRQHGI
51  EGMGFDFKQI FRHVQSSNRQ NGRQPVCTKP PNTASLQTAL SRPAVFGYNA
101 DIKRIL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m669/g669 96.2% identity in 106 aa overlap

	10	20	30	40	50	60
m669.pep	M R R I I K K H Q P I N A P H I V L E I R I M K L H R A F V F L G R K R P H H H D S S L R R Q H G I E G M G F D F K Q I					
g669	M R R I V K K H Q P V N A P H I V L E I R I M K L H R A F V F L G R K R P H H H D R S L R R Q H G I E G M G F D F K Q I					
	10	20	30	40	50	60
	70	80	90	100		

1073

```

m669.pep    FRHVQSSNRQNGRQPVCTKPPNTASLQTALSRPAVFGYNADIKRILX
             |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g669        FRHVQSSNRQSGRQPVCTKPPNTASLQTALSRPAVFGYNADIKRILX
             70      80      90      100

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2187>:

```

a669.seq
1  ATGCGCCGCA TCATTAATAA ACACCAGCCC GTAAACGCGC CACATATCGT
51  TTTGGAAATT CGGATAATGA AACTGCATCG CGCGTTTGTC TTCCTTGGGC
101 GGAACGTC CCATCATCAT GACGCGAGCC TTCGGCGGCA ACACGGAATC
151 GAAGGGATGG GTTTCGATT CAAGCAGATT TTCAGACACG TTCAATCCTC
201 CAACAGGCAA AACGGCAGAC AGCCGGTTTG CACCAAACCG CCAAACACGG
251 CAAGCCTTCA AACAGCATT TCACGCCCTG CCGTTTTCGG TTACAATGCC
301 GACATCAAC GGATACTGTA A

```

This corresponds to the amino acid sequence <SEQ ID 2188; ORF 669.a>:

```

a669.pep
1  MRRIKKHQF VNAPHIVLEI RIMKLHRAV FLGRKRPHHH DRSLRRQHGI
51  EGMGFDFKQI FRHVQSSNRQ NGRQPVCTKP PNTASLQTAL SRPAVFGYNA
101 DIKRIL*

```

m669/a669 98.1% identity in 106 aa overlap

```

              10      20      30      40      50      60
m669.pep    MRRIKKHQPINAPH_VLEIRIMKLHRAVFLGRKRPHHHDRSLRRQHGI EGMGFDFKQI
             |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a669        MRRIKKHQPVNAPH_VLEIRIMKLHRAVFLGRKRPHHHDRSLRRQHGI EGMGFDFKQI
              10      20      30      40      50      60

              70      80      90      100
m669.pep    FRHVQSSNRQNGRQPVCTKPPNTASLQTALSRPAVFGYNADIKRILX
             |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a669        FRHVQSSNRQNGRQPVCTKPPNTASLQTALSRPAVFGYNADIKRILX
             70      80      90      100

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2189>:

```

g670.seq
1  ATGACTTGTT GCAGGAAC TGCTGGCGCGT TCGTGTTCG GGTGGTGAA
51  AAACGCTTCC GCGGTTTCGT CTTCAAGGAT TTGCCCTTTA TCGACGAAAA
101 TCACGCGGTC GGCAACTTCG CGGGCAAACC CCATTTCGTG GGTACGCAC
151 ATCATCGTCA TGCCGCTTTC CGCCAAGTCT TTCATCACTT TCAACACTTC
201 GCCGACCATT TCGGGTCGA GTGCGGAAGT CGGCTCGTCA AACAGCATCA
251 CGCGCGGCTC CATCGCCAGC CCGCGCGCAA TCGCCACGCG TTGCTGCTGG
301 CCGCCGGAAG GTTGGGAAGG GAAGGCGTCT TTTTGTGTG CCAGTCCGAC
351 GCGTTCCAAA AGCTCCATTG CCTTTTCTC CGCCTGTCC GCATTTGCC
401 CCTTAACCTT CATCGGTGCG AGGGTGATGT TGTCCAACAC GGTGAGGTGC
451 GGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2190; ORF 670.ng>:

```

g670.pep
1  MTCCRNCLAR SCFGLVKNAS GVSSSRICPL STKITRSATS RANPISWVTH
51  IIVMPLSAKS FITFNTSPTI SGSSAEVGSS NSITRGSIAS PRAIATRCW
101 PPESWEGKAS FLCASPTRSK SSIAFFSACS AFCPLTFIGA RVMLSNTVRC
151 G*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2191>:

```

m670.seq
1  ATGACCTGTT GCAGGAAC TGCTGGCGCGT TCGTGTTCG GGTGGTGAA
51  AAACGCTTCC GCGGTTTCGT CTTCAAGGAT TTGCCCTTTA TCGACGAAAA
101 TCACGCGGTC GGCAACTTCG CGGGCAAACC CCATTTCGTG GGTACGCAC
151 ATCATCGTCA TGCCGCTTTC TGCCAAGTCT TTCATCACTT TCAACACTTC
201 GCCGACCATT TCGGGTCGA GTGCGGAGGT CGGTTCTGTC AACACATTA

```

1074

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251 CGCGCGGTTC CATCGCCAAA CCGCGTGCAA TCGCCACGCG TTGCTGCTGG
301 CCGCCGGAAA GTTGGGAAGG GAAGGCGTCT TTTTGTGTG CCAGTCCGAC
351 GCGTTCCAAA AGCTCCATTG CCTTTTCTC CGCCTGTTCC GCATTTTGCC
401 CCTTAACCTT CATCGGTGCG AGGTAATGT TTTCCAACAC GGTGAGGTGC
451 GGGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2192; ORF 670>:

```

m670.pep
  1 MTCCRNCLAR SCFGLVKNAS GVSSSRICPL STKITRSATS RANPISWVTH
  51 IIVMPLSAKS FITFNTSPTI SGSSAEVGSS NNITRGSIAK PRAIATRCCW
 101 PPESWEGKAS FLCASPTRSK SSIAFFSACS AFCPLTFIGA RVMFSNTVRC
 151 G*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m670/g670 98.0% identity in 151 aa overlap

```

              10      20      30      40      50      60
m670.pep      MTCCRNCLARSCFGLVKNASGVSSSRICPLSTKITRSATS RANPISWVTHIIVMPLSAKS
               |||
g670           MTCCRNCLARSCFGLVKNASGVSSSRICPLSTKITRSATS RANPISWVTHIIVMPLSAKS
              10      20      30      40      50      60

              70      80      90     100     110     120
m670.pep      FITFNTSPTISGSSAEVGSSNNITRGSIAKPRAIATRCCWPPESWEGKASFLCASPTRSK
               |||
g670           FITFNTSPTISGSSAEVGSSNITRGSIAKPRAIATRCCWPPESWEGKASFLCASPTRSK
              70      80      90     100     110     120

              130     140     150
m670.pep      SSIAFFSACSAFCPLTFIGARVMSNTVRCGX
               |||
g670           SSIAFFSACSAFCPLTFIGARVMSNTVRCGX
              130     140     150

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2193>:

```

a670.seq
  1 ATGACCTGTT GCAGGAACGT CTTGGCGCGT TCGTGTTTCG GGTGTTGTAAG
  51 AAACGCTTCC GGCCTTTTCT CTTCGAGGAT TTGCCCTTTA TCGACGAAAA
 101 TCACGCGGTC GGCAACTTCG CGGGCAAACC CCATTTCTGTG GGTACGCAC
 151 ATCATGGTCA TACCGCTTTC CGCCAAGTCT TTCATCACTT TCAACACTTC
 201 GCCGACCATT TCGGGGTGGA GTGCGGAGGT CGGTTCTGCA AACAAACATTA
 251 CGCGCGGTTC CATCGCCAAA CCGCGTGCAA TCGCCACGCG TTGCTGCTGG
 301 CCGCCGGAAA GTTGGGAAGG GAAGGCGTCT TTTTGTGTG CCAGTCCGAC
 351 GCGTTCCAAA AGTTCCATCG CTTTTTCTC TGCCTGTTCC GCATTTTGAC
 401 CTTTAACCTT CATCGGTGCG AGGTAATGT TTTCCAACAC GGTGAGGTGC
 451 GGGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2194; ORF 670.a>:

```

a670.pep
  1 MTCCRNCLAR SCFGLVKNAS GVSSSRICPL STKITRSATS RANPISWVTH
  51 IMVIPLSAKS FITFNTSPTI SGSSAEVGSS NNITRGSIAK PRAIATRCCW
 101 PPESWEGKAS FLCASPTRSK SSIAFFSACS AF*PLTFIGA RVMFSNTVRC
 151 G*

```

m670/a670 98.0% identity in 151 aa overlap

```

              10      20      30      40      50      60
m670.pep      MTCCRNCLARSCFGLVKNASGVSSSRICPLSTKITRSATS RANPISWVTHIIVMPLSAKS
               |||
a670           MTCCRNCLARSCFGLVKNASGVSSSRICPLSTKITRSATS RANPISWVTHIMVIPLSAKS
              10      20      30      40      50      60

```

1075

	70	80	90	100	110	120
m670.pep	FITFNTSPTISGSSAEVGSNNITRGSIAKPRAIATRCWPPESWEGKASFLCASPTRSK					
a670	FITFNTSPTISGSSAEVGSNNITRGSIAKPRAIATRCWPPESWEGKASFLCASPTRSK					
	70	80	90	100	110	120
	130	140	150			
m670.pep	SSIAFFSACSAFCPLTFIGARVMFSNTVRCGX					
a670	SSIAFFSACSAFXPLTFIGARVMFSNTVRCGX					
	130	140	150			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2195>:

g671.seq

1	ATGATCAGCA	GGTAACAAT	CAAAACGCCT	TTCAATGCAC	CGAATACACC
51	GCCCAAAATG	CGGTTGGCAA	AGCCAGACC	GACCGCCGAA	ACTGCGCUGG
101	TCAGCAGCGA	ACGAGGCATT	TTCTGGATCA	GACAGGCAAT	GACGAACAGG
151	GAAATGAATG	ACAGagccaa	TGCAAAACagg	cggggTTGGA	ACGaggCAAA
201	GGCGAGGTcg	gcgaaggGTG	CGGCaaAGAG	TTTggcaaAA	AAGAaggAAA
251	ccaccCATGC	cACCATCgaa	ccTGCTTCGG	CAATCACGCC	GCGCATCGTG
301	GAAATGACGA	TGCAGGCGGC	GATGACGGcg	gAGGCGAGGA	GGTCGGCAAT
351	GGGGAGGCTA	TTCATTCGTT	ACCTGGCCGG	CGATGCCGTG	CACGCGCAGT
401	TTGTTCAAAT	CGCGTTCGGC	ATCCCTTGCG	TTTTTATAGT	TGCTTGA

This corresponds to the amino acid sequence <SEQ ID 2196; ORF 671.ng>:

g671.pep

1	MISRVTIKTP	FNAPNTPPKM	RLAKPRPTAE	TAPVSSERSI	FWIRQAMTNR
51	EMNDRANANR	RGWNEAKARS	AKGAAKSLAK	KKETTHATIE	PASAITPRIV
101	EMTMQAAMTA	EARRSAMGRL	FIRYLAGDAV	HAQFVQIAFG	IPCVFIVA*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2197>:

m671.seq

1	ATGACCAGCA	GGTAACAAT	CAAAACGCCT	TTCAATGCAC	CGAATACGCC
51	GCCCAAAATG	CGGTTGGCAA	AGCCCAAACC	GACCGCCGAA	ACTGCGCTGG
101	TCAGCAGCGA	ACGAGGCATT	TTCTGGATCA	GACAGGCAAT	GACGAACAGG
151	GAAATGAACG	ACAGAGCCAA	TGCAAAACAGG	CGGGGTGGA	ACGAGGCCAA
201	GGCGAGGTCG	GCGAAGGAGG	CGGCAAAAGAG	TTTGGCGAAA	AAGAAGGAAA
251	CCACCCATGC	CGCCATTGAG	CCTGCCTCCG	CAATCACGCC	GCGCATCGCG
301	GATAGCACGA	TGCAGGCGGC	GATGACGGCG	GAGACGAGGA	GGTCGGCAAT
351	GGGGAGGCTA	TTCATTCGTT	ACCTGACCGG	CGATACCGTG	TACGCGCAAT
401	TTGTTCAAAT	CGCGTTCGCG	ATCCCTTGCG	TTTTTATAGT	TGCTTGA

This corresponds to the amino acid sequence <SEQ ID 2198; ORF 671>:

m671.pep

1	MTSRVTIKTP	FNAPNTPEKM	RLAKPKPTAE	TALVSSERSI	FWIRQAMTNR
51	EMNDRANANR	RGWNEAKARS	AKEAAKSLAK	KKETTHAAIE	PASAITPRIA
101	DSTMQAAMTA	ETRRSAMGRL	FIRYLTGDTV	YAQFVQIAFG	IPCVFIVA*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m671/g671 91.9% identity in 148 aa overlap

	10	20	30	40	50	60
m671.pep	MTSRVTIKTPFNAPNTPPKMRLAKPKPTAETALVSSERSIFWIRQAMTNREMNDRANANR					
g671	MISRVTIKTPFNAPNTPPKMRLAKPRPTAETAPVSSERSIFWIRQAMTNREMNDRANANR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m671.pep	RGWNEAKARSAKEAAKSLAKKKETTHAAIEPASAITPRIADSTMQAAMTAETRRSAMGRL					

```

g671      ||||| | : ||||| : : ||||| : |||||
          RGWNEAKARSAKGAASKLAKKETTHATIEPASAITFRIVETMQAAMTAEARRSAMGRL
              70           80           90           100          110          120

                130         14C        149
m671.pep   FIRYLTGDTVYAQFVQIAFGIPCVFIVAX
          ||||| : ||| : ||||| |||||
g671       FIRYLAGDAVHAQFVQIAFGIPCVFIVAX
                130         14C

```

```
a671.seq
1  ATGACCAGCA GGGTAATAAT CAAATGCCT TTCAATGCAC CGAATACGCC
51  GCCCAAAATG CGGTGGCAA AGCCCAAACC GACCGCGGAA ACTGCCCCGG
101 TCAGCAGCGA CGCGAGTATT TTCTGGATCA GACAGGCAAT GACGAATAGG
151 GAAATGAACG ACAGAGCCAA TGCAACACAG CGGGGTGGA ACATGCAAA
201 GCGATGTCTG GCGAAGGSTG CGGCAAGAG TTGGCGAAA AAAAAGGCAA
251 CCACCATGCG CGCCATTGAG CCAGCCTCCG CAATCACGCC GCGCATCGCG
301 GATAGCAGCA TGCAGGCCTG GATGATGGCG GAGACAGGGA GGTGCGCAAC
351 GGGGAGGTTA TTCATTCTGT ACCTGACCCG CGATACCGTG TACGCGCAAT
401 TTGTTCAAAT CGCGTTCGCG ATCCCTTGCG TTTTATAGT TGCTTGA
```

```
a671.pep
1  MTSRVIKMP  FNAPNTPPKM  RLAKPKPTAE  TAPVSSERSI  FWIRQAMTNR
51  EMNDRANANR  RGWNDAKAMS  AKGAAKSLAK  KKATTHAAIE  PASAITPRIA
101 DSTMQAAMMA  ETRRSATGRL  FIRYLTGDTV  YAQFVOIAFG  IPCVFIVA*
```

	10	20	30	40	50	60
m671.pep	MTSRVTIKTPFNAPNTPPKMLAKPKPTAETALVSSERSIFWIRQAMTNREMNDRANANR					
a671	MTSRVLIKMPFNAPNTPPKMLAKPKPTAETAPVSSERSIFWIRQAMTNREMNDRANANR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m671.pep	RGWNEAKARSAKEAAKSLAKKKETHAAIEFPASAITPRIADSTMQAAMTAETRRSAMGRL					
a671	RGWNDAKAMSAKGAASKLAKKKATHAAIEFPASAITPRIADSTMQAAMMAETRRSATGRL					
	70	80	90	100	110	120
	130	140	149			
m671.pep	FIRYLTGDTVYAQFVQIAFGIPCVFIVAX					
a671	FIRYLTGDTVYAQFVQIAFGIPCVFIVAX					
	130	140				

```

g672.seq
1  ATGAGGAAAA  TCCGCACCAA  AATCTGCGGC  ATCACCACAC  CGGAAGACGC
51  ACTGTATGCC  GCCACGCCG  GCGCAGACGC  ATTGGGACTG  GTTTTTTTAC
101  CCAAAGCC   CCGCGCTATC  GACATCATTA  AAGCAAAAA  AATCGCGCC
151  GCATGCGCG  CGTTTGTGAC  CSTTGCGCC  CTTTTCGTCA  ACGAAAGCG
201  GCAAAAGCAT  CGCCGCATCC  TTGCCGAAGT  CGCGATACAC  ATCATCCAAT
251  TCCACGGCGA  CGAAGACGAT  GCATTCTGCC  GGCAGTTGGA  CGCCCTTAT
301  ATTAAGCCA  TTCGTGTTCA  GACGGCATCA  GACATCCGAA  ACGCCGCCAC
351  GCGCTTCCC  AACGCTCAG  CACTGCTGTT  CGATGCCTAT  CACCCTTCGG
401  AATACGGCG  CACCGACAC  CGCTTCGact  GGacgtgtt  ggcggAATAT
451  TCGGGCAAG  CGTGGGTGCT  TGCGCGCGGG  CTGACCTCTG  AAAACGTCGG
501  CGAAGCCGT  CGCATCACCG  GAGCGGAAGC  GGTGCACGTA  TCCGGCGGCG
551  TGAAGCGTC  TAAAGGCAA  AAGACCCCG  CCAAAGTCGC  CGCCTTTATC
601  GCAACCGCCA  ACCGCCATC  CGGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2202; ORF 672.ng>:

```
g672.pep
  1 MRKIRTKICG ITTPEDALYA AHAGADALGL VFYFQSPRAI DIIKAQKIAA
 51 ALPPFVSVVA LFNESAQNI RRILAEVPIH IIQFHGDEDD AFCRQFDRPY
101 IKAIRVQTAS DIRNAATREF NAQALLFDAY HPSEYGGTGH RFDWTLLEAY
151 SGKPWVLAGG LTPENVGEAV RITGAEAVDV SGGVEASKGK KDPKVAEFI
201 ATANRLSR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2203>:

```
m672.seq
  1 ATGAGGAAAA TCCGCACCAA AATCTGCGGC ATCACCACAC CGGAAGACGC
 51 AGCTGCCGCC GCAGCGGCAG GTGCGGATGC CGTCGGGCTG GTCTTTTTC
101 AAGGCAGCAG CCGGGCCGTC GATATTGCCG CGCCCAAAAA AATCACCGCC
151 GCACCTGCCGC CGTTTGTCTC CGTTGTCTGC CTTTTCGTCA ACGAAAGCGC
201 GCAAAACATC CGCCGCATCC TTGCCGAAGT GCCGATACAC ATCATCCAAT
251 TCCACGGCGA CGAAGACGAC GCATTCTGCC GCCAGTTCCA CCGCCCCTAT
301 ATCAAAGCCA TTCGTGTTCA GACGGCATCA GACATCCGAA ACGCCGCCAC
351 GCGCTTCCCC GACGCTCAGG CACTGCTGTT CGATGCCTAC CATCCTTCGG
401 AATACGGCGG CACCGGAAAC CGCTTCGACT GGACGCTGCT GCGGGAATAT
451 TCGGGCAAAC CGTGGGTGCT TGCCGGCGGG CTGACCCCTG AAAACGTCGG
501 CGAAGCCGTC CGCATCACCG GAGCGGAATC GGTCGATGTA TCCGGCGGTG
551 TGGAAGCGTC TAAAGGCAAA AAAGATGCCG CCAAAGTCGC CGCCTTTATC
601 GCAACGCCCA ACCGCCTATC CCGTTAA
```

This corresponds to the amino acid sequence <SEQ ID 2204; ORF 672>:

```
m672.pep
  1 MRKIRTKICG ITTPEDAAAA AAAGADAVGL VFFQSSRAV DIARAKKITA
 51 ALPPFVSVVA LFNESAQNI RRILAEVPIH IIQFHGDEDD AFCRQFHRPY
101 IKAIRVQTAS DIRNAATREF DAQALLFDAY HPSEYGGTGN RFDWTLLEAY
151 SGKPWVLAGG LTPENVGEAV RITGAESVDV SGGVEASKGK KDAAKVAEFI
201 ATANRLSR*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m672/g672 91.3% identity in 208 aa overlap

	10	20	30	40	50	60
m672.pep	MRKIRTKICG	ITTPEDAAAA	AAAGADAVGL	VFFQSSRAV	DIARAKKITA	ALPPFVSVVA
g672	MRKIRTKICG	ITTPEDALYA	AHAGADALGL	VFYFQSPRAI	DIIKAQKIAA	ALPPFVSVVA
	10	20	30	40	50	60
m672.pep	LFVNESAQNI	RRILAEVPIH	IIQFHGDEDD	AFCRQFHRPY	IKAIRVQTAS	DIRNAATREF
g672	LFVNESAQNI	RRILAEVPIH	IIQFHGDEDD	AFCRQFDRPY	IKAIRVQTAS	DIRNAATREF
	70	80	90	100	110	120
m672.pep	DAQALLFDAY	HPSEYGGTGN	RFDWTLLEAY	SGKPWVLAGG	LTPENVGEAV	RITGAESVDV
g672	NAQALLFDAY	HPSEYGGTGH	RFDWTLLEAY	SGKPWVLAGG	LTPENVGEAV	RITGAEAVDV
	130	140	150	160	170	180
m672.pep	SGGVEASKGK	KDAAKVAEFI	ATANRLSRX			
g672	SGGVEASKGK	KDPKVAEFI	ATANRLSRX			
	190	200	209			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2205>:

a672.seq

1078

```

1  ATGAGGAAAA TCCGCACCAA AATCTGCGGC ATCACCACAC CGGAAGACGC
51  ACTGTATGCC GCCCAGCGCG GCGCAGACGC ATTGGGACTG GTTTTTTACC
101 CCCAAAGCCC CCGCGCTGTC GACATCATT AAGCACAAAA AATCACCGCC
151 GCACTGCCGC CGTTTGTCTAG CGTTGTCTGCC CTTTTCGTCA ACGAAAGCGC
201 GCAAAACATC CGCCGCATCC TTGCCGAAGT ACCGATACAC ATCATCCAAT
251 TCCACGGCGA CGAAGACGAC GCATTCTGCC GCCAGTTCCA CCGCCCCTAT
301 ATCAAGGCCA TTCGTGTTCA GACGGCATCA GACATCCGAA ACGCCGCCGA
351 CCGCTTCCCC GACGCTCAGG CACTGCTGTT CGATGCCTAC CATCCTTCGG
401 AATACGGCGG CACCGGACAC CGCTTCGACT GGACGCTGTT GCGGGAATAT
451 TCGGGCAAAC CGTGGGTGCT TGCCGGCGGG CTGACCCCTG AAAACGTGCA
501 CGAAGCCATC CGCATCACCG GAGCGGAAGC GGTCGATGTA TCCGGCGGCG
551 TGGAAGCGTC TAAAGGCAAA AAAGACCCAG CCAAAGTTGC CGCCTTTATC
601 GCAACGCCCA ACCGCCTATC CCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2206; ORF 672.a>:

```

a672.pep
1  MRKIRTKICG ITTPEDALYA AHAGADALGL VFYPQSPRAV DIIKAQKITA
51  ALPPFVSVVA LFNESAQNI RRILAEPVPIH IIQFHGDEDD AFQRQFHRPY
101 IKAIRVQTAS DIRNAADRF DAQALLFDAY HPSEYGGTGH RFDWTLLEAY
151 SGKWPVLAGG LTPENVDEAI RITGAEAVDV SGGVEASKGK KDPKVAFAFI
201 ATANRLSR*

```

m672/a672 91.8% identity in 208 aa overlap

	10	20	30	40	50	60
m672.pep	MRKIRTKICG	ITTPEDAAAA	AGADAVGLV	FFQGSRAVD	DIARAKKITA	ALPPFVSVVA
a672	MRKIRTKICG	ITTPEDALYA	AHAGADALGL	VFYPQSPRAVD	IIKAQKITA	ALPPFVSVVA
	10	20	30	40	50	60
	70	80	90	100	110	120
m672.pep	LFVNESAQN	IRRLAEVPIH	IIQFHGDEDD	AFQRQFHRPY	IKAIRVQTAS	DIRNAATRF
a672	LFVNESAQN	IRRLAEVPIH	IIQFHGDEDD	AFQRQFHRPY	IKAIRVQTAS	DIRNAADRF
	70	80	90	100	110	120
	130	140	150	160	170	180
m672.pep	DAQALLFDAY	HPSEYGGTGN	RFDWTLLEAY	SGKWPVLAGG	LTPENVGEAVR	ITGAESVDV
a672	DAQALLFDAY	HPSEYGGTGH	RFDWTLLEAY	SGKWPVLAGG	LTPENVDEAIR	ITGAEAVDV
	130	140	150	160	170	180
	190	200	209			
m672.pep	SGGVEASKGK	DAKVAFAFI	ATANRLSRX			
a672	SGGVEASKGK	DPKVAFAFI	ATANRLSRX			
	190	200				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2207>:

```

g673.seq
1  ATGGATATTG AAACCTTCCT TGCAGGGGAA CGCGCCGCCG GCGGATACCG
51  TTGCGGCTTC GTGGCGATTG TCGGTCGTCC GAACGTGGGC AAATCAACGC
101 TGATGAACCA TCTCATCGGT CAGAAAATCA GTATTACCAG CAAAAAGCGG
151 CAGACGACGC GCAACCGCGT AACGGGGATT TATACCGACG ATACCGCGCA
201 GTTCGTGTTT GTCGATACGC CGGGCTTTCA AACCACCACG CGCAACGCGC
251 TCAACGACAG GCTGAATCAA AATGTTACCG AGCGCTCGG CGGTGTGGAT
301 GTGGTGGTTT TCGTCGTGGA GCGATGCGC CTTACCGATG CCGACCGCGT
351 CGTGTTGAAA CAACTGCCCA AGCACACGCC GGTCAATTTA GTGATCAACA
401 AAATCGACAA GGACAAGGCG AAAGACCGTT ACGCGCTGGA GCGGTTTGTT
451 GCCCAAGTGC GCGCCGAATT TGAATTTGCG GCGGCGGAGG CGGTCAGTGC
501 GAAACACGGT TTGCGGATTG CCAACCTGTT GGAGCTGCTC AAGCCGTATC
551 TGCCCGAAAG CGTACCGATG TATCCGAAG ACATGGTTAC GGACAAATCG
601 GCGCGTTTTT TGGCGATGGA AATCGTGCCT GAAAACTCT TCCGCTATT

```

1079

```

651 GGGCGAGGAG CTGCCTTATG CGATGAACGT CGAAGTGGAG CAGTTTGAAG
701 AGGGAGACGG TTTGAACCGC ATCTACatcg cCGTTTTGGT CGACAAAGAA
751 AGCCAAAAGG CGATTTTGAT CGGTAAAGGC GGGGAGCGTT TGAAAAAAT
801 TTCCACCGAA GCGCGGCTGG ATATGGAAAA ACTGTTTGAT AACAAAGTAT
851 TTTTGAAGGT CTGGGTCAAA GTCAAATCCG GTTGGGCAGA CGACATTCGC
901 TTCCTGCGCG AGCTGGGTTT GTAG

```

This corresponds to the amino acid sequence <SEQ ID 2208; ORF 673.ng>:

g673.pep

```

1 MDIETFLAGE RAAGGYRCGF VAIVGRPNVG KSTLMNHLIG QKISITSKKA
51 QTRNRVTGI YTDDTAQFVF VDTPGFQTDH RNALNDRLNQ NVTEALGGVD
101 VVVVFVEAMR LTDADRVVLK QLPKHTPVIL VINKIDKDKA KDRYALEAFV
151 AQVRAEFEEFA AAEAVSAKHG LRIANLLELL KPYPESVPM YPEDMVTDKS
201 ARFLAMEIVR EKLFRYLGE E LPYAMNVEVE QFEEGDGLNR IYIAVLVDKE
251 SQKAILIGKG GERLKKISTE ARLDMEKLFD NKVFLKVWVK VKSGWADDIR
301 FLRELGL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2209>:

m673.seq

```

1 ATGGATATTG AAACCTTCCT TGCAGGGGAA CGCGCCGCCG GCGGATACCG
51 TTGCGGCTTC GTAGCGATTG TCGGCCGTCC GAACGTGGGC AAATCAACGC
101 TGATGAACCA TCTCATCGGT CAGAAAATCA GTATTACCAG CAAAAAGGCG
151 CAGACGACGC GCAACCGCGT AACGGGGATT TATACCGACG ATACCGCGCA
201 GTTCGTGTTT GTCGATACGC CCGGCTTTCA AACCGACCAC CGCAACGCGC
251 TCAACGACAG GCTGAATCAA AATGTTACCG AGGCGCTCGG CGGCGTGGAT
301 GTGGTGGTTT TCGTCGTGGA GCGCATGCGC TTTACCGATG CCGACCGCGT
351 CGTGTGAAA CAACTGCCCA AGCACACGCC GGTCATTTTA GTGGTCAACA
401 AAATCGACAA GGACAAGGCG AAAGACCGTT ACGCGCTGGA GCGGTTTGT
451 GCCCAAGTGC GCGCCGAATT TGAATTTGCG GCGGCGGAGG CCGTCAGCGC
501 GAAACACGGA TTGCGGATTG CCAACCTGTT GGAGCTGATT AAGCCGTATC
551 TGCCCGAAAG CGTGCCGATG TATCCCGAAG ATATGGTTAC GGACAAATCG
601 GCGCGTTTTT TGGCGATGGA AATCGTGCCT GAAAAATTGT TCCGCTATTT
651 GGGCGAGGAA TTGCCTTATG CGATGAACGT CGAAGTGGAG CAGTTTGAAG
701 AGGAAGACGG TTTGAACCGC ATCTATATCG CCGTTTGGT CGATAAGGAA
751 AGCCAAAAGG CAATTTTAAT CGGTAAAGGC GGAGAACGTT TGAAGAAAAT
801 TTCCACCGAA GCGCGGTTGG ATATGGAAAA ACTGTTTGAT ACCAAAGTAT
851 TTTTGAAGGT CTGGGTCAAA GTCAAATCCG GTTGGGCGGA CGACATCCGC
901 TTCCTGCGCG AGCTGGGTTT GTAG

```

This corresponds to the amino acid sequence <SEQ ID 2210; ORF 673>:

m673.pep

```

1 MDIETFLAGE RAAGGYRCGF VAIVGRPNVG KSTLMNHLIG QKISITSKKA
51 QTRNRVTGI YTDDTAQFVF VDTPGFQTDH RNALNDRLNQ NVTEALGGVD
101 VVVVFVEAMR LTDADRVVLK QLPKHTPVIL VVNKIDKDKA KDRYALEAFV
151 AQVRAEFEEFA AAEAVSAKHG LRIANLLELI KPYPESVPM YPEDMVTDKS
201 ARFLAMEIVR EKLFRYLGE E LPYAMNVEVE QFEEEDGLNR IYIAVLVDKE
251 SQKAILIGKG GERLKKISTE ARLDMEKLFD TKVFLKVWVK VKSGWADDIR
301 FLRELGL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m673/g673 98.4% identity in 307 aa overlap

```

              10      20      30      40      50      60
m673.pep      MDIETFLAGERAAAGGYRCGFVAIVGRPNVGKSTLMNHLIGQKISITSKKAQTRNRVTGI
              |||||
g673           MDIETFLAGERAAAGGYRCGFVAIVGRPNVGKSTLMNHLIGQKISITSKKAQTRNRVTGI
              10      20      30      40      50      60

              70      80      90     100     110     120
m673.pep      YTDDTAQFVFVDTPGFQTDHNRNALNDRLNQNVTEALGGVDVVVFVEAMRFTDADRVVLK
              |||||

```


1080

```

g673      YTDDTAQVFVVDTPGFQTDHRNALNDRLNQNVTEALGGVDVVVFVVEAMRLTDADRVVLK
           70      80      90      100     110     120

           130     140     150     160     170     180
m673.pep  QLPKHTPVILVVKIDKDKAKDRYALEAFVAQVRAEFEEFAAAEAVSAKHGLRIANLLELI
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g673      QLPKHTPVILVINKIDKDKAKDRYALEAFVAQVRAEFEEFAAAEAVSAKHGLRIANLLELL
           130     140     150     160     170     180

           190     200     210     220     230     240
m673.pep  KPYPLESVPMYPEDMVTDKSARFLAMEIVREKLFYRLGEELPYAMNVEVEQFEEDGLNR
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g673      KPYPLESVPMYPEDMVTDKSARFLAMEIVREKLFYRLGEELPYAMNVEVEQFEEDGLNR
           190     200     210     220     230     240

           250     260     270     280     290     300
m673.pep  IYIAVLVDKESQKAILIGKGERLKKISTEARLDMEKLFDTKVFLKVWVKVKS GWADDIR
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g673      IYIAVLVDKESQKAILIGKGERLKKISTEARLDMEKLF DNKVFLKVWVKVKS GWADDIR
           250     260     270     280     290     300

m673.pep  FLRELGLX
           |||||
g673      FLRELGLX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2211>:

```

a673.seq
1  ATGGATATTG AACCTTCCT TGCAGGGGAA CGCGCCGCCG ACGGATACCG
51  TTGCGGCTTC GTAGCGATTG TCGGCCGTCC GAACGTGGGC AAATCAACGC
101 TGATGAATCA TCTCATCGGT CAGAAAATCA GTATTACCAG CAAAAGGCG
151 CAGACGACGC GCAACCGCGT AACGGGGATT TATACCGACG ATACCGCGCA
201 GTTTGTGTTT GTCGATACGC CCGGTTTTC AACCGACCAC CGCAACGCGC
251 TCAACGACCG TTTGAATCAA AACGTTACCG AGGCACTCGG CGGCGTGGAT
301 GTGGTGGTTT TCGTCGTGGA AGCGATGCGT TTTACCGATG CCGACCGCGT
351 CGTGTGAAA CAACTGCCCA AGCACACGCC GGTCATTTTA GTGGTCAACA
401 AAATCGATAA GGACAAGGCG AAAGACCGTT ACGCGCTGGA GCGTTTGT
451 GCCCAGGTGC GCGCCGAATT TGAATTTGCG GCGGCGGAGG CGGTCAAGCG
501 GAAACACGGA TTGCGGATTG CCAACCTGTT GGAGCTGATT AAGCCGTATC
551 TCCCCGAAAG CGTGCCGATG TATCCCGAAG ATATGGTTAC GGACAAATCG
601 GCGCGTTTTT TAGCGATGGA AATCGTGCGT GAAAAATTGT TCCGCTATTT
651 GGGCGAGGAA TTGCCTTATG CGATGAACGT CGAAGTGGAG CAGTTTGAAG
701 AGGAAGACGG TTTGAACCGC ATCTATATCG CCGTTTGGT CGATAAGGAA
751 AGCCAAAAGG CGATTTTAAT CGGCAAAGGC GGGGAGCGTT TGAAGAAAAT
801 TTCCACCGAA GCGCGGTTGG ATATGGAAAA ACTGTTTGAT ACCAAAGTAT
851 TTTTGAAGGT CTGGGTCAAA GTCAAATCCG GTTGGGCGGA CGACATCCGC
901 TTCTGCGCG AGCTGGGTTT GTAG

```

This corresponds to the amino acid sequence <SEQ ID 2212; ORF 673.a>:

```

a673.pep
1  MDIETFLAGE RAADGYRCGF VAIVGRPNVG KSTLMNHLIG QKISITSKKA
51  QTRNRVTGI YTDQTAQVFV VDTPGFQTDH RNALNDRLNQ NVTEALGGVD
101 VVVFVVEAMR FTDADRVVLK QLPKHTPVIL VVNKIDKDKA KDRYALEAFV
151 AQVRAEFEEFA AAEAVSAKHG LRIANLLELI KPYPLESVPM YPEDMVTDKS
201 ARFLAMEIVR EKLFYRLGEE LPYAMNVEVE QFEEDGLNR IYIAVLVDKE
251 SQKAILIGKG GERLKKISTE ARLDMEKLF DT KVFLKVWVK VKS GWADDIR
301 FLRELGL*

```

m673/a673 99.7% identity in 307 aa overlap

```

           10      20      30      40      50      60
m673.pep  MDIETFLAGERAAGGYRCGFVAIVGRPNVGKSTLMNHLIGQKISITSKKAQTRNRVTGI
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a673      MDIETFLAGERAADGYRCGFVAIVGRPNVGKSTLMNHLIGQKISITSKKAQTRNRVTGI
           10      20      30      40      50      60

```

1081

	70	80	90	100	110	120
m673.pep	YTDDTAQFVFVDTPGFQTDHRNALNDRINQNVTEALGGVDVVVFVVEAMRFTDADRVLK					
a673	YTDDTAQFVFVDTPGFQTDHRNALNDRINQNVTEALGGVDVVVFVVEAMRFTDADRVLK					
	70	80	90	100	110	120
	130	140	150	160	170	180
m673.pep	QLPKHTPVILVVKIDKDKAKDRYALEAFVAQVRAEFEEFAAAEAVSAKHGLRIANLLELI					
a673	QLPKHTPVILVVKIDKDKAKDRYALEAFVAQVRAEFEEFAAAEAVSAKHGLRIANLLELI					
	130	140	150	160	170	180
	190	200	210	220	230	240
m673.pep	KPYLPESVPMYPEDMVTDKSAREFLAMEIVREKLFYRLGEELPYAMNVEVEQFEEDGLNR					
a673	KPYLPESVPMYPEDMVTDKSAREFLAMEIVREKLFYRLGEELPYAMNVEVEQFEEDGLNR					
	190	200	210	220	230	240
	250	260	270	280	290	300
m673.pep	IYIAVLVDKESQKAILIGKGERLKKISTEARLDMEKLFDTKVFVKVWVKVSGWADDIR					
a673	IYIAVLVDKESQKAILIGKGERLKKISTEARLDMEKLFDTKVFVKVWVKVSGWADDIR					
	250	260	270	280	290	300
m673.pep	FLRELGLX					
a673	FLRELGLX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2213>:

```

g674.seq
1  ATGAAAACAG CCCGCCGCGG TTCCCGCGAG CTGCGCGTAC AAGCCGTTTA
51  CCAATCCCTT ATCAACCGCA CCGCCGCGCC CGAAATTGCT AAAAACATCC
101 GCGAAATGTC CGACTTTGCC AAGCGGACG AAGAATTGTT CAACAACTC
151 TTCTTCGGCA CACAAACCAA TGCAGCGGAC TACATCCAAA AAATCCGCCC
201 GCTGCTCGAC AGGGACGAAA AAGACCTCAA CCCCATCGAA CGCGCCGTTT
251 TGCTGACCGC CTGCCACGAG CTTTCCGCTA TGCCCGAAAC GCCCTACCCC
301 GTATTATCA ACGAAGCCAT CGAAGTTACC AAAACCTTCG GCGGCACGGA
351 CGGGCACAAA TTCGTCACG GCATCCTCGA CAAACTCGCC GCCCAAATCC
401 GCCCAGACGA GCCCAAACGC CGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2214; ORF 674.ng>:

```

g674.pep
1  MKTARRRSRE LAVQAVYQSL INRTAAPEIA KNIREMSDFA KADEELFNKL
51  FFGTQTNAAD YIQKIRPLLD RDEKDLNPIE RAVLLTACHE LSAMPETYPY
101 VIINEAIEVT KTEGGTDGKH FVNGILDKLA AQIRPDEPKR R*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2215>:

```

m674.seq
1  ATGAAAACAG CCCGCCGCGG TTCCCGCGAG CTGCGCGTAC AAGCCGTTTA
51  CCAATCCCTT ATCAACCGCA CCGCCGCGCC CGAAATTGCT AAAAACATCC
101 GCGAAATGTC CGACTTTGCC AAGCGGACG AAGAATTGTT CAACAACTT
151 TTCTTCGGCA CGCAAACCAA TGCAGCGGAC TATATCCGAC AAATCCGCCC
201 GCTACTTGAC AGGGACGAAA AAGACCTCAA CCCCATCGAA CGCGCCGTTT
251 TGCTGACCGC CTGCCACGAG CTGTCCGCCA TGCCCGAAAC GCCCTACCCC
301 GTATTATCA ACGAAGCCAT CGAAGTTACC AAAACCTTCG GCGGCACGGA
351 CGGGCACAAA TTCGTCACG GCATCCTCGA CAAACTCGCC GCCCAAATCC
401 GCCCCGACGA GCCCAAACGC CGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2216; ORF 674>:

```

m674.pep
1  MKTARRRSRE LAVQAVYQSL INRTAAPEIA KNIREMSDFA KADEELFNKL

```

1082

51 FFGTQTNAAE YIRQIRPLLD RDEKDLNPIE RAVLLTACHE LSAMPETPYP
 101 VIINEAIEVT KTFGGTDGHK FVNGILDKLA AQIRPDEPKR R*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m674/g674 97.9% identity in 141 aa overlap

	10	20	30	40	50	60
m674.pep	MKTARRRSRELAVQAVYQSLINRTAAPEIAKNIREMSDFAKADEELFNKLFFGTQTNAAE					
g674	MKTARRRSRELAVQAVYQSLINRTAAPEIAKNIREMSDFAKADEELFNKLFFGTQTNAAD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m674.pep	YIRQIRPLLDREKDLNPIERAVLLTACHELSAMPETPYPVIINEAIEVTKTFGGTDGHK					
g674	YIQKIRPLLDREKDLNPIERAVLLTACHELSAMPETPYPVIINEAIEVTKTFGGTDGHK					
	70	80	90	100	110	120
	130	140				
m674.pep	FVNGILDKLAAQIRPDEPKRRX					
g674	FVNGILDKLAAQIRPDEPKRRX					
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2217>:

a674.seq
 1 ATGAAACAG CCCGCCGCGC TTCCCGCGAG CTGCGGTAC AAGCCGTTTA
 51 CCAATCCCTT ATCAACC3CA CCGCCGCGCC CGAGATTGCT AAAAACATCC
 101 GCGAAATGCC CGACTTTGCC AAGGCAGACG AAGAATTGTT CAACAACTT
 151 TTCTTCGGCA CGCAAACCAA TGCGGCAGAG TACATCCGAC AAATCCGCCC
 201 CCTGCTCGAC CGCGACGAAA AAGACCTCAA CCCCATCGAA CGCGCCGTCC
 251 TGCTGACCGC CTGCCACGAG CTGTCCGCCA TGCCCGAAAC GCCCTACCCC
 301 GTCATCATCA ACGAAGCCAT CGAAGTAACC AAAACCTTCG GCGGCACGGA
 351 CGGGCACAAA TTCGTCAACG GCATCCTCGA CAAACTCGCC GCCCAAATCC
 401 GTCCCGACGA GCCCAAACGC CGTTGA

This corresponds to the amino acid sequence <SEQ ID 2218; ORF 674.a>:

a674.pep
 1 MKTARRRSRE LAVQAVYQSL INRTAAPEIA KNIREMPDFA KADEELFNKL
 51 FFGTQTNAAE YIRQIRPLLD RDEKDLNPIE RAVLLTACHE LSAMPETPYP
 101 VIINEAIEVT KTFGGTDGHK FVNGILDKLA AQIRPDEPKR R*

m674/a674 99.3% identity in 141 aa overlap

	10	20	30	40	50	60
m674.pep	MKTARRRSRELAVQAVYQSLINRTAAPEIAKNIREMSDFAKADEELFNKLFFGTQTNAAE					
a674	MKTARRRSRELAVQAVYQSLINRTAAPEIAKNIREMPDFAKADEELFNKLFFGTQTNAAE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m674.pep	YIRQIRPLLDREKDLNPIERAVLLTACHELSAMPETPYPVIINEAIEVTKTFGGTDGHK					
a674	YIRQIRPLLDREKDLNPIERAVLLTACHELSAMPETPYPVIINEAIEVTKTFGGTDGHK					
	70	80	90	100	110	120
	130	140				
m674.pep	FVNGILDKLAAQIRPDEPKRRX					
a674	FVNGILDKLAAQIRPDEPKRRX					
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2219>:

```
g675.seq
  1  ATGAACACCA TCGCCCCcaa cctcgacgGC AAACACCTCC GCATCGGCAT
 51  CGTACAGGCA CGCTTCACCA ACGAAATCGG CAGCCAAATG CTCAAAGTCT
101  GCTGCCGCAC CCTCCAAGAA TTGGGCGTAG CAGACGAAAa catcaccgtc
151  gCCACCGTAC CCGGCGCGCT TGAATCCCC ATCGCGCTGA TGAACTTTGC
201  CTCTCCGAA AAATTGACG CACTGATTGC CATCGGCGTC GTCATCCGTG
251  GCGAAACCTA CCATTTCGAG CTGTTGCCA ACGAATCCGG CGCAGGGATC
301  GGCCGCGTCG CACTCGACTA CAACATCCCG ATTGCCAACG CCGTCCTGAC
351  CACCGAAAAC GACGCGCAGG CAATTGAACG GATTGGAGAA AAAGCCTCGG
401  ATGCCGCCAA AGTCGCCGTA GAATCGCCA ACCTCGTCAA CCTTCTGCTC
451  GAAGAACAGT TTGAAGACGA AGAATAA
```

This corresponds to the amino acid sequence <SEQ ID 2220; ORF 675.ng>:

1084

g675.pep

```

1  MNTIAPNLDG KHLRIGIVQA RFTNEIGSQM LKVCCTRLQE LGVADENITV
51  ATVPGALEIP IALMNFASSE KFDALIAIGV VIRGETYHFE LVANESGAGI
101 GRVALDYNIP IANAVLT TEN DAQAIERIGE KASDAAKVAV ECANLVNLLL
151 EEQFEDEE*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2221>:

m675.seq

```

1  ATGAACACCA TCGCCCCCAA CCTCGACGGC AAACACCTCC GCATCGGCAT
51  CGTACAGGCA CGCTTCACCA ACGAAATCGG CAGCGAAATG CTCAAAGTCT
101 GCTGCCGCAC CCTCCAAGAA TTGGGCGTGG CAGACGAAAA CATTACCGTC
151 GCCACCGTAC CCGGCGCGCT TGAAATCCCC ATCGCGCTGA TGAACCTTGC
201 CTCTTCCGAA AAGTTTGACG CACTGATTGC CATCGGCGTC GTCATCCGTG
251 GCGAAACCTA CCATTTCGAG CTGGTTTCCA ACGAATCCGG AGCAGGCGTC
301 AGCCGCGTCG CACTCGACTA CAATATCCCG ATTGCCAATG CCGTCCTAAC
351 CACCGAAAAC GACGCGCAGG CAATCGAACG GATTGAAGAA AAAGCCTCGG
401 ATGCCGCCAA AGTCGCGGTC GAATGCGCCA ACCTCGTCAA CCTGCTGCTC
451 GAAGAACAGT TTGAAGACGA AGAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2222; ORF 675>:

m675.pep

```

1  MNTIAPNLDG KHLRIGIVQA RFTNEIGSEM LKVCCTRLQE LGVADENITV
51  ATVPGALEIP IALMNFASSE KFDALIAIGV VIRGETYHFE LVSNEGAGV
101 SRVALDYNIP IANAVLT TEN DAQAIERIEE KASDAAKVAV ECANLVNLLL
151 EEQFEDEE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m675/g675 96.8% identity in 158 aa overlap

	10	20	30	40	50	60
m675.pep	MNTIAPNLDGKHLRIGIVQARFTNEIGSEMLKVCCTRLQELGVADENITVATVPGALEIP					
g675	MNTIAPNLDGKHLRIGIVQARFTNEIGSQMLKVCCTRLQELGVADENITVATVPGALEIP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m675.pep	IALMNFASSEKFDALIAIGVVIRGETYHFE LVSNEGAGVSRVALDYNIPIANAVLT TEN					
g675	IALMNFASSEKFDALIAIGVVIRGETYHFE LVANESGAGIGRVALDYNIPIANAVLT TEN					
	70	80	90	100	110	120
	130	140	150	159		
m675.pep	DAQAIERIEEKASDAAKVAVECANLVNLLLEEQFEDEEX					
g675	DAQAIERIGE KASDAAKVAVECANLVNLLLEEQFEDEEX					
	130	140	150			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2223>:

a675.seq

```

1  ATGAACACCA TCGCCCCCAA CCTCGACGGC AAACACCTCC GCATCGGCAT
51  CGTACAGGCA CGCTTCACCA ACGAAATCGG CAGCGAAATG CTCAAAGTCT
101 GCTGCCGCAC CCTCCAAGAA TTGGGCGTGG CAGACGAAAA CATTACCGTC
151 GCCACCGTAC CCGGCGCGCT TGAAATCCCC ATCGCGCTGA TGAACCTTGC
201 CTCTTCTGAA AAATTGACG CACTGATTGC CATCGGCGTC GTTATCCGTG
251 GCGAAACCTA CCATTTCGAG CTGGTTTCCA ACGAATCCGG AGCAGGGGTC
301 AGCCGCGTCG CACTCGACTA CAACATCCCG ATTGCCAATG CCGTCCTGAC
351 CACCGAAAAC GACGCGCAGG CAATCGAACG GATTGAAGAA AAAGCCTCGG
401 ATGCCGCCAA AGTCGCGGTA GAATGCGCCA ACCTCGTCAA CCTCCTGCTC
451 GAAGAACAGT TTGAAGACGA AGAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2224; ORF 675.a>:

a675.pep

```

1  MNTIAPNLDG KHLRIGIVQA RFTNEIGSEM LKVCCTRLQE LGVADENITV
51  ATVPGALEIP IALMNFASSE KFDALIAIGV VIRGETYHFE LVSNEGAGV

```

1085

101 SRVALDYNIP IANAVLTEN DAQAIERIEE KASDAKVAV ECANLVNLLL
 151 EEQFEDEE*

m675/a675 100.0% identity in 158 aa overlap

	10	20	30	40	50	60
m675.pep	MNTIAPNLDGKHLRIGIVQARFTNEIGSEMLKVCRTLQELGVADENITVATVPGALEIP					
a675	MNTIAPNLDGKHLRIGIVQARFTNEIGSEMLKVCRTLQELGVADENITVATVPGALEIP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m675.pep	IALMNFASSEKFDALIAIGVVIRGETYHFELVSNEAGVSRVALDYNIPIANAVLTEN					
a675	IALMNFASSEKFDALIAIGVVIRGETYHFELVSNEAGVSRVALDYNIPIANAVLTEN					
	70	80	90	100	110	120
	130	140	150	159		
m675.pep	DAQAIERIEEKASDAKVAVECANLVNLLLEEQFEDEEX					
a675	DAQAIERIEEKASDAKVAVECANLVNLLLEEQFEDEEX					
	130	140	150			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2225>:

g677.seq
 1 ATGCCGCAGA TTTTGGTGCG GATTTTCCTC ATTCGGTATT CCTTTATTg
 51 ggAAACGGTG CGCTTGTGCC GTTTCAGACG GCATTCCCGA TCAGTCGATT
 101 TTGATGTATT CGACAGAAAG GATTTCAATT TCCTCACGGC CTTCGGCGCT
 151 GTTCAAAACC ACTTCGTCGC CTTCGGCGCG TTTAATCAGG CAACGCGCCA
 201 ACGGCGAAAT CCAAGAAATT TTGTTTTGCG CGGTATCGAT TTCATCGACG
 251 CCGACGATT TGACGGTTTG CTCGGCGCCG TCGCCGCGCA ACAGACCGAC
 301 GGTGCGCGCG AAAAATACTT GGTGCGTCGC TTCGCGCAAT TCGGGATCGA
 351 CGACGACGGC AGCCTCCAAA CGTTTGGTCA GGAAACGGAT GCGGCGGTGCG
 401 ATTTGCGGCA TACGGCGTTT GCCGTAAAGA TAGTCGCGCT TTTGCGTGCG
 451 GTCGCGGTTG CCTGCGGCCC AGTTGACGAT TTGGACGATT TCGGGGCGTT
 501 CTTTATTGAC CAGTTGATAA AGCTCGTCTT TCAATGCCTG CCATCCGGCG
 551 GCGGTAATGT AGTTTTTGGT TTCGGTACTC ATATTGTGTG CGGATGA

This corresponds to the amino acid sequence <SEQ ID 2226; ORF 677.ng>:

g677.pep
 1 MPQILVRIFL IRYFSIWETV RLCRFRHRSR SVDFDVDRK DFNFLTAFRR
 51 VQNHFAFAR FNQATRRRRN PRNFVLRGID FIDADDFDGL LAPVAAQQTQ
 101 GRAEKLVRG FAQFGIDDDG SLQTFGQETD AAVDFAHATF AVKIVAVFAA
 151 VAVACRPVDD LDDFGAFFID QLIKLVFQCL PSGGRNVVFG FGTHIVCG*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2227>:

m677.seq
 1 ATGCCGCAGA TTTTGGTGCG GATTTTCCTC ATTCGGTATT CCTTTATTG
 51 GGAAACGGCG CGCTTTTGCC GTTTCAGACG GCATTCCCGA TCAGTCGATT
 101 TTGATGTATT CGACAGAAAG GATTTCAATT TCCTCACGCC CTTCGGCGCT
 151 GTTCAAAACC ACTTCGTCGC CTTCGGCGCG TTTAATCAGA CAACGAGCCA
 201 GCGGCGAAAT CCAAGAAATT TTGTTTTGCG CGGTATCGAT TTCATCGATG
 251 CCGACGATT TGACGGTTTG CTCGGCGCCG TCGTCGCGCA ACAGTCGAC
 301 CGTCGCGCGG AAAAATACTT GGTGCGTCGC TTCGCGCAAT TCGGGATCGA
 351 CGACGACGGC AGCCTCCAAA CGTTTGGTCA GGAAACGGAT GCGGCGGTGCG
 401 ATTTGCGGCA TACGGCGTTT GCCGTAAAGA TAGTCGCGCT TTTGCGTGCG
 451 GTCGCGGTTG CCTGCGGCCC AGTTGACGAT TTGGACGATT TCGGGGCGTT
 501 CTTTGTGAC CAGTTGATAA AGCTCGTCTT TCAATGCCTG CCATCCGGCG
 551 GCGGTAATGT AGTTTTTGGT TTCGGTACTC ATATTGTGTG CGGATGA

This corresponds to the amino acid sequence <SEQ ID 2228; ORF 677>:

m677.pep
 1 MPQILVRIFL IRYFSIWETA RLCRFRHRSR SVDFDVDRK DFNFLTPFRR

1086

51 VQNHVFAR FNQTSQRRN PRNFVLRGID FIDADDFDGL LAPVVAQSD
 101 RRAEKHLVGR FAQFGIDDDG SLQTFGQETD AAVDFAHTAF AVKIVAVFAA
 151 VAVACRPVDD LDDEGAFFVD QLIKLVFQCL PSGGRNVVFG FGTHIVCG*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m677/g677 94.9% identity in 198 aa overlap

m677.pep	10	20	30	40	50	60
	MPQILVRIFLIRYSFIWETARFCRFRHRSRSVDFDVFDRKDFNFLT	PFRRVQNHVFAR				
g677	10	20	30	40	50	60
	MPQILVRIFLIRYSFIWETVRLCRFRHRSRSVDFDVFDRKDFNFLT	AFRRVQNHVFAR				
m677.pep	70	80	90	100	110	120
	FNQTSQRRNPRNFVLRGIDFIDADDFDGLLAPVVAQSDRRAEKHLVGRFAQFGIDDDG					
g677	70	80	90	100	110	120
	FNQATRQRRNPRNFVLRGIDFIDADDFDGLLAPVAAQQTGGRAEKYLVRFAQFGIDDDG					
m677.pep	130	140	150	160	170	180
	SLQTFGQETDAAVDFAHTAFVAVFAAVAVACRPVDDLDDDEGAFFVDQLIKLVFQCL					
g677	130	140	150	160	170	180
	SLQTFGQETDAAVDFAHTAFVAVFAAVAVACRPVDDLDDDEGAFFIDQLIKLVFQCL					
m677.pep	190	199				
	PSGGRNVVFGFGTHIVCGX					
g677	190	199				
	PSGGRNVVFGFGTHIVCGX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2229>:

a677.seq

1	ATGCCGCAGA	TTTTGGTGCG	GATTTTCCTC	ATTCGGTATT	CCTTTATTG
51	GGAAACGGCG	CGTTGTGCG	GTTTCAGACG	GCATTCCCGA	TCAGTCGATT
101	TTGATGTATT	CGACAGAAAG	GATTTCAATT	TCCTCACGCC	CTTCCGGCGT
151	GTTTAAACC	ACTTCGTCGC	CTTCACGGCG	TTAATCAGA	CAACGAGCCA
201	GCGGCGAAAT	CCAAGAAATT	TTGTTTTGCG	CGGTATCGAT	TTCATCGATG
251	CCGACGATT	TGACGGTTG	CTCGCGCCG	TCGCCGCGCA	ACAGACCGAC
301	GGTCGCGCG	AAAAACACTT	GGTCGGTCGC	TTCGCGCAAT	TCGGGATCAA
351	CGACGACGCG	GGCTTCCAAA	CGCTTGGTCA	GGAAACGGAT	GCGGCGGTCG
401	ATTTCGCGCA	TACGGCGTTT	GCCGTAAAGG	TAGTCGCCGT	TTTCGCTGCG
451	GTCGCCGTTG	CCTGCCGCC	AGTTGACGAT	TTGGACGATT	TCGGGGCGTT
501	CTTTATTAA	CAGTTGATAA	AGCTCGTCTT	TCAATGCCTG	CCATCCGCGC
551	GGCGTAATGT	AGTTTTTGGT	TTCGGTACTC	ATATTGTGTG	CGGATGA

This corresponds to the amino acid sequence <SEQ ID 2230; ORF 677.a>:

a677.pep

1	MPQILVRIFL	IRYSFIWETA	RLCRFRHRSR	SVDFDVFDRK	DFNLT	PFRR
51	V*NHVFATR	FNQTSQRRN	PRNFVLRGID	FIDADDFDGL	LAPVAAQQT	D
101	GRAEKHLVGR	FAQFGINDDG	GFQTLGQETD	AAVDFAHTAF	AVKVVAVFAA	
151	VAVACRPVDD	LDDEGAFFIN	QLIKLVFQCL	PSGGRNVVFG	FGTHIVCG*	

m677/a677 93.4% identity in 198 aa overlap

m677.pep	10	20	30	40	50	60
	MPQILVRIFLIRYSFIWETARFCRFRHRSRSVDFDVFDRKDFNFLT	PFRRVQNHVFAR				
a677	10	20	30	40	50	60
	MPQILVRIFLIRYSFIWETARLCRFRHRSRSVDFDVFDRKDFNFLT	PFRRVXNHVFATR				
	70	80	90	100	110	120

1087

```

m677.pep  FNQTTSQRRNPRNFVLRGIDFIDADDDFGLLAPVVAQQSDRRAEKHLVGRFAQFGIDDDG
          |||||
a677      FNQTTSQRRNPRNFVLRGIDFIDADDDFGLLAPVAAQQTDRRAEKHLVGRFAQFGINDDG
          70      80      90      100     110     120

          130     140     150     160     170     180
m677.pep  SLQTFGQETDAAVDFAHTAFVAVKIVAVFAAVAVACRPVDDLDDFGAFFVDQLIKLVFQCL
          ::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a677      GFQTLGQETDAAVDFAHTAFVAVKVVAVFAAVAVACRPVDDLDDFGAFFINQLIKLVFQCL
          130     140     150     160     170     180

          190     199
m677.pep  PSGGRNVVFGFGTHIVCGX
          |||||
a677      PSGGRNVVFGFGTHIVCGX
          190

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2231>:

```

g678.seq
1  ATGAATAGCC TCCCCATTGC CGACCTCCTC GCCTcgcCG TCATCGCCGC
51 CTGCATCGTC ATTTCCACGA TCGCGGCGGT GATTGCGGAA GCAGgttcGA
101 TGGTgGCATG ggtggTTTcc tTCTTTtttg ccAAACTCTt tGCCGCACcc
151 ttegcgcACC TCGCCTTTGc ctCGTTCCAA ccccgccTGT TTGCAttggc
201 tCTGTCATTC ATTCCCTGT TCGTCATTGC CTGTCTGATC CAGAAAATGC
251 TCCGTTCGCT GCTGACCGGC GCAGTTTCGG CGGTCGGTCT GGGCTTTGCC
301 AACCGCATTT TGGGCGGTGT ATTCGGTGCA TTGAAAGGCG TTTTGATTGT
351 TACCCTGCTG ATCATGCTTG CTTCAAAAC CGACCTGCC GATACCGAAG
401 AATGGCAACA GTCCTATACC GTACCGTTT TCGTATCGCT TTCCGAAGCG
451 GTGTTAAACC atacggaCAA CGCaccgaa tCCCTcgacg acgactaa

```

This corresponds to the amino acid sequence <SEQ ID 2232; ORF 678.ng>:

```

g678.pep
1  MNSLPIADLL ASAVIAACIV ISTMRGVIAE AGSMVAWVVS FFFAKLFAAP
51 FADLAFASFQ PRLFALALSF ISLFVIACLI QKMLRSLLTG AVSAVGLGFA
101 NRILGGVFGA LKGV LIVTLL IMLASKTDLP DTEEWQSYT VPFFVSLSEA
151 VLNHTDNAPE SLDD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2233>:

```

m678.seq
1  ATGAATAGCC TCCCCATTGC CGACCTCCTC GTCTCCGCG TCATCGCCGC
51 CTGCATCGTG CTATCCGCGA TCGCGGCGGT GATTGCGGAG GCAGGCTCAA
101 TGGCGGCATG GGTGGTTTCC TTCTTTTTCG CCAAACCTT TGCCGCCTCC
151 TTCGCCGACC TCGCCTTTGC CTGTTCCAA CCCCgcCTGT TTGCATTGGC
201 TCTGTCGTT ATTCCCTGT TCGTCATTGC CTGTCTGATC CAGAAAATGC
251 TCCGTTCGCT GCTGACCAGC GCAGTTTCGG CGGTCGGTTT GGGCTTTGCC
301 AACCGCATTT TGGGCGGCGT ATTCGGTGCA TTGAAAGGCG TTTTGATTGT
351 TACCCTGCTG GTCATGCTTG CTTCAAAAC CGACCTGCC GATACCGAAG
401 AATGGCGGCA ATCTTACACA CTGCCGTTT TCGTATCGCT TTCCGAAGCC
451 GTGTTGAACC ATAGCGGCG CACGGCGGAA ACTCCGAAG ACGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 2234; ORF 678>:

```

m678.pep
1  MNSLPIADLL VSAVIAACIV LSAMRGVIAE AGSMAWVVS FFFAKLFAAS
51 FADLAFASFQ PRLFALALSF ISLFVIACLI QKMLRSLTTS AVSAVGLGFA
101 NRILGGVFGA LKGV LIVTLL VMLASKTDLP DTEEWQSYT LPFFVSLSEA
151 VLNHSGGTAE TPEDD*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m678/g678 89.7% identity in 165 aa overlap

1088

	10	20	30	40	50	60
m678.pep	MNSLPIADLLVSAVIAACIVLSAMRGVIAEAGSMAAWVVSFFFAKLFAASFADLAFASFQ					
g678	MNSLPIADLLASAVIAACIVISTMRGVIAEAGSMVAWVVSFFFAKLFAAPFADLAFASFQ					
	10	20	30	40	50	60
m678.pep	70	80	90	100	110	120
	PRLFALALSFISLFVIACLIQKMLRSLTSAVSAVGLGFANRILGGVFGALKGV LIVTLL					
g678	PRLFALALSFISLFVIACLIQKMLRSLTGA VSAVGLGFANRILGGVFGALKGV LIVTLL					
	70	80	90	100	110	120
m678.pep	130	140	150	160		
	VMLASKTDLDPTEEWQSYTLPFFVSLSEAVLNHSGGTAETPEDDX					
g678	IMLASKTDLDPTEEWQSYTVPFFVSLSEAVLNHTDNAPESLDDDX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2235>:

```

a678.seq
1  ATGAATAACC TCCCCGTTGC CGACCTCCTC GTCTCCGCCA TCATCGCCGC
51  CTGCATCGTG CTATCCGCGA TGCGCGGCGT GATTGCGGAG GCTGGCTCAA
101 TGGCGGCATG GGTGGTTGCC TTTTTCG CCAAACTCTT TGCCGCACCC
151 TTCGCCGACA TCGCCTTTCG ATCGTTCCAA CCCGCCCTGT TTGCATTGGC
201 TCTGTCGTTT ATTTCCCTAT TCGTCATTGC CTGTCTGATC CAGAAAATAC
251 TCCGCTCGCT GCTGACCGGG GCAGTTTCGG CGGTCGGTTT GGGCTTTGCC
301 AACCGCATTT TGGGCGGCGT ATTCGGTGCA TTGAAAGGCA TTTGATTAT
351 TACCCTGCTG GTCATGCTCG CTCAAAAAC CGACCTGCCC GATACCGAAG
401 AATGGCGGCA ATCTTACACA CTGCCGTTT TCGTATCGCT TTCCGAAGCC
451 GTGTTGAACC ATAGCGGCGG CACGGCGGAA ACTCCGAAG ACGATTGA
  
```

This corresponds to the amino acid sequence <SEQ ID 2236; ORF 678.a>:

```

a678.pep
1  MNNLPVADLL VSAIIAACIV LSAMRGVIAE AGSMAAWVVA FFFAKLFAAP
51  FADIAFASFQ PRLFALALSF ISLFVIACLI QKILRSLLTG AVSAVGLGFA
101 NRILGGVEGA LKGILIIITLL VMLASKTDLF DTEEWQSYT LPFFVSLSEA
151 VLNHSGGTAE TPEDD*
  
```

m678/a678 93.9% identity in 165 aa overlap

	10	20	30	40	50	60
m678.pep	MNSLPIADLLVSAVIAACIVLSAMRGVIAEAGSMAAWVVSFFFAKLFAASFADLAFASFQ					
a678	MNNLPVADLLVSAIIAACIVLSAMRGVIAEAGSMAAWVVAFFFAKLFAAPFADIAFASFQ					
	10	20	30	40	50	60
m678.pep	70	80	90	100	110	120
	PRLFALALSFISLFVIACLIQKMLRSLTSAVSAVGLGFANRILGGVFGALKGV LIVTLL					
a678	PRLFALALSFISLFVIACLIQKILRSLTGA VSAVGLGFANRILGGVFGALKGILIIITLL					
	70	80	90	100	110	120
m678.pep	130	140	150	160		
	VMLASKTDLDPTEEWQSYTLPFFVSLSEAVLNHSGGTAETPEDDX					
a678	VMLASKTDLDPTEEWQSYTLPFFVSLSEAVLNHSGGTAETPEDDX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2237>:

```

g680.seq
1  ATGACGAAGG GCAGTTCGGC GATGTCCAGC CCACGCGCGG CGATATCGGT
51  GGCGACGAGG ACGCGCAGGC TGCCGTCTTT GAAGGCGTTG AGTGTTCGA
101 GCCTGCTTTG TTGGGAACGG TCGCCGTGTA TCGCCTGTGC GGACAGGTTG
  
```

1089

```

151 CGGCGCACCA GTTCGCGCGT TACGCGGTCG ACGCTTTGTT TGGTtttgCA
201 AAAGACGATA ACTTGGTTCA TATGCAGATC GACAATCAGC CGTTTCAGCA
251 GGTTCGCTT TTGGAAGGTA TCGACGGCGA TGATGTgttg ttcGACGTTG
301 GCGTTGGTGG TGTTTTGGGC GGCAACCTCG ACGGTTTCGG GCGCGTTCAT
351 GAAGTCTTGC GCCAGTTTGC GTATCGGTGC GGAGAAGGTG GCGGAAAAGA
401 GCAGGGTTTG GCGTTGGCGG GGCAGCATCT GCATGATTTT GCGGATGTCG
451 TCGATAAACC CCATATCCAA CATGCGGTCT GCTTCGTCCA GAACGACGAT
501 TTCGGCTTTG TTTAAACTGA TGTTTTTCTG TTTCACATGG TCGAGCAGCC
551 GTCGACGGT GCGCAGCACT ATTTGCGAGC CGGCACGCAG GTCGCGCGTT
601 TGTTTTGTCCA TGTTGACACC GCCGAAGAGG ACGGTATGCC GCAGCGGCAG
651 GTTTTTTAATg tag

```

This corresponds to the amino acid sequence <SEQ ID 2238; ORF 680.ng>:

```

g680.pep
1 MTKGSSAMSS PRAAISVATR TRRLPSLKAL SVSSLLCWER SPCACADRL
51 RRTSSRVTRS TLCLVLQKTI TWFICRSTIS RSSRLRFWKV STAMMCCSTL
101 ALVVFWAATS TVSGAFMKSC ASLRIGAELV AEKSRVVRWR GSICMILRMS
151 SINPISNMRS ASSRTTISAL FKLMEFCFTW SSSRPTVATT ISQPARRSAV
201 CLSMLTPPKR TVCRSGRFLM *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2239>:

```

m680.seq
1 ATGACGAAGG GCAGTTCGGC AATGTCCAGC CCGCGCGCGG CGATGTCGGT
51 GGCGACGAGG ACGCGCAGGT TGCCGTCTTT GAAGGCGTTG AGTGTTCGA
101 GCCGGCTTTG TTGGGAACGG TCGCCGTGTA TCGCCTGTGC GGACAGGTTG
151 CGGCGCACCA GTTCGCGCGT TACGCGGTCG ACGCTTTGTT TGGTTTTGCA
201 GAACACGATG ACCTGGTTCA TATGCAAATC GACAATCAGC CGTTCGAGCA
251 GGTTCGCTT CTGAATGGTA TCGACGGCGA TGATGTGCTG CTCGACGTTG
301 GCGTTGGTGG TGTTTTGGCG GCGCACTTCG ACGGTTTCGG GCGCGTTCAT
351 GAAGTCTTGC GCCAGTTTGC GTATCGGGG GAGAAGGTG GCGGAAAAGA
401 GCAGGGTTTG GCGTTGGCGG GGCAGCATCT GCATGATTTT GCGGATGTCG
451 TCGATAAACC CCATATCCAG CATACGGTCG GCTTCGTCCA AAACGACGAT
501 TTCGACTTTG TTCAAATGGA TGTTTTTCTG TTTCACGTGG TCGAGCAGCC
551 TTCGACGGT GCGCAGCACT ATTTGCGAGC CGGCACGCAG GTCGCGCGTC
601 TGTTTTGTCCA TATTCATACC GCCGAACAAG ACGGTGTGGC GCAGCGGCAG
651 GTTTTGTATG TAG

```

This corresponds to the amino acid sequence <SEQ ID 2240; ORF 680>:

```

m680.pep
1 MTKGSSAMSS PRAAMSVATR TRRLPSLKAL SVSSRLCWER SPCACADRL
51 RRTSSRVTRS TLCLVLQNTM TWFICKSTIS RSSRLRF*MV STAMMCCSTL
101 ALVVFCAATS TVSGAFMKSC ASLRIGAELV AEKSRVVRWR GSICMILRMS
151 SIKPISSIRS ASSKTTISTL FKWMFFCFTW SSSRPTVATT ISQPARRSAV
201 CLSIFIPPNK TVWRSGRFLM *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

```

m680/g680 90.9% identity in 220 aa overlap

          10      20      30      40      50      60
m680.pep  MTKGSSAMSSPRAAMSVATRTRRLPSLKALSVSSRLCWERSPCACADRLRRTSSRVTRS
          |||
g680      MTKGSSAMSSPRAAISVATRTRRLPSLKALSVSSLLCWERSPCACADRLRRTSSRVTRS
          10      20      30      40      50      60

          70      80      90      100     110     120
m680.pep  TLCLVLQNTMTWFICKSTISRSSRLRFKXVSTAMMCCSTLALVVFWAATSTVSGAFMKSC
          |||
g680      TLCLVLQKTIITWFICRSTISRSSRLRFWKVSTAMMCCSTLALVVFWAATSTVSGAFMKSC
          70      80      90      100     110     120

          130     140     150     160     170     180
m680.pep  ASLRIGAELVAEKSRVVRWRGSICMILRMSSIKPISSIRSASSKTTISTLFKWMFFCFTW

```

1090

```

g680      |||||
          ASLRIGA EKVAEKSRVWRWRSICMILRMSSINPISNMRSASSRTTISALFKLMFFCFTW
          130      140      150      160      170      180

          190      200      210      220
m680.pep  SSSRPTVATTISQPARRSAVCLSI FIPNKT VWRSGRFLMX
          |||||
g680      SSSRPTVATTISQPARRSAVCLSM LTPKRTVCRSGRFLMX
          190      200      210      220

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2241>:

```

a680.seq
1  ATGACGAAGG GCAGTTCGGC AATATCCAGC CCCCGCGCGG CGATATCGGT
51  GCGGACGAGG ACGCGCAGGT TGCCGTCTTT GAAGGCGGTG AGTGTTCGA
101 GCCGGCTTTG TTGGGAACGG TCGCCGTGTA TCGCCTGTGC GGACAGGTTG
151 CGGCGCACCA GTTCGCGCGT TACGCGGTGC ACGCTTTGTT TGGTTTTCGA
201 GAACACGATG ACCTGGTTCA TATGCAAATC GACAATCAGC CGTTCGAGCA
251 GGTTCGCGTT CTGAATGGTA TCGACGGCGA TGATGTGCTG CTCGACGTTG
301 CGCTTGGTGG TGTCTTGGCG GCGGACTTCG ACGGTTTCGG GCGCGTTCAT
351 GAAGTCTTGC GCCAGTTTGC GTATCGGGGC GGAGAAGGTG GCGGAAAAGA
401 GCAGGGTTTG GCGTTGGCGG GGCAGCATCT GCATGATTTT GCGGATGTCG
451 TCGATAAAAC CCATATCCAG CATA CGGTTCG GCTTCGTCCA AAACGACGAT
501 TTCGACTTGG TTCAAATGGA TGTTTTCTG TTTCACGTGG TCGAGCAGCC
551 GTCCGACGGT GCGGACGACG ATTTCCGAGC CGGCACGCAG GTCGGCGGTC
601 TGTTCGTCCA TATTCATACC GCCGAACAAG ACGGTGTGGC GCAGCGGCAG
651 GTTTTGTATG TAG

```

This corresponds to the amino acid sequence <SEQ ID 2242; ORF 680.a>:

```

a680.pep
1  MTKGSSAISS PRAAISVATR TRRLPSLKAL SVSSRLCWER SPCACADRL
51  RRTSSRVTRS TLCLVLQNTM TWFIKSTIS RSRRLRF*MV STAMMCCSTL
101 ALVVSCAATS TVSGAFMKSC ASLRIGA EKVAEKSRVWRWR GSICMILRMS
151 SIKPISSIRS ASSKTTISTL FKWMFFCFTW SSSRPTVATT ISQPARRSAV
201 CLSIFIPNKT TVWRSGRFLM *

```

m680/a680 98.6% identity in 220 aa overlap

```

          10      20      30      40      50      60
m680.pep  MTKGSSAMSSPRAAMS VATRTRRLPSLKALSVSSRLC WERSPCACADRLRRTSSRVTRS
          |||||
a680      MTKGSSAISSPRAAISVATRTRRLPSLKALSVSSRLC WERSPCACADRLRRTSSRVTRS
          10      20      30      40      50      60

          70      80      90      100     110     120
m680.pep  TLCLVLQNTMTWFIKSTISRSSRLRFXMVSTAMMCCSTLALVV FCAATSTVSGAFMKSC
          |||||
a680      TLCLVLQNTMTWFIKSTISRSSRLRFXMVSTAMMCCSTLALVV SCAATSTVSGAFMKSC
          70      80      90      100     110     120

          130     140     150     160     170     180
m680.pep  ASLRIGA EKVAEKSRVWRWRSICMILRMSSIKPISSIRSASSKTTISTLFKWMFFCFTW
          |||||
a680      ASLRIGA EKVAEKSRVWRWRSICMILRMSSIKPISSIRSASSKTTISTLFKWMFFCFTW
          130     140     150     160     170     180

          190     200     210     220
m680.pep  SSSRPTVATTISQPARRSAVCLSI FIPNKT VWRSGRFLMX
          |||||
a680      SSSRPTVATTISQPARRSAVCLSI FIPNKT VWRSGRFLMX
          190     200     210     220

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2243>:

```

g681.seq
1  ATGACGACGC CGATGGCAAT CAGTGCCTCA AATTTTTCGG AAGAGGCAAA
51  GTTCATCAGC GCGATGGGGA TTTCAAGCGC GCCGGGTACG GTGGcgacgg

```

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```

101  tgatgtTTTC GTCTGCTACG CCCAATTCTT GGAGGGTGCG GCAGCAGACT
151  TTGAGCATTT GGCTGCCGAT TTCGTTGGTG AAGCGTGCCT GTACGATGCC
201  GATGCGGAGG TGTTTGCcgt cgaggttgGG GGCGATGGTG TTCATTGGGT
251  GTCCTTTGGT ATTCGGGGTT TCGGAATGCC GTCTGAAGGT TTCAGTCTTG
301  CGGCTGCCAG TCGGCAACGG TTTGGAATGT GCCGTCTTCG GCAAGCTCCC
351  ACGCGCTGCC TTCGGGTTGG GAAAGCAGTG CGGCGGTTTC AGGGTTGGTT
401  TTGGTGATGT CGGCGAGGCT GACGATGCTG AAGTTGTCCG GGTCTGCGGT
451  GTATTCTCGC GTTTCGTGCG CGCTGAAGAA ACGCCAGCCG CTGTCTGTTT
501  CAAAAACGGG CGCTTCGCGG TAAAGGAAGC CGACGGGCCG GTTTTGTTTG
551  GCGACGGTGT TGGTGGCGAT GCAGCGTTCG AGTGCCGAGG AAAGTGCTTG
601  TGCAAAATGCG TTCATTGCGG GAATACGTTG GGGGGGGGGA AACTTGCGGA
651  TTTTACCAGC ATCCCGCGT TGTCGGCAGA CGGCGGCGGT TTGGTGGTAC
701  AATGTGCCCC GTTTCGAGCC TTAAGGTGTT TCTGTATTTT TGGAGTATGG
751  AAACGCATTC GGGCTGTTTT TTGCGGAAGA CGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2244; ORF 681>:

```

g681.pep
1  MTPMAISAS NFSEEAKFIS AMGISSAPGT VATVMFSSAT PNSWRVRQQT
51  LSIWLPISLV KRACTMPMR CLPSRLGAMV FIGCPLVFGV SECRLKVSVL
101 RLPVGNGLC AVFGKLPRAA FGLGKQCGGF RVGFGDVGEA DDAEVGVVVG
151 VFVGFVAAEE TPAAVVFKNG GFAVKEADGP VLFGDGVGGD AAVECRGKCL
201 CKCVHCGNTL GGGKLADFTT IFALSADGGG LVVQCAPFAA LRCFCIFGVW
251 KRIRAVFCGR R*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2245>:

```

m681.seq
1  ATGACGACGC CGATGGCAAT CAGTGCCTCA AACTTTTTCG AAGAGGCAAA
51  GTTCATCAGC GCGATGGGGA TTTCAAGCGC GCCGGGTACG GTGGCGACGG
101 TAATGTTTTT GTCTGCCACG CCCAATTCTT GGAGGGTGCG GCAGCAGACT
151 TTGAGCATTT CGCTGCCGAT TTCGTTGGTG AAGCGTGCCT GTACGATGCC
201 GATGCGGAGG TGTTTGCCGT CGAGGTGGG GGCGATGGTG TTCATTGGGT
251 GTCCTTTGGT ATTCGGAGTT TCGGAATGCC GTCTGAAGGT TTCAGTCTTG
301 CGSCTGCCAG TCGGCGACGG TTTGGAATGT GCCGTCTTCG GCAAGCTCCC
351 ATGCGCTGCC TTCGGGTTGG GAGAGCAGTG CGGCGGTTTC AGGGTTGGTT
401 TTGGCGATGT CGGCGAGGCT GACGATGCTG AAGTTGTCCG GATCTGCGGT
451 GTATTCTCGC GTCTCGTTCG CGCTGAAGAA ACGCCAGCCG CTGTCTGTTT
501 CAAAAACGGG GGCTTCGCGG TAGAGGAAGC CGACGGGCCG GTTTTGTTTG
551 GCGACGGTGT TGGTGGCGAT ACAGCGGTTC AGTGCCGAGG AAAGTGCTTG
601 TGCAAAATGCG TTCATTACGG GAATACGTTG GGGG.AAAAC TTACGGATT
651 TACCACGATT CGTGCGTTGT CGGCAGACGG CGGCGGTTTG GTGGTACAAT
701 GTGCGCCGTT TGCAGCCTTA AGGTGTTTCT GTATTTTGG AGTATGGAAA
751 CGCATTCGGG CTGTTTTTTG CGGAAGACGG TAA

```

This corresponds to the amino acid sequence <SEQ ID 2246; ORF 681>:

```

m681.pep
1  MTPMAISAS NFSEEAKFIS AMGISSAPGT VATVMFSSAT PNSWRVRQQT
51  LSISLPISLV KRACTMPMR CLPSRLGAMV FIGCPLVFGV SECRLKVSVL
101 RLPVGDGLEC AVFGKLPCAA FGLGEQCGGF RVGFGDVGEA DDAEVVRIVG
151 VFVGLVAAEE TPAAVVFKNG GFAVEEADGP VLFGDGVGGD TAVECRGKCL
201 CKCVHYGNTL GXKLTDFTT RALSADGGGL VVQCAPFAAL RCFCIFGVWK
251 RIRAVFCGRR *

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 681 shows 94.6% identity over a 261 aa overlap with a predicted ORF (ORF681.a) from *N. gonorrhoeae*:

m681/g681

```

          10      20      30      40      50      60
m681.pep  MTPMAISASNFSEEAKFISAMGISSAPGTVATVMFSSATPNSWRVRQQTLSISLPISLV
          |||
g681       MTPMAISASNFSEEAKFISAMGISSAPGTVATVMFSSATPNSWRVRQQTLSIWLPISLV
          10      20      30      40      50      60

```

1092

	70	80	90	100	110	120
m681.pep	KRACTMPMRRCLPSRLGAMVFIGCPLVFGVSECRLKVSVLRLPVGDGLECAVFGKLPCAA					
	: : : : :					
g681	KRACTMPMRRCLPSRLGAMVFIGCPLVFGVSECRLKVSVLRLPVGNGLECAVFGKLPRAA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m681.pep	FGLGEQCGGFRVGFVDVGEADDAEVVRIVGVFVGLVAAEETPAAVVFKNGGFAVEEADGP					
	: : : : : :					
g681	FGLGKQCGGFRVGFVDVGEADDAEVVGVGVGFVAAEETPAAVVFKNGGFAVKEADGP					
	130	140	150	160	170	180
	190	200	210	220	230	239
m681.pep	VLFGDGVGGDTAVECRGKCLCKCVHYGNTLGX-KLTDFTTIRALSADGGGLVVQCAPFAA					
	: : : : : :					
g681	VLFGDGVGGDAAVECRGKCLCKCVHCGNTLGGGKLADFTTIPALSADGGGLVVQCAPFAA					
	190	200	210	220	230	240
	240	250	260			
m681.pep	LRCFCIFGVWKIRAVFCGRRX					
	: : :					
g681	LRCFCIFGVWKIRAVFCGRRX					
	250	260				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2247>:

```

a681.seq
1   ATAACGACGC CGATGGCAAT CAGTGCCTCA AATTTTTCAG AAGAGGCAAA
51  GTTCATCAGC GCGATGGGGA TTTCAAGCGC GCCGGGTACG GTGGCGACGG
101 TAATGTTTTTTC GTCTGCCACG CCAATTCTT GGAGGGTGC GACAGAGACT
151 TTGAGCATTT CGCTGCCGAT TTCGTTGGTG AAGCGTGCCT GTACGATGCC
201 GATGCGGAGG TGTTCGCCGT CGAGGTTGGG GCGATGGTG TTCATTGAGT
251 GTCCTTTGGT ATTCGGAGGT TTCGGAATGC CGTCTGAAGG GTCAGTCCTT
301 AGGTGCCCAG TCGCGACCGG TTTGGAATGT GCCGTCTTCT GCCAATTCCC
351 ACGCGCTGCC TTCAGGTTGG GAGAGCAGTG CGCGGTTTC AGGGTTGGTT
401 TTGGTGATAT CGGCGAGGCT GACGATGCTG AAGTTGTCCG GGTCTCGGTT
451 GTATTCGTCG GTCTCGTCGC CGCTGAAGAA ACGCCAGCCG CTGTCGTTTT
501 CAAAACGGG GGCTTCGCGG TAGAGGAAGC CGACGGGCTG GTTTTGTGTTG
551 GCGACGGTGT TGTGCGCGAT GCAGCGGTCG AGTGCCGAGG AAAGTGCTTG
601 TGCAAAATGCG TTCATTGCGG GAATACGTT GGGGGAAAAC TTGCGGATTT
651 TACCACGATT CTTGCGTTGT CGGCAGACGG CGCGGTTTG GTGGTACAAT
701 GTGCGCCGTT TGCAGCCTTA AGGTGTTTCT GTATTTTGG AGTATGGAAA
751 CGCATTCCGG CTGTTTTTTC CGGAAGACGG TAA

```

This corresponds to the amino acid sequence <SEQ ID 2248; ORF 681.a>:

```

a681.pep
1   ITPMAISAS NFSEEAKFIS AMGISSAPGT VATVMFSSAT PNSWRVRQQT
51  LSISLPISLV KRACTMPMRR CLPSRLGAMV FIECPLVFGG FGMPSEGSVL
101 RLPVGDGLEC AVFCQFPRAA FRLGEQCGGF RVGFGDIGEA DDAEVVRVVG
151 VFVGLVAAEE TPAAVVFKNG GFAVEEADGL VLFGDGVGGD AAVECRGKCL
201 CKCVHCGNTX GGLADFTTI LALSADGGGL VVQCAPFAAL RCFCIFGVWK
251 RIRAVFCGRR *

```

m681/a681 90.8% identity in 260 aa overlap

	10	20	30	40	50	60
m681.pep	MTTPMAISASNFSEEAKFISAMGISSAPGTVATVMFSSATPNSWRVRQQTLSISLPISLV					
	: : : : : :					
a681	ITTPMAISASNFSEEAKFISAMGISSAPGTVATVMFSSATPNSWRVRQQTLSISLPISLV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m681.pep	KRACTMPMRRCLPSRLGAMVFIGCPLVFGVSECRLKVSVLRLPVGDGLECAVFGKLPCAA					
	: : : : :					
a681	KRACTMPMRRCLPSRLGAMVFIECPLVFGGFGMPSEGSVLRLPVGDGLECAVFCQFPRAA					
	70	80	90	100	110	120

1093

	130	140	150	160	170	180
m681.pep	FGLGEQCGGFRVGF	GDVGEADDAEVVR	IVGVFVGLVAAEET	PAAVVFKN	GGFAVEEADGP	
a681	FRLGEQCGGFRVGF	DIGEADDAEVVR	VGVFVGLVAAEET	PAAVVFKN	GGFAVEEADGL	
	130	140	150	160	170	180
	190	200	210	220	230	240
m681.pep	VLFGDGVGGDTAVE	CRGKCLCKCVHYG	NLTGXKLTDFTTI	RALSADGGGLVV	QCAPFAAL	
a681	VLFGDGVGGDAAVE	CRGKCLCKCVHCG	NLTGXKLTDFTTI	LALSADGGGLVV	QCAPFAAL	
	190	200	210	220	230	240
	250	260				
m681.pep	RCFCIFGVWKRIR	AVFCGRRX				
a681	RCFCIFGVWKRIR	AVFCGRRX				
	250	260				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2249>:

g682.seq

```

1  ATGCGCGATT TCGCCGTATG GGTGCCTTAC GGGGAACGGC GGAAAAATTG
51  GGACATAAGG TATTGCCTCC CGCACCTTAT TCGCCTGAGC CCAACCCGAT
101 TGAGAAAGTG TGGGCGAATA TTAAGCGGTA TCTGCGAACC GTTTTGTCTG
151 ATTACGCCCC ATTTGACGAT GCACTACTGT CCTATTTGA TTTTAATTGA
201 CTATATTGTG GTGAATGATG AAATAAAAT GCCGTCTGAA CCCGATTGGA
251 TTCAGACGGC ATTTTGTATG GCAGGATTTA TTCGCTTCC AACTGACCGA
301 CCCATTCTGA CAAGGCAGTC AGCGTTGTT CGGATTTCGC CACGAACGGG
351 TTTTCGGTAT CCCACGCGTA GCCTGCCAAA ATCGAAGAAA GCATACGGCT
401 GA

```

This corresponds to the amino acid sequence <SEQ ID 2250; ORF 682>:

g682.pep

```

1  MRDFAVWVPY GERRKNWDIR YCLPHLIRLS PTRLRKCGRI LSGICEPFCL
51  ITPDLTMHYC PILILIDYIC VNDEIKMPSE PDWIQTAFCM AGFIREPTDR
101 PILTRQSGVV RISPRTGFRY PTRSLPKSKK AYG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2251>:

m682.seq

```

1  ATGCGTGATT TCACCGTATG GGTGTCTTAC GGGAAATGGC GGAAAAATTG
51  GGACATAAGG TATTGCCTCT TGCACCTTAT TCACCTGAGC TCAACCCGAT
101 TGAGAAAGTG TGGGCGAATA TTAAGCGGTA TCTGCGAACC GTTTTGTCTG
151 ATTACGCCCC ATTTGACGAT GCACTACTGT CCTATTTGA TTTTAATTGA
201 CTAT..... GAAA TGGCAATGCC GTCTGAACCC GATTGGATTC
251 AGACGGCATT TTGTATGGCG TACGGATTTA TTCGGTTTCC AACTGACCGA
301 CCCATTCTGA CAAGGCAGTC AGCGTTGTT CGGATTTCGC CACGAACGGG
351 TTTTCGGTAT CCCACGCGTA GCCTGCCAAA ATCGAAGAAA GCATACGGCT
401 GA

```

This corresponds to the amino acid sequence <SEQ ID 2252; ORF 682>:

m682.pep

```

1  MRDFTVWVSY GKWRKNWDIR YCLLHLIHLs STRLRKCGRI LSGICEPFCL
51  ITPDLTMHYC PILILIDY.. ..EMAMFSEP DWIQTAFDMA YGFIREPTDR
101 PIRTRQSGVV RISPRTGFRY PTRSLPKSKK AYG*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* menA with menB

ORF 682 shows 88.1% identity over a 134 aa overlap with a predicted ORF (ORF682.a) from *N. gonorrhoeae*:

m682/g682

1094

```

      10      20      30      40      50      60
m682.pep  MRDFTVWVSYGKWRKNWDIRYCLLHLIHLSSTRLRKCGRILSGICEPFCLITPDLTMHYC
          |||:||||| ||: ||||| |||: || ||||| ||||| ||||| ||||| |||||
g682      MRDFAVWVPYGERRKNWDIRYCLPHLIRLSPTRLRKCGRILSGICEPFCLITPDLTMHYC
          10      20      30      40      50      60

      70      80      90      100     110
m682.pep  PILILIDY----EMAMPSEPDWQIQTAFCMAYGFIREFTDRPIRTRQSGVVRISPRTGFR
          ||||| ||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g682      PILILIDYICVNDEIKMPSEPDWQIQTAFCMAYGFIREFTDRPIRTRQSGVVRISPRTGFR
          70      80      90      100     110

      120     130
m682.pep  YPTRSLPKSKKAYGX
          ||||| |||||
g682      YPTRSLPKSKKAYGX
      120     130

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2253>:

```

a682.seq
1  ATGCGCGATT TTACCGTATG GGTGTCTTAC GGGAAATGGC GGAAAAATTG
51 GGACATAAGG TATTGCCTCT TGCACCTTAT TCACCTGAGC TCAACCCGAT
101 TGAGAAAGTG TGGCGGAATA TTAAGCGGTA TCTGCGAACC GTTTGTCTG
151 ATTACGCCCG ATTTGACGAT GCACTACTGT CCTATTTTGA TTTAATTGA
201 ATAT.....
251 .....TATA TTCGGTTTCC AACTGACCGA
301 CCCATTCTGA CAAGGCCGAC AGGCGTTGTT CGGATTTCGC CACGAACGGG
351 TTTTCGGTAT CCCACGCGTA GCCTGCCAAA ATCGAAGAAA GCATACGGCT
401 GA

```

This corresponds to the amino acid sequence <SEQ ID 2254; ORF 682.a>:

```

a682.pep
1  MRDFTVWVSY GKWRKNWDIR YCLLHLIHL STRLRKCGRI LSGICEPFCL
51 ITPDLTMHYC PILILIEY.. ..YIRFPTDR
101 PILTRPTGVV RISPTGFRY PTRSLPKSKK AYG*

```

m682/a682 80.6% identity in 129 aa overlap

```

      10      20      30      40      50      60
m682.pep  MRDFTVWVSYGKWRKNWDIRYCLLHLIHLSSTRLRKCGRILSGICEPFCLITPDLTMHYC
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a682      MRDFTVWVSYGKWRKNWDIRYCLLHLIHLSSTRLRKCGRILSGICEPFCLITPDLTMHYC
          10      20      30      40      50      60

      70      80      90      100     110     120
m682.pep  PILILIDYEMAMPSEPDWQIQTAFCMAYGFIREFTDRPIRTRQSGVVRISPRTGFRYPTRS
          ||||| ||: ||||| ||||| ||||| ||||| ||||| ||||| |||||
a682      PILILIEY-----YIRFPTDRPILTRPTGVVRISPRTGFRYPTRS
          70      80      90      100

      130
m682.pep  LPKSKKAYGX
          ||||| |||||
a682      LPKSKKAYGX
      110

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2255>

```

g683.seq
1  ATGATTAAGG AAACCTAAT GCGCCCAATC TTCCTATCTT TCGTTTACT
51 CCCTATTTTG ATAACCGCCT GCAGCACACC GGACAAGTCT GCCCGATGGG
101 AAAATATCGG CACAATCTCA AACGGCAATA TTCATACATA TATTAATAAA
151 GACAGTGTGA GAAAAACGG AAATCTGATG ATTTCCAAG ATAAAAAAGT
201 TGTTACCAAT CTGAAACAAG AACGTTTTCG CAACACCCCC GCATACAAGA
251 CTGCCATTGC CGAGTGGGAA ATCCACTGCA ACAACAAAAC ATACCGCTTA
301 AGTTTCGCTAC AGTTATTGA TACAAAAAAC ACGGAATTT CCACACAAA
351 CTACACAGCC TCTTCCTCC GCCCGATGAG CATCCTGTCC GGGACATTAA

```

401 CTGAAAAACA ATATGAAACC GTATGCGGGA AAAAAGCTCTG A

This corresponds to the amino acid sequence <SEQ ID 2256; ORF 683 >:

m683.pep
 1 MIKETLMRPI FLSFVLLPIL ITACSTPDKS ARWENIGTIS NGNIHTYINK
 51 DSVRKNGNLM IFQDKKVVVN LKQERFANTP AYKTAIAEWE IHCNNKTYRL
 101 SSLQLFDTKN TEISTQNYTA SSLRPMISLS GTLTEKQYET VCGKKL*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2257>:

m683.seq.
 1 ATGATTAAGG AAACCTAAT GCGCCCAATC TTCCTATCTT TCGTTTATT
 51 CCCTATTTTG ATAACCGCCT GCAGCACACC GGACAAGTCT GCCCGATGGG
 101 AAAATATCGG CACAATCTCA AACGGCAATA TTCATACATA TATCAATAAA
 151 GACAGCGTGA GAAAAACGG AAATCTGATG ATTTTCCAAG ATAAAAAAGT
 201 TGTTACCAAT CTAAAAACAAG AACGTTTTCG CAACACCCCC GCATACAAGA
 251 CTGCCATTGC CGAGTGGGAA ATCCACTGCA ACAACAAAAC ATACCGCTTA
 301 AGTTCGCTAC AGTTGTTTGA TACAAAAAAC ACGGAAATTT CCACACAAAA
 351 CTACACAGCC TCTTCCCTCC GCCCGATGAG CATCCTGTCC GGGACATTAA
 401 CCGAAAAACA ATATGAAACC GTATGCGGAA AAAAAGCTCTG A

This corresponds to the amino acid sequence <SEQ ID 2258; ORF 683>:

m683.pep.
 1 MIKETLMRPI FLSFVLPIL ITACSTPDKS ARWENIGTIS NGNIHTYINK
 51 DSVRKNGNLM IFQDKKVVVN LKQERFANTP AYKTAIAEWE IHCNNKTYRL
 101 SSLQLFDTKN TEISTQNYTA SSLRPMISLS GTLTEKQYET VCGKKL*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 683 shows 99.3% identity over a 146 aa overlap with a predicted ORF (ORF 683) from *N. gonorrhoeae*:

m683/g683 99.3% identity in 146 aa overlap

m683.pep	10	20	30	40	50	60
	MIKETLMRPI	FLSFVLPIL	ITACSTPDKS	ARWENIGTIS	NGNIHTYINK	DSVRKNGNLM
g683	MIKETLMRPI	FLSFVLPIL	ITACSTPDKS	ARWENIGTIS	NGNIHTYINK	DSVRKNGNLM
	10	20	30	40	50	60
m683.pep	70	80	90	100	110	120
	IFQDKKVVVN	LKQERFANTP	PAYKTAIAEWE	IHCNNKTYRL	SSLQLFDTKN	TEISTQNYTA
g683	IFQDKKVVVN	LKQERFANTP	PAYKTAIAEWE	IHCNNKTYRL	SSLQLFDTKN	TEISTQNYTA
	70	80	90	100	110	120
m683.pep	130	140				
	SSLRPMISLS	GLTEKQYET	VCGKKLX			
g683	SSLRPMISLS	GLTEKQYET	VCGKKLX			
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2259>

a683.seq
 1 ATGATTAAGG AAACCTAAT GCGCCCAATC TTCCTATCTT TCGTTTATT
 51 CCCTATTTTG ATAACCGCCT GCAGCACACC GGACAAGTCT GCCCGATGGG
 101 AAAATATCGG CACAATCTCA AACGGCAATA TTCATACATA TATCAATAAA
 151 GACAGCGTGA GAAAAACGG AAATCTGATG ATTTTCCNAG ATAAAAAAGT
 201 TGTTACCAAT CTAAAAACAAG AACGTTTTCG CNACACCCCC GCATACAAGA
 251 CTGCCATTGC CGAGTGGGAA ATCCACTGCA ACAACAAAAC ATACCGCTTA
 301 AGTTCGCTAC AATGTTTGA TACAAAAAAC ACGGAAATTT CCACACAAAA
 351 NTACACAGCC TCTTCCCTCC GCCCGATGAG CATCCTGTCC GGGACATTAA
 401 CCGAAAAACA ATATGAAACC GTATGCGGAA AAAAAGCTCTG A

This corresponds to the amino acid sequence <SEQ ID 2260; ORF 683.a>:

a683.pep
 1 MIKETLMRPI FLSFVLPIL ITACSTPDKS ARWENIGTIS NGNIHTYINK
 51 DSVRKNGNLM IFXDKKVVVN LKQERFAXTP AYKTAIAEWE IHCNNKTYRL

101 SSLQLFDTKN TEISTQXYTA SSLRPMSILS GTLTEKQYET VCGKKL*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 683 shows 97.9% identity over a 146 aa overlap with a predicted ORF (ORF 683) from *N. meningitidis*:

m683/a683 97.9% identity in 146 aa overlap

	10	20	30	40	50	60
m683.pep	MIKETLMRPIFLSFVLPILITACSTPDKSARWENIGTISNGNIHTYINKDSVRKNGNLM					
a683	MIKETLMRPIFLSFVLPILITACSTPDKSARWENIGTISNGNIHTYINKDSVRKNGNLM					
	10	20	30	40	50	60
	70	80	90	100	110	120
m683.pep	IFQDKKVVTNLKQERFANTPAYKTAIAEWEIHCNNKTYRLSSLQLFDTKNTEISTQNYTA					
a683	IFQDKKVVTNLKQERFANTPAYKTAIAEWEIHCNNKTYRLSSLQLFDTKNTEISTQNYTA					
	70	80	90	100	110	120
	130	140				
m683.pep	SSLRPMSILSGTLTEKQYETVCGKKLX					
a683	SSLRPMSILSGTLTEKQYETVCGKKLX					
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2261>

g684.seq

1	ATGCGCCTTT	TCCCATCGC	CGCCGCCCTG	ACGCTTGCCG	CCTGCGGTAC
51	TGTGCAAAGC	ACACAATATT	TCGTGTTGCC	CGACAGCCGC	TACATCCGTC
101	CTGCAACGCA	AGGCGGCGAA	ACCGCCGTCG	AAGTCCGTCT	TGCCGAACCG
151	CTCAAACGCG	GCGGACTGGT	CTATCAAAAC	GACCCCTACC	GCATCAACAC
201	CGCACAAAAC	CATGTTGGG	CAGACACCTT	GGACGATATG	CTCGAAGCGG
251	CGTTGAGCAA	TGCATTCAAC	CGTTTGGACA	GCACACGCAT	CTTTGTTCTT
301	GCCTCACGCA	GCGGCAGTAC	CGACAAATGG	ACGGTCTATA	TCGACGCATT
351	CCAAGGCAGC	TACACGGGCA	AAACCCTCAT	CAGCGGCTAC	GCCGTCCTAC
401	CCGACGGTAC	GAACAGACCC	TTCCATATCG	AAACCGAACA	GCAGGGTGAC
451	GGCTACGCCG	CCATGACCGC	CGCACTCGAA	CAGGGACTGA	AACAGGCGGC
501	GCAACAGATG	GTCGAGTAA			

This corresponds to the amino acid sequence <SEQ ID 2262; ORF 684>:

g684.pep

1	MRLFPAAAL	TAAACGTVQS	TOYFVLPDSR	YIRPATQGGG	TAVEVRLAEP
51	LKRGLVYQT	DPYRLNTAQN	HVWADTLDDM	LEAALSNAFN	RLDSTRIFVP
101	ASRSGSTDKW	TVYIDAFQGS	YTGKTLISGY	AVLPDGTNRP	FHIETEQQGD
151	GAAAMTALE	QGLKQAAQOM	VE*		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2263>:

m684.seq

1	ATGCGCCTTT	TCCCGATTGC	CGCCGCCCTG	TCGCTTGCCG	CCTGCGGTAC
51	TGTGCAAAGC	ACACAATATT	TCGTGTTGCC	CGACAGCCGC	TACATCCGTC
101	CTGCAACGCA	AGGCGGCGAA	ACTGCCGTCG	AAGTCCGTCT	TGCCGAACCG
151	CTCAAACGCG	GCGGACTGGT	CTATCAAAAC	GACCCCTACC	GCCTCAACAC
201	CGCACAAAAC	CACGTCTGGG	CAGACACCTT	GGACGATATG	CTCGAAGCGG
251	CGTTGAGCAA	TGCATTCAAC	CGTTTGGACA	GCACACGCAT	CTTTGTTCTT
301	GCCTCACGCA	GCGGCAGTAC	CGAAAAATGG	ACGGTCTATA	TCGACGCATT
351	CCAAGGCAGC	TACACGGGCA	AAACCCTCAT	CAGCGGCTAC	GCCGTCCTAC
401	CCGACGGTAC	GAACAGACCC	TTCCATATCG	AAACCGAACA	GCAGGGTGAC
451	GGCTACGCCG	CGATGACCGC	CGCACTCGAA	CAGGGACTGA	AACAGGCGGC
501	GCAACAGATG	GTCGAGTAA			

This corresponds to the amino acid sequence <SEQ ID 2264; ORF 684>:

m684.pep

1	MRLFPAAAL	SLAACGTVQS	TOYFVLPDSR	YIRPATQGGG	TAVEVRLAEP
51	LKRGLVYQT	DPYRLNTAQN	HVWADTLDDM	LEAALSNAFN	RLDSTRIFVP
101	ASRSGSTEKW	TVYIDAFQGS	YTGKTLISGY	AVLPDGTNRP	FHIETEQQGD

151 GYAAMTAALE QGLKQAAQOM VE*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 684 shows 97.7% identity over a 172 aa overlap with a predicted ORF (ORF 684) from *N. gonorrhoeae*:

m684/g684 97.7% identity in 172 aa overlap

m684.pep	10	20	30	40	50	60
	MRLFP	IAAALSLAAC	GTQSTQYFVLP	DSRYIRPATQ	GGETA	VEVRLAEPLKRGGLVYQT
g684	10	20	30	40	50	60
	MRLFP	IAAALSLAAC	GTQSTQYFVLP	DSRYIRPATQ	GGETA	VEVRLAEPLKRGGLVYQT
m684.pep	70	80	90	100	110	120
	DPYRLNTAQN	HVWADTLD	DMLEAALSNA	FNRLDSTRIF	VPASRSGST	EKWTVYIDAFQGS
g684	70	80	90	100	110	120
	DPYRLNTAQN	HVWADTLD	DMLEAALSNA	FNRLDSTRIF	VPASRSGST	EKWTVYIDAFQGS
m684.pep	130	140	150	160	170	
	YTGKTLISGY	AVLPDGTNR	PFHIETEQQ	GDGYAAMTAA	LEQGLKQAAQOMVEX	
g684	130	140	150	160	170	
	YTGKTLISGY	AVLPDGTNR	PFHIETEQQ	GDGYAAMTAA	LEQGLKQAAQOMVEX	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2265>

a684.seq

1	ATGCGCCTCT	TCCCGATTGC	CGCCGCCCTG	ACGCTTGCCG	CCTGCGGTAC
51	TGTGCAAGC	ACACAATATT	TCGTGTTGCC	CGACAGCCGC	TACATCCGTC
101	CTGCAACGCA	AGGCGCGCAA	ACTGCCGTCG	AAGTCCGTCT	TGCCGAACCG
151	CTCAAACGCG	GCGGACTGGT	CTATCAAACC	GACCCCTACC	GCCTCAACAC
201	CGCACAAAAC	CACGTCTGGG	CAGACACCTT	GGACGATATG	CTCGAAGCGG
251	CGTTGACCAA	TGCATTCAAC	CGTTTGACA	GCACACGCAT	CTTTGTTCTT
301	GCCTCACGCA	GCGGCAGTAC	CGAAAAATGG	ACGGTCTATA	TCGACGCATT
351	CCAAGGCAGC	TACACGGGCA	AAACCCTCAT	CAGCGGCTAC	GCCGTCCTAC
401	CCGACGGTAC	GAACAGACCC	TTCCATATCG	AAACCGAACA	GCAGGGTGAC
451	GGCTACGCCG	CCATAGCCGC	CGCACTCGAA	CAGGGACTGA	AACAGGCGGC
501	GCAACAGATG	GTCGAGTAA			

This corresponds to the amino acid sequence <SEQ ID 2266; ORF 684.a>:

a684.pep

1	MRLFP	IAAAL	TLAAC	GTQSTQYFVLP	DSRYIRPATQ	GGETA	VEVRLAE
51	LKRGGLVYQT	DPYRLNTAQN	HVWADTLD	DMLEAALSNA	FNRLDSTRIF	VP	
101	ASRSGST	TEKWT	TVYIDAFQGS	YTGKTLISGY	AVLPDGTNR	PFHIETEQQ	GD
151	GYAAMTAALE	QGLKQAAQOM	VE*				

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 684 shows 99.4% identity over a 172 aa overlap with a predicted ORF (ORF 684) from *N. meningitidis*

m684/a684 99.4% identity in 172 aa overlap

m684.pep	10	20	30	40	50	60
	MRLFP	IAAALSLAAC	GTQSTQYFVLP	DSRYIRPATQ	GGETA	VEVRLAEPLKRGGLVYQT
a684	10	20	30	40	50	60
	MRLFP	IAAALSLAAC	GTQSTQYFVLP	DSRYIRPATQ	GGETA	VEVRLAEPLKRGGLVYQT
m684.pep	70	80	90	100	110	120
	DPYRLNTAQN	HVWADTLD	DMLEAALSNA	FNRLDSTRIF	VPASRSGST	EKWTVYIDAFQGS
a684	70	80	90	100	110	120
	DPYRLNTAQN	HVWADTLD	DMLEAALSNA	FNRLDSTRIF	VPASRSGST	EKWTVYIDAFQGS
	130	140	150	160	170	

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g685.00q
1  TTGTTTTCGC GTATCGGGAA TTTTCGCTTT TCGCGCGTGG TTTCTGCAGG
51  TTGTTTTCCT AATAATAAAC ATTCTATTCT GTATGCAAAg GAACCGCACA
101 CCGTGAACGc GCGTTTTTAT TTGGCAGcct GCGCGCTCCT GCGCGCGCCc
151 TGTTCGCCCC AACCTGCCGC CGAAAAAAcT GTATcgcCG CATCCCAAGC
201 CGCATCCACA CCFGTCCGCA CGCTGACCGT GCCGACCgCG CCGGGCGGATG
251 CGGTTTGTCc GAAGAATCCC GAACgcgtcg cegtgtAcga CTgggCGGCG
301 TtggATACGC TGACCCGATG GGGCGTGAAT GTGGGCGCAA CCACCGCGCC
351 GGTGCGCGTC GACTATTGCT AGCCTGCAAT TGACAAGGCG GCAACCGGTG
401 GGACGCTGTT TGAGCCCGAT TGCGAATCCC TGCACCGCCA CAATTCCGAG
451 TTTGTCATTA CCGCGGGGCC GGGTGCGGAA GCGTATGAAC AATTGGCGAA
501 AAGCGCGACC ACCATAGATT TGACGGTGGA CAACGGCAAT TAACCGCACA
551 CGGGCGAGAA GCAGATTGGAG ACCCTGTCGC GATTTTTCG TAAGGAAGCG
601 CGCGTGGCGG AATTGAATGC GCAGATTGAC GCGCTGTTCG CCAAAAAGCG
651 CGAAGCGGCC AAGGCAAAAG GACGCGGGCT GGTGCTGTGC GTTACAGCCA
701 ACAAGGTGTC CGCCTTCGCG ACGCAATCGC GGTGGCAAG TTGGATACAC
751 GCGGACATCG GCCTGCGCGC CGTGACGAA TCTTTACGA ACGAAGGCGA
801 CGGGCAGGCC GTTTCCTTCG AATACATCAA AGAGAAAAAG CCCGCTTGA
851 TTTTCATCAT CGAGCCGACC GCCGCCATCG GGCAGGAAGG CCGCGCTGCC
901 TTGGAAGTGT TEGATAACGC CTGTTATGCG GCGACGACG CTTTGAAGCG
951 CAAGCAAATC ATCGTCATGC CTGCGCGAA CTACATTGTC GCGGGCGGCG
1001 CGCGCGCACT GTACAGCGCG GCGGAACAGT TGAAGCGGCG GTTTGAAAAG
1051 GCAGAACCCG TTGCGCGCGA GTAG

```

g685.pap

1	LFCRIGNFAP	CGVSAGCLL	NNKHSYSYAK	EPHTVKPRFY	WAACAVLPAA
51	CSEPEAEK	VSASQAAS	PVATLTVP	RGDAVVPKPN	ERVAVDWQA
101	LDLTLP	EGVNVG	ATTA	PVRV	DYLPQAFDKA
151	FVITGGP	GAEE	ALYQLAKNAT	TIDLTVDVNS	IRTSGEKOME
201	RVAEINQA	IF	ALPQAKREAA	KGKGRGLVGL	VTGNKVSAPG
251	GDIGLPP	VDSE	SLRNEGHGQP	VSFEYIKEKN	PGWIFIIDRT
301	VEVLDA	NALV	GTNAWKRKQI	IVMPAANYIV	AGGARQLIQA
351	AEPAAG	*			AEQLKAAFEK

```
m685.seq
1      TTGTTTTGCC GTATCGGGAA TTTTGC GTTT TGCGCGTGG TTTCTGCAGG
5      TTGTTTGCTT AATAATAAAC ATTCTTATTC GTATGCAAAAG GAACCGCACA
101    CCGTGAACCTT GCGTTTTTAT TTGGGACCGT GCGCGCTCCT GTCAGCCGCC
151    TGTTTCGCCCG AACCTCGCCG CGAAAAAATC GTATCCGCCG CATCCGCATC
201    TGCCGCCACG CTGACCGTGC CGACCGCGCG GGGCGATGCC GTTGTGCGCA
251    AGAATCCCGA ACSCGTGCGC GTGTACGACT GGGCGCGCGT GGATACGTGA
301    ACCGAATTGG GCGTGAATGT GGGCGCAACC ACCGCGCCGG TGCGCGTGGA
351    TTATTTTGAC CTGTCATTTT ACAAGGCGCG AACCGTGGGG ACGCTGTTTCG
401    AGCCCGATTA CGAAGCCCTG CRCCGCTACA ATCCTCAGCT TGTCAATTAC
451    GCGGGGCGCG GCGCGGAAGC GTATGAACAG TTAGCGAAAA ACGCGGATCC
501    CATAGATCTG ACCGTGGACA ACGGCAATAT CGCGACCAGC GCGGAAAAAG
551    AGATGGAGAC CTTTGGCGGG ATTTTGGCCA AGGAAGCGCG CGCGCGCGAA
601    TTGAAGGCGC AGATTGACGC GCTGTTCCGC CAACCGCGCG AAGCGCGCAA
651    AGGCAAAAGG ACGCGGCTGG TGCTGTCCGT TACGGGCAAC AAGGTGTCCG
701    CCTTCGGCAC CGACTCGCG TTGGCAAGTT GGATACACGC CGCATCTCGC
751    CTACCGCCTG TAGACGAATC TTTAGCAAC GAGGGGACAG GCGACCGTGT
801    TTCTTTCGAA TACATCAAAG AGAAAAAGCC CGATTGGATT TTCATCATCG
851    ACCGTACCGC CGCCATCGGG CAGGAAGGCG CGCGGCTGT CGAAGTATTG
901    GATAACGCGC TGTGACGCGG CACGACGCT TGGAAAGCGA AGCAATCAT
951    CGTCATGCTT CGGCGCAATT ACATTGTGCG GGGCGGCGCG CGGCAAGTGA
1001   TTCAGGCGGC GGAGCAGTT AGGGCGCGCT TTAATAAGGC AGAACCCGTT
1051   GCGCGGGGGA AAAAGTAG
```

W685 . p8p

1099

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1  LFCRIGNFAF CGVVSAGCLL NNKHSYSYAK EPHTVKPRFY WAACAVLLTA
51 CSPEPAAEKT VSAASASAAT LTVPTARGDA VVPKNPERVA VYDWAALDTL
101 TELGVNVGAT TAPVRVDYLO PAFDKAATVG TLFEPDYEAL HRYNPQLVIT
151 GGPGEAEAYEQ LAKNATTIDL TVDNGNI RTS GEKQMETLAR IFGKEARAAE
201 LKAQIDALFA QTREAAKKGK RGLVLSVTGN KVSAGFTQSR LASWIHGDIG
251 LPPVDESLRN EGHGQPVSE YIKEKNPDWI FIIDRTAAIG OEGPAAVEVL
301 DNALVRGTNA WKRKQIIVMP AANYIVAGGA RQLIQAAEQL KAAFKKAEPV
351 AAGKK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 685 shows 94.4% identity over a 356 aa overlap with a predicted ORF (ORF 685) from *N. gonorrhoeae*:

m685/g685 94.4% identity in 356 aa overlap

```

m685.pep      10      20      30      40      50      60
LFCRIGNFAFCGVVSAGCLLNNKHSYSYAKEPHTVKPRFYWAACAVLLTACSPEPAAEKT
g685          10      20      30      40      50      60
LFCRIGNFAFCGVVSAGCLLNNKHSYSYAKEPHTVKPRFYWAACAVLPAACSPEPAAEKT

m685.pep      70      80      90      100     110
VSAASASA----ATLTVPTARGDAVVPKNPERVAVYDWAALDTLTELGVNVGATTAPVRV
g685          70      80      90      100     110     120
VSAASQAASFPVATLTVPTARGDAVVPKNPERVAVYDWAALDTLTPGVNVGATTAPVRV

m685.pep     120     130     140     150     160     170
DYLQPAFDKAATVGTLEFEPDYEALHRYNPQLVITGGPGAAYEQLAKNATTIDLTVDNGN
g685         120     130     140     150     160     170     180
DYLQPAFDKAATVGTLEFEPDCESLHRHNPQFVITGGPGAAYEQLAKNATTIDLTVDNGN

m685.pep     180     190     200     210     220     230
IRTSGEKQMETLARIFGKEARAAELKAQIDALFAQTREAAKKGKRGVLVSVTGNKVSAGF
g685         180     190     200     210     220     230     240
IRTSGEKQMETLSRIFGKEARVAELNAQIDALFAKREAAKKGKRGVLVSVTGNKVSAGF

m685.pep     240     250     260     270     280     290
TQSRLASWIHGDI GLPPVDESLRNECHGQPVSEFYIKEKNPDWIFIIDRTAAIGOEGPAA
g685         240     250     260     270     280     290     300
TQSRLASWIHGDI GLPPVDESLRNECHGQPVSEFYIKEKNPDWIFIIDRTAAIGOEGPAA

m685.pep     300     310     320     330     340     350
VEVLDNALVRGTNANKRKQIIVMPAANYIVAGGARQLIQAAEQLKAAFKKAEPVAAKKX
g685         300     310     320     330     340     350
VEVLDNALVCGTNANKRKQIIVMPAANYIVAGGARQLIQAAEQLKAAFEKAEPVAAQX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2271>

```

a685.seq
1  TTGTTTGGCC GTATCGGGAA TTTTGCCTTT TGCGGCGTGG TTCTGCGAGG
51 TTGTTTGGCTT AATATAAAC ATTCTTATTC GTATGCAAAG GAACCGCACA
101 CCGTGAAACC GCGTTTTTAT TGGGCAGCCT GCGCCGTCCT GCTGACCGCC
151 TGTTCGCCCC AACCTGCCGC CGAAAAACT GTATCCGCCG CATCCGCATC
201 TGCCGCCACA CTGACCGTGC CGACCGCGCG GGGCGATGCC GTTGTGCCGA
251 AGAATCCCGA ACGCGTCGCC GTGTACGACT GGGCGGCGTT GGATACGCTG
301 ACCGAATTGG GTGTGAATGT GGGCGCAACC ACCGCGCCGG TCGCGTGGGA
351 TTATTTGCAG CCTGCATTGT ACAAGCGGCG AACGGTGGGG ACCTGTTCG
401 AGCCCGATTA CGAAGCCCTG CACCGCTACA ATCCTCAGCT TGTCATTACC
451 GCGCGGCCGG GCGCGGAAGC GTATGAACAG TTGGCGAAAA ACGCGACCAC
501 CATAGATCTG ACGGTGGACA ACGGCATAT CCGCACCAGC GCGGAAAAGC
551 AGATGGAGAC CTTGGCGCGG ATTTTCGCA ASGAAGCGCG CGCGCGGAA
601 TTGAAGGCGC AGATTGACGC GCTGTTCGCC CAAACGCGCG AAGCCGCCAA
651 AGGCAAAAGG CGCGGCTGG TGCTGTCCGT TACGGGCAAC AAGGTGTCCG
701 CCTTCGGCAC GCAGTCGCGG TTGGCAAGTT GSATACACGG CGACATCGGC
751 CTACCGCCTG TAGACGAATC TTTACGCAAC GAGGGGCACG GGCAGCCTGT
801 TTCCTTCGAA TACATCAAAG AGAAAAACCC CGATTGGATT TTATCATCG

```

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```

851 ACCGTACCGC CGCCATCGGG CAGGAAGGGC CGGCGGCTGT CGAAGTATTG
901 GATAACGGC TGGTACGGC CACGAACGCT TGGAAAGCGA AGCAAAATCAT
951 CGTCATGCCT GCCGCGAACT ACATTGTCGC GGGCGGCTCG CGGCAGTTGA
1001 TTCAGGCGGC GGAGCAGTTG AAGGAGGCGT TTGAAAAGGC AGAACCCGTT
1051 CCGCGGGGA AAGAGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2272; ORF 685.a>:

```

a685.pep
1  LFCRIGNFAF CGVVSAGCLL NNKHSYSYAK EPHTVKPRFY WAACAVLLTA
51  CSPEPAAEKT VSAASASAAT LTVPTARGDA VVPKNPERVA VYDWAALDTL
101 TELGVNVGAT TAPVRVDYLO PAFDKAATVG TLFEPDYEAL HRYNPQLVIT
151 GGPGEAEAYEQ LAKNATTIDL TVDNGNIRTS GEKQMETLAR IFGKEARAAE
201 LKAQIDALFA QTREAAKGKG RGLVLSVTGN KVSAGTQSR LASWINGDIG
251 LPPVDESIRN EGHGQPVSEF YIKEKNPDWI FIIORTAAIG QEGPAAVEVL
301 DNALVRGTNA WKRKQIIVMP AANYIVAGGS RQLIQAAEQL KEAFEKAEPV
351 AAGKE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 685 shows 98.9% identity over a 355 aa overlap with a predicted ORF (ORF 685) from *N. meningitidis*:

```

m685/a685 98.9% identity in 355 aa overlap

m685.pep      10      20      30      40      50      60
LFCRIGNFAFCGVVSAGCLLNNKHSYSYAKEPHTVKPRFYWAACAVLLTACSPEPAAEKT
a685          10      20      30      40      50      60
LFCRIGNFAFCGVVSAGCLLNNKHSYSYAKEPHTVKPRFYWAACAVLLTACSPEPAAEKT

m685.pep      70      80      90      100     110     120
VSAASASAATLTVPTARGDAVVPKNPERVAVYDWAALDTLTELGVNVGATTAPVRVDYLQ
a685          70      80      90      100     110     120
VSAASASAATLTVPTARGDAVVPKNPERVAVYDWAALDTLTELGVNVGATTAPVRVDYLQ

m685.pep     130     140     150     160     170     180
PAFDKAATVGTLEFDPYEALHRYNPQLVITGGPGEAEAYEQLAKNATTIDLTVDNGNIRTS
a685         130     140     150     160     170     180
PAFDKAATVGTLEFDPYEALHRYNPQLVITGGPGEAEAYEQLAKNATTIDLTVDNGNIRTS

m685.pep     190     200     210     220     230     240
GEKQMETLARIFGKEARAAELKAQIDALFAQTREAAKGKRGVLVSVTGNKVSAGTQSR
a685         190     200     210     220     230     240
GEKQMETLARIFGKEARAAELKAQIDALFAQTREAAKGKRGVLVSVTGNKVSAGTQSR

m685.pep     250     260     270     280     290     300
LASWINGDIGLPPVDESIRNEGHGQPVSEFYIKEKNPDWIFIIDRTAAIGQEGPAAVEVL
a685         250     260     270     280     290     300
LASWINGDIGLPPVDESIRNEGHGQPVSEFYIKEKNPDWIFIIDRTAAIGQEGPAAVEVL

m685.pep     310     320     330     340     350
DNALVRGTNAWKRKQIIVMPAANYIVAGGARQLIQAAEQLKAAFKKAEPVAAGKKX
a685         310     320     330     340     350
DNALVRGTNAWKRKQIIVMPAANYIVAGGSRLIQAAEQLKEAFEKAEPVAAGKEX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2273>

```

g686.seq (partial)
1  ..AATTTCCTCT GCCGCGCCGA TGATGTTTTT GACGATATCT GCAGTGCCGT
51  TGAAGGGCTTC ggcgcATTG CCCGATCTGT CCAGCTCGGG GCTGTATCGG
101 TTGGCGCGTT TGAATCCGTC CCTACTCCT TGCCTCAGCA TAGCGCCGGC
151 ATTGTGGAAG CGGTCGGCAA CCCGTTGTCC GGTGCTCGCG TTGTCGGTCA
201 GGTGAGCGCG GATATTTTGG GCAACGCCCT TTATGTCGTA GCTGTATATA
251 TCCCTCGCGC CTTGGGAGC GGGATAGCCG CCGCCCTGTG GCCCGTCATA
301 GCCGTCGGCG GGATGGTGTT CGTATCCGTC CCAATGGATG CGGTAAAGGC
351 TGAATCCGTC AACGGGACTA CCGGCTTCGT CAGAATCGGA ATGTGA

```

This corresponds to the amino acid sequence <SEQ ID 2274; ORF 686 >:

```
g686.pep (partial)
1  ..NFSCRADDVF DDICSAVEGF GGIARSVQLG AVSGGAFESV AYSLRQHSAG
51  IVETVGRPLS GAAVVGQVEA DILGNAFYVV AVYIPRAFGS GIAAALWPVI
101 AVGGMVFVSV PMDAVKAESV NGTTGFVRIG M'
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2275>:

```
m586.seq.
1  ATGATGTTGA AAAAATTCGT ACTCGGCGGT ATTGCCGCAT TGCTTTTGGC
51  GGCCTGCGGC GGTTCGGAAG GCGGCAGCGG AGCGNNNNNN NNNNNNAATT
101 TCTCCTGCAG CGCCGATGAT GTTTTAAACG ATATCTGCAG TGCCGTTGAA
151 GGCTTCGGCG GCATTGCCCG ATCTGTCCAG CTCGGGGCTG TATCGGGTGG
201 CGCGTTTGAA TCCGTCGCCT ACTCCTTCCG TCAGCATACT ACCGGCATTG
251 TGGAAACGGT CGGCAAGCCG TTGTCCGGTG CTGCGGTTGT CGGTCAGGIT
301 GAGGCGGATA TTTTGGGCAA CGCCTTTTAT CTCGTAGCTG TATATATCCC
351 TCGCGCCTTT GGGAGCGGGA TAGCCGCCGC CCTGTGGCCC GTCATAGCCG
401 TCGGCGGGAT GGTGTTTCGTA TCCGTCCCAA TGGATCGCGT AAAGGCTAAA
451 TCCGTCAACG GGACTACCGG CTCATCAGA ATCGGAATGT GA
```

This corresponds to the amino acid sequence <SEQ ID 2276; ORF 686>:

```
m686.pep
1  MMLKKEVLGG IAAVLAAACG GSEGGSGAXX XXNFSCSADD VFNDICSAVE
51  GFGGIARSVQ LGAVSGGAFE SVAYSIRQHT TGIVETVGKP LSGAAVVGQV
101 EADILGNAFY VVAVYIPRAF GSGIAAALWF VIAVGGMVFY SVPMDAVKAK
151 SVNGTTGFIR IGM'
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 686 shows 95.4% identity over a 131 aa overlap with a predicted ORF (ORF 686) from *N. gonorrhoeae*

g686/m686 95.4% identity in 131 aa overlap

g686.pep				10	20	30
				NFSCRADDVFDDICSAVEGFGGIARSVQLG		
m686	LKRFVLGGIAALVLAACGSGEGSGAXX	XXXXNFSCSADDVFNDICSAVEGFGGIARSVQLG				
	10	20	30	40	50	60
g686.pep		40	50	60	70	80
		AVSGGAFESVAYSRLRQHSAGIVETVGKPLSGAAVVGQVEADILGNAFYVVAVYIPRAFGS				
m686		AVSGGAFESVAYSRLRQHTTGIVETVGKPLSGAAVVGQVEADILGNAFYVVAVYIPRAFGS				
		70	80	90	100	110
g686.pep		100	110	120	130	
		GIAAALWPVIAVGGMVFSVPMDAVKAESVNGTTGFVRIGMX				
m686		GIAAALWPVIAVGGMVFSVPMDAVKAESVNGTTGFVRIGMX				
		130	140	150	160	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2277>

```
a686.seq (partial)
1  ..AATTTCCTCCT GCCGCGCCGA TGATGTTTTT GACGATATCT GCAGTGCCGT
51  TGAAAGCTTC GCGGCATTG CCCGATCTGT CCAGCTCGGG GCTGTATCGG
101 GTGGCGCGTT TGAATCCGTC GCCTACTCCT TCGCTCAGCA TACTACCGGT
151 ATGTGTGAAA CGGTCGACAA GCCGTTGTCC GGTGCTGCGG TTGTCGGTCA
201 GGTGAGGCGG GATATTTTGG GCAACGCCTT TTATGTCGTA GCTGTATATA
251 TCCTTCGCGC CTTTGGGAGC GGGATAGCCG CCGCCCTGTG GCCCGTCATA
301 GCCGTCGCGC GGATGGTGTG CGTATCCGTC CCAATGGATG CGGTAAGGC
351 TGAATCCGTC AACGGGACTA CCGGCTTCAT CAGARTCGGA ATGTGA
```

This corresponds to the amino acid sequence <SEQ ID 2278; ORF 686.a>:

```
a686.pep (partial)
```

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```

1  ..NFSCRADDVF DDICSAVESF GGIARSVOLG AVSGGAFESV AYSLRQHTTG
51  IVETVDKPLS GAAVVGQVEA DELGNIFYV AVYIPRAFGS GIAAALWPVI
101 AVGGMVFEVS PMDAVKAESV NGTGFIRIG M*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 686 shows 96.2% identity over a 131 aa overlap with a predicted ORF (ORF 686) from *N meningitidis*:

m686/a686 96.2% identity in 131 aa overlap

```

              10      20      30      40      50      60
m686.pep      LKKFVLGGIAALVLAACGGSEGGSGAXXXNFSCSADDVFNDICSAVEGFGGIARSVQLG
a686              ||| |||||:|||||:|||||:|||||:|||||:|||||
              NFSCRADDVFDDICSAVESFGGIARSVQLG
                      10      20      30

              70      80      90      100     110     120
m686.pep      AVSGGAFESVAYSLRQHTTGIVETVGKPLSGAAVVGQVEADILGNIFYVVAVYIPRAFGS
a686              ||| |||||:|||||:|||||:|||||:|||||:|||||
              AVSGGAFESVAYSLRQHTTGIVETVDKPLSGAAVVGQVEADILGNIFYVVAVYIPRAFGS
                      40      50      60      70      80      90

              130     140     150     160
m686.pep      GIAAALWPVIAVGGMVFEVSPMDAVKAKSVNGTGFIRIGMX
a686              ||| |||||:|||||:|||||:|||||:|||||:|||||
              GIAAALWPVIAVGGMVFEVSPMDAVKAESVNGTGFIRIGMX
                      100     110     120     130

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2279>

```

g687.seq
1  ATGAAATCCA GACACCTCGC CCTCGCCCTC GCGGTGCGG CCCTGTTCGC
51  CCTTGCCCGG TGCGACAGCA AAGTCCAAC CAGCGTCCCC GCCGACAGCG
101 CGCCTGCCGC TTCGGCAGCC GCCGCCCGG CAGGACTGGT CGAAGGGCAA
151 AACTACACCG TCCTTGCCAA CCGGATTCCC CAACAGCAGG CAGGCAAGGT
201 TGAAGTGCTT GAGTTTTCG GCTATTTTG TCCGCACTGC GCCCGCCTcg
251 AACCTGTTTT GAGCAAACAC GCCAAGTCTT TTAAAGACGA TATGTACCTG
301 CGTACCGAAC ACGTGCTCTG GCAGAAAGAA ATGCTGCCGC TGGCAGGCct
351 cGCCGCGGCC GTCGATATGG CTGCCGCCGA AAGCAAAGAT GTGGCGAACA
401 GCCATATTTT CGATGCGATG GTCAACCAAA AAATCAAGCT GCAAGAGCCG
451 GAAGTCCTCA AAAATGGCT GGGCGAACaa ACcgcttTG ACGGCAAAAA
501 AGTCCTTGCC GCCTACGAAT CCCCAGAAAG TCAGGCGCGC GCcggcAAAA
551 TGCAGGAGCT GACCGAAACC TTCCAAATCG ACGGTACGCC CACGGTTA*c
601 GTCGGCGGCA AATATAAAGT CGAATTGCG GACTGGGAGT CCGGTATGAA
651 CACCATCGAC CTTTGGCGG ACAAAGTACG TGAAGAACAA AAAGCCGCGC
701 AGTAG

```

This corresponds to the amino acid sequence <2280 ID 724; ORF 687>:

```

g687.pep
1  MKSRHLALAL GVAALFALAA CDSKVQTSVP ADSAPAASAA AAPAGLVEGQ
51  NYTVLANPIP QQOAGKVEVL EFFGYFCPHC ARLEPVLSKH AKSFKDDMYL
101 RTEHVWQKE MLPLARLAAA VDMAAESKD VANSIFDAM VNQIKLQEP
151 EVLKKWLGEQ TAFDGKKVLA AYESPESQAR AGKMQLTET FQIDGTPTVI
201 VGGRYKVEFA DWESGMNTID LLADKVREEQ KAAQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2281>:

```

m687.seq
1  ATGAAATCCA GACACCTTGC CCTCGGCGTT GCGGCCCTGT TCGCCCTTGC
51  CGCGTGCGAC AGCAAAGTCC AAACCAAGCT CCCCGCCGAC AGCGCGCTG
101 CCGCTTCGCG AGCCGCCGCC CCGGCAGGGC TGGTCGAAGG GCAAACTAT
151 ACCGTCCPTG CCAACCCGAT TCCCAACAG CAGGCAGGCA AAGTCGAAGT
201 CCTTGAGTTT TTCGGCTATT TCTGTCCGCA CTGCGCCAC CTCGAACCTG
251 TTTTAAGCAA ACACGCCAAG TCTTTAAAG ACGATATGTA CCTGCGTACC
301 GAACACGTCG TCTGGCAGAA AGAAATGCTG ACGCTGGCAC GCCTCGCCGC
351 CGCCGTGCGT ATGGCTGCCG CCGACAGCAA AGATGTGGCG AACAGCCATA
401 TTTTCGATGC GATGGTCAAC CAAAAATCA AGCTGCAAAA TCCGGAAGTC
451 CTCAAAAAT GGCTGGGCGA ACAAACCGCC TTTGACGGCA AAAAAGTCCT

```

m687.pgp

1	MKSRLHLAGV	AALFALAA	CD	SKVQTSVP	AD	SAPAASAAAA	PAGLVEGQNY
51	TVLANPIPQ	QAGKVEVLEF		FGYFCPHCAH		LEPVLSKHAK	SFKDDMYLRT
101	EHVVWQKEML	TLARLAAAVD		MAAADSKDVA		NSHIFDAMVN	QKIKLQNPFEV
151	LKKLWGEQTA	FDGKKVLAAY		ESPESQARAD		NKMELTETFQ	IDGTPTVIVG
201	GKYKVEFADW	ESGMNTIDLL		ADKRVREOKA		AO*	

Homology with a predicted ORF from *N. gonorrhoeae*

m687/g687 97.0% identity in 234 aa overlap

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2283>

a687.seq

1	ATGAAATCCA	AACACCTCGC	CCTCGGCGTT	GCCGCCCTGT	TCGCACTTGC
51	CGCGTGGCAC	AGCAAAGTCC	AAACCGAGGT	CCCCGCCGAC	AGCGGCGCTG
101	CGCTTTCGGC	AGCCCGCCGC	CCGGCAGGCT	TGGTCTGAAG	GCAGAACTAT
151	ACTGTCTCTG	CCAAACCGAT	TCCCAACAGC	CAGGCAGGCA	AAGTCGAAGT
201	CCTTGAGTTT	TTCGCTTAAT	TCTGTCCGCA	CTGCGCCAC	CTCGAACCTG
251	TTTTAAGCAA	ACAGCCTAAG	TCTTTTAAAG	ACGATATGTA	CCTCGGTACG
301	GAACACGCTG	TCTGGCAGAA	AGAAATGCTG	ACGCTGCAC	GCGTCGCGCG
351	CGCCGTGCGT	ATGGCTGCCG	CCGACAGCAA	AGATGTGGCG	AACAGCCATA
401	TTTTCGATGC	GATGGTGCAC	CAAAAAATCA	AGCTGCAGA	GCCGGAAGTC
451	CTCAAAAATAT	GGCTGGGCGA	ACAAACGCCC	TTTGACGGCA	AAAAAGTCTCT
501	TGCGCGTTAC	GAATCTCCCG	AAAGCCAGGC	GCGCGCCGAC	AAATGCAAGT
551	AGCTGACCGA	AACCTTCCAA	ATCGACGGTA	CGCCACCGGT	TATCGTCCGC
601	GGCAATATTA	AAGTCGAATT	TGCCCACTTG	GAGTCCGGTA	TGAACACCAT
651	CGACCTTTTG	GCGGACAAGG	TACGGCAAGA	ACAAAAAGCC	GCGCACTAA

a687.pap

```

1  MKSKHLALGV AALFALAA CD SKVQTSVPAD SAPAASAAAA PAGLVEGQNY
51 TVLANPIPQQ QAGKVEVLEF FGYFCPHCAH LEPVLSKHAK SFKDDMYLRT
101 EHVVWQKEML TLARLAAAVD MAASQKSDVA NSHIFDAMVN QKIKLQEPFV
151 LKKWLGEQTA FSGKTVLAA Y ESPESQARAD KMQELTETFO IDGTPTVIVG
201 GYKYVEFADN EDGNTIDLL ADKRVREOKA AH*

```


Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 687 shows 98.7% identity over a 232 aa overlap with a predicted ORF (ORF 687) from *N meningitidis*:

m687/a687 98.7% identity in 232 aa overlap

	10	20	30	40	50	60
m687.pep	MKSRHLALGV	ALFALAACDSKV	QTSVPADSA	PAASAAAAPAGL	VEGONYTVLAN	PIPQQ
a687						
	10	20	30	40	50	60
	70	80	90	100	110	120
m687.pep	QAGKVEVLEFF	GYFCPHCAHLEP	VLSKHAKSFKD	DMYLRTEHV	VVWQKEMTLAR	LAAAVD
a687						
	70	80	90	100	110	120
	130	140	150	160	170	180
m687.pep	MAAADSKDVAN	SHIFDAMVNQK	IKLQNPVLK	KWLGEQTA	FDGKKVLAAYE	PESQARAD
a687						
	130	140	150	160	170	180
	190	200	210	220	230	
m687.pep	KMQELTET	FQIDGTP	TVIVGGKYK	VEFADWESGM	NTIDLLADK	VREEQKAAQX
a687						
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2285>

g688.seq

1	GTGCTACACT	AGACATCCCG	ATTTGCACAG	AAAGGTTCTC	CCGTGAACAA
51	AACCTCATC	CTCGCCCTTT	CCGCCCTGTT	CAGCCTGACC	GCGTGCAGCG
101	TCGAACGCGT	CTCGCTGTTT	CCCTCCTACA	AACTCAAAAT	CATCCAAGGC
151	AACGAACTCG	AACCGCGCGC	CGTTGCCGCC	CTGCCGCCCG	GCATGACCAA
201	AGACCAAGTC	CTGCTCCTGC	TCGGCAGCCC	CATACTGCGC	GACGCTTTCC
251	ATACCGACCG	CTGGGACTAT	ACCTTCAACA	CCTCCCGCAA	CGGCATCATC
301	AAAGAACGCA	GCAACCTGAC	CGTCTATTTT	GAAAACGGCG	TACTCGTCCG
351	CACCGAAGGC	GACGCCCTCC	AAAATGCCGC	CGAAGCCCTC	CGCGCGAAAC
401	AAAACGCAGA	CAAACAATAA			

This corresponds to the amino acid sequence <SEQ ID 2286; ORF 688 >:

g688.pep

1	VLH*TSRFAQ	KGSPVNKTLI	LALSALFSLT	ACSVVERVSLF	PSYKLKIIQG
51	NELEPRVAA	LRPGMTKDQV	LLLLGSPILR	DAFHTDRWDY	TFNTSRNGII
101	KERSNLTVYF	ENGVLVRTEG	DALQNAEAL	RAKQNAQKQ*	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2287>:

m688.seq

1	GTGTTACACT	ACCCATCCCG	ATTTGCACAG	AAAGGCATT	CCGTGAACAA
51	AACCTCATC	CTCGCCCTTT	CCGCCCTCCT	CGGCCTTGCC	GCGTGCAGTG
101	CCGAACGCGT	TTCAGTGTC	CCCTCGTACA	AACTCAAAAT	CATACAGGGC
151	AACGAACTCG	AACCGCGCGC	CGTTGCCGCC	CTCCGCCCGC	GCATGACCAA
201	AGACCAAGTC	CTGCTCCTGC	TCGGCAGCCC	CATACTGCGC	GACGCATTCC
251	ATACCGACCG	CTGGGACTAT	ACCTTCAACA	CCTCCCGCAA	CGGCATCATC
301	AAAGAACGCA	GCAATCTGAC	CGTCTATTTT	GAAAACGGCG	TACTCGTCCG
351	CACCGAAGGC	GACGCTCTGC	AAACGCTGC	CGAAGCCCTC	AAAGACGGCC
401	AAACACAGA	CAAACCATAA			

This corresponds to the amino acid sequence <SEQ ID 2288; ORF 688>:

m688.pep

1	VLHPSRFAQ	KGISVNKTLI	LALSALLGLA	ACSAERVSLF	PSYKLKIIQG
51	NELEPRVAA	LRPGMTKDQV	LLLLGSPILR	DAFHTDRWDY	TFNTSRNGII
101	KERSNLTVYF	ENGVLVRTEG	DVLQNAEAL	KDRQNTDKP*	

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Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 688 shows 90.6% identity over a 138 aa overlap with a predicted ORF (ORF 688) from *N. gonorrhoeae*:

m688/g688 90.6% identity in 138 aa overlap

```

      10      20      30      40      50      60
m688.pep  VLHYPSRFAQKGISVNKTLILALSALLGLAACSVERVSLFSPYKLIKIQGNELEPRVAA
          ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g688       VLHXTSRFAQKGSVPNKTLLALSALFSLTACSVERVSLFSPYKLIKIQGNELEPRVAA
          10      20      30      40      50      60

      70      80      90     100     110     120
m688.pep  LRPGMTKDQVLLLLGSPILRDAFHTDRWDYTFNTSRNGI IKERSNLT VYFENGVLVRTEG
          ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g688       LRPGMTKDQVLLLLGSPILRDAFHTDRWDYTFNTSRNGI IKERSNLT VYFENGVLVRTEG
          70      80      90     100     110     120

      130     140
m688.pep  DVLQNAAEALKDRQNTDKPX
          ||||| ||||| |||||
g688       DALQNAAEALRAKQNAADKQX
          130     140

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2289>

```

a688.seq
1  GTGTTACACT ACCCATCCCG ATTTGCACAG AAAGGCATT CCGTGAACAA
51 AACCCTCATC CTCGCCCTTT CGGCCCTCCT CGGCCTTGCC GCGTGCAGCG
101 TCGAACCGCT TTTACTGTTC CCCTCGTACA AACTCAAAAT CATACAGGGC
151 AACGAACTCG AACCTCGCGC CGTCGCCTCC CTCCGCCCCG GTATGACCAA
201 AGACCAAGTC CTGCTCCTGC TCGGCAGCCC CATACTGCGC GACGCATTCC
251 ATACCGACCG CTGGGACTAT ACCTTCAACA CCTCCCGCAA CGGCATCATC
301 AAAGACCGAA GCAATCTGAC CGTCTATTTT GAAAACGGCG TGCTCGTCCG
351 CACCGAAGGC AACGCCCTGC AAAATGCCGC CGAAGCCCTC CGCGTAAAC
401 AAAACGCAGA CAAACAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2290; ORF 688.a>:

```

a688.pep
1  VLHYPSRFAQ KGISVNKTLI LALSALLGLA ACSVERVSLF PSYKLIKIQG
51  NELEPRAVAS LRPGMTKDQV LLLLGSPILR DAFHTDRWDY TFNTSRNGII
101 KDRSNLT VYF ENGVLVRTEG NALQNAAEAL RVKQNAADKQ*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 688 shows 93.5% identity over a 138 aa overlap with a predicted ORF (ORF 688) from *N. meningitidis*

m688/a688 93.5% identity in 138 aa overlap

```

      10      20      30      40      50      60
m688.pep  VLHYPSRFAQKGISVNKTLILALSALLGLAACSVERVSLFSPYKLIKIQGNELEPRVAA
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a688       VLHYPSRFAQKGISVNKTLILALSALLGLAACSVERVSLFSPYKLIKIQGNELEPRVAA
          10      20      30      40      50      60

      70      80      90     100     110     120
m688.pep  LRPGMTKDQVLLLLGSPILRDAFHTDRWDYTFNTSRNGI IKERSNLT VYFENGVLVRTEG
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a688       LRPGMTKDQVLLLLGSPILRDAFHTDRWDYTFNTSRNGI IKERSNLT VYFENGVLVRTEG
          70      80      90     100     110     120

      130     140
m688.pep  DVLQNAAEALKDRQNTDKPX
          ||||| ||||| |||||
a688       NALQNAAEALRVKQNAADKQX
          130     140

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2291>

```
g689.seq (partial)
1  ..TCTCCGCCCC TTCCTCCGAT GAGCGGAAAA CTGATGGCGG TTTTGATGGC
51  GGTACTGGTC GCGCTGATGC CGTTTTCAT CGATGCCTAC CTGCCCAGCA
101 TTCCCGAAAT GCGCAGCCG CTGAACGCGG ATATCCACCG TATCGAATAG
151 AGTCTGAGTT TGTTTATGTT CGSCACGGCG TTCGGGCAAG TGGCCGCGCG
201 CGCGGTGTCC GACATCAAAG GCGCAAACC CGTCGCCCTG ACCGGTTTGA
251 TTGTATATTG CCTTGCCGTT GCCGCCATCG TATTTGCTTC GAGTACCGAA
301 CAGCTCCTTA ACCTGCGTGC GGTACAGGCG TTCGGCGCAG GCATGGCTGT
351 AGTCATCGTC ggtgcatggt tgcgcgatTA TTATTCGGGA CGCAAAGCCG
401 cgcAGATGTT TGCCCTTATC GGCAATCATT TGATGGTTGT GCCGCTGGCC
451 GCACCCATGC TCGGCGCATT GTTGCAGGGA TTGGGCGGAT GCGGGGCGAT
501 TTTCGTTTTG ttggcGgcgT ATTCGCCGGT GCTGCCCGGT TTGGTACAGT
551 ATTTCTCTGC CAATCCCGCC GTCGGCGGCA AAATCGGCAG GGATGTGTTC
601 GGGCTGGTGG CGGGGCGGTT CAAGCGCGTA TTGAAAACCC GTGCCGCGAT
651 GGGTtatCTG TTTTTCAGG CATTACGCTT CGGTTTCGATG TTCGCCTTTC
701 TGACCGAATC TTCCTTCGTG TACCGGCAGC TCTACCACGT TACGCCGCAC
751 CGGTACGCAT GGGTGTTCG ACTCAACATC ATCACGATGA TGTTTTTCAG
801 CGCGCTTACC GCGTGGCGGC TTAACACCGG CGCGCATCCG CAAAGCATCC
851 TGCTCGGGGG GATTGTCGTC CAATTGCGG CCAACCCGTC CCAACTCGCC
901 GCCGTGCTGT TTTTCGCGTT GCCCCCGTTT TGGGTGCCGG TCGCGTGCCT
951 GATGTTTTTC GTCGGTACGC AGGGCCTGGT CGGTGCGGAC ACGCAGGCAT
1001 GCTTTATGTC TTATTTCAAA GAAGAGGGCG GCAGCGCGAA CGCCGTGTTCG
1051 GGTGTATTCC GGTCTTAAT CGGCGCGGCG GTGGTCATGG CGGCAACCGT
1101 GATGGCGGCA ACCATGACCG CGTCCGCTC TTGCGGCATT GCGCTTTTGT
1151 GGCTCTGCTC GCACAAGGCG TGGAGGAAA ACGAAAAAA GCGAATACTT
```

This corresponds to the amino acid sequence <SEQ ID 2292; ORF 689>:

```
g689.pep (partial)
1  ..SPPLPPMSGK LMAVLMVAVL ALMPFSIDAY LPAIPEMAQP LNADIHRIE*
51  SLSLFMFSTA FGQVAGGAVS DIKGRKPVAL TGLIVYCLAV AAIVFASSTE
101 QLLNLRAVQA FGAGMAVVIV GAMVRDYYSR RKAQMFLI GIIIMVPLA
151 APMVGALLQG LGGWRAIFVF LAAYSPLVLP LVQYFLPNFA VGGKIGRDVF
201 GLVAGRFRKRV LKTRAAMGYL FFQAFSFGSM FAFLETSEFV YRQLYHVTPH
251 RYAWVFALNI ITMFFSRVT ANRLKTGAHP QSILLRGIVV QFAANPSQLA
301 AVLFFGLPEF WLPVACVMFS VGTQGLVGAD TOACFMSYFK EEGGSANAVS
351 GVFRSLIGAG VVMAATVMAA TMTASASCGI ALLWLCSHKA WKENEKKRIL
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2293>:

```
m689.seq
1  TTGTTAATCC ACTATATCGT TCCGGTTCGT CCGGTTTTGC CGGGGCTTTT
51 GTTGCCGCTT GTTGTGCGG GTGTGTAAAT ATTTTCCGTT TCCGCGTATT
101 GTGTTTTCCG CCGCCGGGCG GTTGTGTTGC GAATCGGACG AGAATTTATG
151 CCTTCGTCCT ATTATCCTGA AATGAGCGAA AAATGATGG CGGTTTTGAT
201 GCGGATGCTG GTTACGCTGA TCGCGTTTC CATCGATGCC TACCTGCCCG
251 CGATTCGCGA AATGGCGCAA TCGCTGAACG CGGATGTTCA CCGCATCGAA
301 CAGAGTTTGA GTTGTGTTAT GTTCGGCAGC GCGTTTCGGAC AGGTGGTCGG
351 CCGTTTCGGT TCCGACATCA AAGGGCGCAA ACCCGTCGCC CTGACCGGTT
401 TGATTGTATA TTGCCCTTGC GTTGCCGCCA TCGTATTGTT TTCGAGTGCC
451 GAACAGCTCC TCAACCTGCG CGTCGTGCAG GCATTTCGGT CGGGCATGAC
501 TGTGGTCATC GTCGGCGCAA TGGTGCAGCA TTATTATTCC GGACGCAAG
551 CCGCCAGATG GTTGTCCCTT ATCGGCATCA TTTTGATGGT TGTGCCGCTG
601 GTCGCACCCA TGGTCCGCGC ATTGTTGCAG GGCTTGGGTG GCTGGCAGGC
651 GATTTTTGTT TTTCTGGCGG CGTATTGCTT GGTGCTGCTC GGTTTGGTAC
701 AGTATTTCCT GCCAAGCCG GCCGTCGGCG GCAAAATCGG ACGGGACGTG
751 TTCGGGCTGG TGGCGGGGCG GTTCAAGCGC GTATTGAAAA CCCGTGCTGC
801 GATGGGTATC CTGTTTTTTC AGGCATTGAG CTTGCGTTTC ATGTTCCGCT
851 TTCTGACCGA ATCTTCTTTC GTGTACGAGC AGCTCTACCG TGTACGCTT
901 CATCAATACG CTTGGGCGTT TGCACCTAAC ATCATCAGCA TGATGTTTTT
951 CAACCGCGTT ACCGCGTGGC GGCTCAAAAC CGGCGTGCA CCGCAAAGCA
1001 TCCTGCTGTG GGGGATTGTC GTCCAGTTTG CCGCAACCT GTCCAACTC
1051 GCGCCCGTGC TGTTTTCGG GTTGCCCGG TTTTGGCTGC TGGTCGCGTG
1101 CGTGATGTTT TCCGTCGGTA CGCAGGCTT GGTGCGTGCA AACACGAGG
1151 CGTGTGTTAT GTCCATTTTC AAAGAAGAGG GCGGCAGCGC AAACGCCGTA
1201 TTGGGTGTAT TCCAATCTTT AATCGGCGCG GGGGTGGGTA TGGCGGCGAC
1251 CTTCTGTCAC GACGGTTCGG CAACCGTGAT GCGCGCAACG ATGACCGCGT
1301 CCACCTCTTG CCGCATTGCG CTTCTGTGCG TCTGCTCGCA TCGTCCGTTG
```

1351 AAAGAAAACG GGCAAAGCGA ATACCTTTAA

This corresponds to the amino acid sequence <SEQ ID 2294; ORF 689>:

m689.pep
 1 LLIHIVPVR PVLPGLLLP VCAGVLKFSV SAYCVERRA VCLRIGREFM
 51 PSAHYFEMSE KLMAVLMAML VTLMPFSDA YLPAIPEMAQ SLNADVHRIE
 101 QSLSLFMFGT AFGQVVGGSV SDIKGRKPVA LTGLIVYCLA VAAIVFVSSA
 151 EQLLNLRVQV AFGAGMTVVI VGAMVRDYY GRKAAQMFAL IGIILMVVPL
 201 VAPMVGALLQ GLGGWQAIIV FLAAYSLVLL GLVQYFLPKP AVGGKIGRDV
 251 FGLVAGRFKR VLKTRAAMGY LFFQAFSFGS MFAFLTESSF VYQQLYRVTP
 301 HQYAWAFALN IITMFFNRV TAWRLKTGVH PQSILLWGIV VQFAANLSQL
 351 AAVLFFGLPP FWLLVACVMF SVGTQGLVGA NTQACFMSYF KEEGGSANAV
 401 LGVFQSLIGA GVGMAATFLH DGSATVMAAT MTASTSCGIA LLWLCSHRAW
 451 KENGQSEYL*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 689 shows 88.0% identity over a 408 aa overlap with a predicted ORF (ORF 689) from *N. gonorrhoeae*:

m689/a689 88.0% identity in 408 aa overlap

m689.pep	30	40	50	60	70	80
	CAGVLKFSVSAYCVFRRRAVCLRIGREFMPSAHYFEMSEKLMAVLMAMLVTLMPFSDA					
g689				SPPLPMSGKLMAVLMAVLVALMPFSIDAY		
				10	20	30
m689.pep	90	100	110	120	130	140
	LPAPPEMAQSLNADVHRIEQSLSLFMFGTAFGQVVGGSVSDIKGRKPVALTGLIVYCLAV					
g689	LPAPPEMAQSLNADHRIEXSLSLFMFGTAFGQVAGGAVSDIKGRKPVALTGLIVYCLAV					
	40	50	60	70	80	90
m689.pep	150	160	170	180	190	200
	AAIVFVSSAEQLLNLRVQAFGAGMTVVIVGAMVRDYYSGRKAQMFALIGIILMVVPLV					
g689	AAIVFASSTEQLLNLRVQAFGAGMAVVIVGAMVRDYYSGRKAQMFALIGIILMVVPLA					
	100	110	120	130	140	150
m689.pep	210	220	230	240	250	260
	APMVGALLQGLGGWQAIIVFLAAYSLVLLGLVQYFLPKPAVGGKIGRDVFGVLVAGRFKRV					
g689	APMVGALLQGLGGWRAIVFLAAYSPVLPGLVQYFLPNPAVGGKIGRDVFGVLVAGRFKRV					
	160	170	180	190	200	210
m689.pep	270	280	290	300	310	320
	LKTRAAMGYLFFQAFSFGSMFAFLTESSFVYQQLYRVTPHQYAWAFALNIITMFFNVRT					
g689	LKTRAAMGYLFFQAFSFGSMFAFLTESSFVYRQLYHVTPHRYAWVFALNIITMFFSRVT					
	220	230	240	250	260	270
m689.pep	330	340	350	360	370	380
	AWRLKTGVHPQSILLGIVVQFAANLSQLAAVLFFGLPPFWLLVACVMFSGVTQGLVGAN					
g689	AWRLKTGAHPQSILLRGIVVQFAANPSQLAAVLFFGLPPFWLPVACVMFSGVTQGLVGAD					
	280	290	300	310	320	330
m689.pep	390	400	410	420	430	440
	TQACFMSYFKEEGGSANAVLGVFQSLIGAGVGMAATFLHDGSATVMAATMTASTSCGIAL					
g689	TQACFMSYFKEEGGSANAVSGVFRSLIGAGVMAAT-----VMAATMTASASCGIAL					
	340	350	360		370	380
m689.pep	450	460				
	LWLCSHRAWKENGQSEYLY					
g689	LWLCSHRAWKENKKRIL					
	390	400				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2295>

```
a689.seq
1   TTGTTAATCC ACTATATCGT TCCGGTTCGT CCGGTTTTCG CGGGGCTTTT
51  GTTGCCGCCT GTTTGTGCCG GTGTGTTAAA ATTTTCCGTT TCCGCGTATT
101 GTGTTTTCGG CCGCCGGGCG GTTTGTTTGC GAATCGGACG AGAATTATG
151 CCTTCTGCCG ATTATCCTGA AATGAGCGAA AAATCGATGG CGGTTTGTAT
201 GCGGATGCTG GTTACGCTGA TGCCGTTTTC CATCGATGCC TACCTGCCCG
251 CGATTCCCGA AATGGCGCAG TCGCTGAACG CGGATGTCCA CCGCATCGAA
301 CAGAGCCTGA GTTTGTTTAT GTTCGGCAGC GCGTTCGGAC AGGTGGTCGG
351 CGGTTCCGGT TCCGACATCA AAGGGCGCAA ACCCGTCGGC CTGACCGGAC
401 TGGCCGTCTA CTGCCITGCC GTTGCCGCCA TCGTATTTCG TTCGAGTGCC
451 GAACAGCTCC TCAACCTGCG CGTCGTGCG GCAATCGGTG CCGGCATGAC
501 TGTGGTCATC GTCGGCGCAA TGGTGGCGCA TTATTATTCC GGACGCAAG
551 CCGCCCGAGT GTTTGCCCTT ATCGGCATCA TTTGATGGT TGTGCCGCTG
601 GTCGCACCCA TGGTCGGCGC ATTGTGCGAG GGCTTGGGTG GCTGGCAGGC
651 GATTTTGTGT TTTCTGGCGG CGTATTCGCT GGTGCTGCTC GGTTTGGTAC
701 AGTATTTCCT GCCCAAGCCC GCCGTCGGCG GCAAAATCGG CAGGGATGTG
751 TCCGGGCTGG TGGCTGGGCG GTTCAAACGC GTATTGAAA CCCGTGCCGC
801 GATGGGTTAT CTGTTTTTTC AGGCATTCAG CTTGCGTTCG ATGTTCCGCT
851 TTCTGACCCA ATCTTCCTTC GTGTACCAGC AGCTCTACCA CGTTACGCG
901 CACCAGTACG CTTGGGCGTT TGCATCAAC ATCATCAGCA TGATGTTTTT
951 CAACCGTATT ACCGCGTGGC GGCTCAAAAC CGGCGTGCA CCGCAAAGCA
1001 TCCTGCTGTG GGGGATTGTC GTCCAGTTTG CCGCCAACCT GTCCCAACTC
1051 GCCGCCGTGC TGTTTTTTCG GTTGCCCCCG TTTTGGTGC TGGTCGCGTG
1101 CGTGATGTTT TCCGTCGGTA CGCAGGGCTT GGTGCGTGCA AACACGAGG
1151 CGTGTTTTAT GTCCTATTTC AAAGAAGAGG CGGCGAGCGC AAACGCCGTA
1201 TTGGGTGTAT TCCAATCTTT AATCGGCGCG GGGGTGGGTA TGGCGGCGAC
1251 CTTCTGCAAC GACGGTTCGG CAACCGTGAT GGGCGCAACC ATGACCGCGT
1301 CTACCTCTTC CGGCATTGCG CTTTGTGGC TCTGCTCGCA TCGTGCCTGG
1351 AAAGAAAACG GGCAAAGCGA ATACCTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 2296; ORF 689.a>:

```
a689.pep
1   LLIHIVPVR FVLPGLLLPP VCAGVLKFSV SAYCVFRRRA VCLRIGREFM
51  PSAHYPEMSE KLMAVLMAML VTILMPFSIDA YLPAIPEMAQ SLNADVHRTE
101 QSLSLFMFGT AFGQVVGGSV SDIKGRKPVA LTGLAVYCLA VAAIVFASSA
151 EQLNLNRVVQ AFGAGMTVVI VGAMVRDYYS GRKAAQMFAL IGIILMVVPL
201 VAPMVGALLQ GLGGWQAFV FLAAYSLVLL GLVQYFLPKP AVGGKIGRDV
251 FGLVAGRFRK VLKTRAAMGY LFFQAFSFGS MFAFLTESSF VYQQLYHVTP
301 HQYAWAFALN IITMFFFNRI TAWRLKTGVH PQSILLWGIV VQFAANLSQL
351 AAVLFFGLFP FWLLVACVMF SVGTQGLVGA NTQACFMSYF KEEGGSANAV
401 LGVFQSLIGA GVGMAATFLH DGSATVMAAT MTAATSCGIA LLWLCSHRAW
451 KENGQSEYL*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 689 shows 99.1% identity over a 459 aa overlap with a predicted ORF (ORF 689) from *N. meningitidis*:

```
m689/a689    99.1% identity in 459 aa overlap

          10      20      30      40      50      60
m689.pep    LLIHIVPVRPVLPGLLPPVCAGVLKFSVSAYCVFRRRAVCLRIGREFMPSAHYPEMSE
          |||||||
a689         LLIHIVPVRPVLPGLLPPVCAGVLKFSVSAYCVFRRRAVCLRIGREFMPSAHYPEMSE
          10      20      30      40      50      60

          70      80      90     100     110     120
m689.pep    KLMAVLMAMLVTLMPFSIDAYLPAIPEMAQSLNADVHRIEQSLSLFMFGTAFGQVVGGSV
          |||||||
a689         KLMAVLMAMLVTLMPFSIDAYLPAIPEMAQSLNADVHRIEQSLSLFMFGTAFGQVVGGSV
          70      80      90     100     110     120

          130     140     150     160     170     180
m689.pep    SDIKGRKPVALTGLIVYCLAVAAIVFVSSAEQLNLNRVVQAFGAGMTVVIIVGAMVRDYYS
          |||||||
a689         SDIKGRKPVALTGLAVYCLAVAAIVFASSAEQLNLNRVVQAFGAGMTVVIIVGAMVRDYYS
          130     140     150     160     170     180

          190     200     210     220     230     240
m689.pep    GRKAAQMFALIGIILMVVPLVAPMVGALLQGLGGWQAFVFLAAYSLVLLGLVQYFLPKP
```

1109

```

|||||
a689 GRKAAQMFALIGIILMVPLVAPMVGALLQGLGGWQAI FVFLAAYSLVLLGLVQYFT.PKP
      190      200      210      220      230      240

      250      260      270      280      290      300
m689.pep AVGGKIGRDVFGVLVAGRFKRVLKTRAAMGYLFFQAFSFGSMFAFLTESSEFVYQQLYRVTP
|||||
a689 AVGGKIGRDVFGVLVAGRFKRVLKTRAAMGYLFFQAFSFGSMFAFLTESSEFVYQQLYHVTP
      250      260      270      280      290      300

      310      320      330      340      350      360
m689.pep HQYAWAFALNIIITMMFFNRVTAWRLKTGVHPQSILLWGI VVQFAANLSQLAAVLF FGLPP
|||||
a689 HQYAWAFALNIIITMMFFNRITAWRLKTGVHPQSILLWGI VVQFAANLSQLAAVLF FGLPP
      310      320      330      340      350      360

      370      380      390      400      410      420
m689.pep FWLLVACVMFSVGTQGLVGANTQACFMSYFKEEGGSANAVLGVFQSLIGAGVGM AATFLH
|||||
a689 FWLLVACVMFSVGTQGLVGANTQACFMSYFKEEGGSANAVLGVFQSLIGAGVGM AATFLH
      370      380      390      400      410      420

      430      440      450      460
m689.pep DGSATVMAATMTASTSCGIALLLWLC SHRAWKENGQSEYIX
|||||
a689 DGSATVMAATMTASTSCGIALLLWLC SHRAWKENGQSEYIX
      430      440      450      460

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2297>

```

g690.seq (partial)
1  ATGAAAAACA AAACGTCATC ACTTCCCTTA TGGCTTGCCG CAATCATGCT
51  GGCCGCGCGT TCCCCGAGCA AAGAAGATAA AACGAAAGAA AACGGCGCAT
101 CCGCGCGCTC GTCTTCCGCG TCATCGGCTT CTTCCTCAAC CGATTGCAA
151 CCGGCGCGCAT CCGCCCTGA TAACGTCAAG CAGGCAGAAA GCGCGCCACT
201 GTGAAATTGC ACCGGCCTGC ACCCCGCGCG CGGCATTGGC GATCTCATAC
251 AGCAAAATCGC CGAACACATC GACTCGGACT GTCTGTTTGC CCTTTCCCAT
301 AACGAACTGG AAACCCGTTT CGGCTTACCC GCGCGCGGCT ATGACAACAT
351 ACAGCGGctG CTgtttCCCG ACATCCGCCC TGAAGATCCC GACTACCATC
401 AGAAATCAT GCTGGCAATC GAAGACTTGC GTTACGGAAC GCGCACCATC
451 AGccgGCAGG CACAAGATGC CATAATGGAA CAGGAACGCC gcctccGaGa
501 agCGACGCTG ATGCTGACAC AGGGCAGTCA AAAAACC CGG GgACAAGCGG
551 AGGAACCGAA ACGCGCACGT TATTTGAAAG TTTGCGCAAC ATCtgCctaT
601 TTgaaccggc ACAaacaacGG ACTTggcgGC AATTTCaAT ACATCGGCCA
651 ATTGCCCGGC TATCTGAAAA TGCACGGAGA AATGCTTGAA AACCAATCAC
701 TCTTCCGGCT GTCCAACCGT GAACGCAATC CCGACAAACC GTTTTTAGAC
751 ATCCATTTTG ACGAAAATGG CAAAATCAGC CGTATTGTGC TTTACGAAAA
801 AAATATCTAT...

```

This corresponds to the amino acid sequence <SEQ ID 2298; ORF 690>:

```

g690.pep (partial)
1  MNKNTSSLPL WLAAIMLAAR SPSKEDKKE NGASAASSSA SSASSQTDLQ
51  PAASAPDNVK QAESAPL*NC TGLHPAAGIG DLIQQAIEHI DSDCLFALSH
101 NELETRFGLP GGGYDNIQRL LFPDIRPEDP DYHQIMLAI EDLRYGTRTI
151 SRQAODAIME OERRLREATL MLTQGSQKTR GQGEPEPKRAR YFEVSATSAY
201 LNRHNNGLGG NFOYIGQLPG YLKMHEMLE NQSLFRLSNR ERNPDKPFLL
251 IHFDENGKIT RIVVYEKNIIY ...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2299>:

```

m690.seq..
1  ATGAAAAACA AAACCTCATC ACTTCTCTTA TGGCTTACCG CAATCATGCT
51  GACCGCGTGT TCTCCGAGCA AAGACGATAA AACCAAGAA GTCCGGTGCAI
101 CGCTGCTTC GTCTCCGCG TCATCAGCTC CTTCCTCAAC CGATTGCAA
151 CCGACCGCAT CCGCCCTGA TAACGTCAAG CAGGCAGAAA GCGCGCGGCC
201 GTCAAAATGC ACCAGCCTGC ACCCCGCGCAC CGGCATTGAC GATCTCATGC
251 AGCAAAATCGC CGAACACATT GACTCGGACT GTCTGTTTGC CCTTTCCCAT
301 CACGAACTGG AAACCCGTTT CGGCTTACCC GACGGTGGCT ATGACAACAT
351 ACAGCGGctG CTGTTTCCCG ACATCCGCCC TGAAGATCCC GACTACCATC
401 AGAAATCAT ACTGGCAATT GAAGACTTGC GTTACGGAAA GCGCAGCATC
451 AGCCGGCAGG CACAAAATGC CTTGATGGAA CAGGAACGCC GCCTCCGAGA
501 AGCGACGCTG TTGCTGATAC AGGGCAGTCA AGAAACCCCG GGACAAGCGG

```

1110

```

551 AGGAGCCGAA ACGCAGCGGT TATTTTSAAG TTTCGGCAAC CCCTGCCTAT
601 TCGAGCCGGC ACAACAACGG ACTTGGCGGC AATTTCCAAT ACATCAGCCA
651 ATTGCCCGGC TATCTGAAAA TACACGGAGA AATGCTTGAA AACCAATCAC
701 TCTTCCGGCT GTCCAACCGT GAACGCAATC CCGACAAACC GTTTTtagac
751 ATCCATTTTG ACGAAAATGG CAAAATCACG CGTATTGTCG TTTACGAAAA
801 AAACATCTAC TTCATCCAA ACACGGGGCG AATATAA

```

This corresponds to the amino acid sequence <SEQ ID 2300; ORF 690>:

```

m690.pep
1  MKNKTSLLL WLTAIMLTAC SPSKDDKTKE VGASAASSSA SSAPSQTDLQ
51  PTASAPDNVK QAESAPPSNC TSLHPATGID DLMQQAIEHI DSDCLFALSH
101 HELETRFGLP DGGYDNIQRL LFPDIRPEDP DYHQIILAI EDLRYGKRTI
151 SRQAQNALME OERRLREATL LLIQGSQETR GQGEPEKPTR YFEVSATPAY
201 SSRHNNLGGG NFQYISQLPG YLKIHGEMLE NQSLFRLSNR ERNPKPFLD
251 IHFDENGKIT RIVVYEKNIY FNPNTGRI*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 690 shows 89.3% identity over a 408 aa overlap with a predicted ORF (ORF 690) from *N. gonorrhoeae*:

```

m690/g690 89.3% identity in 408 aa overlap

      10      20      30      40      50      60
m690.pep MKNKTSLLLWLTAIMLTACSPSKDDKTKEVGASAASSSASSAPSQTDLQPTASAPDNVK
||||||| |||:||||| ||||:||||| |||||:||||| |||||:||||| |||||:|||||
g690      MKNKTSLLPLWLAAIMLAARSPSKEDKTENGASAASSSASSAPSQTDLQPAASAPDNVK
      10      20      30      40      50      60

      70      80      90      100     110     120
m690.pep QAESAPPSNCTSLHPATGIDDLMQQAIEHIDSDCLFALSHHELETRFGLPDGGYDNIQRL
||||| |||:||||| |||:||||| |||||:||||| |||||:||||| |||||:|||||
g690      QAESAPLXNCTGLHPAAGIGDLIQQAIEHIDSDCLFALSHNELETRFGLPGGGYDNIQRL
      70      80      90      100     110     120

      130     140     150     160     170     180
m690.pep LFPDIRPEDPDYHQIILAIEDLRYGKRTISRQAQNALMEQERRLREATLLLIQGSQETR
||||||| |||||:||||| |||||:||||| |||||:||||| |||||:||||| |||||:|||||
g690      LFPDIRPEDPDYHQIMLAIEDLRYGTRTISRQAQDAIMEQERRLREATLMLTQGSQKTR
      130     140     150     160     170     180

      190     200     210     220     230     240
m690.pep GQGEPEKPTRYFEVSATPAYSSRHNNLGGNFQYISQLPGYLKIHGEMLENQSLFRLSNR
||||||| |||:||||| |||:||||| |||||:||||| |||||:||||| |||||:|||||
g690      GQGEPEKPRARYFEVSATSAYLNRHNNLGGNFQYIGQLPGYLMHGEMLENQSLFRLSNR
      190     200     210     220     230     240

      250     260     270     279
m690.pep ERNPKPFLDIHFDENGKITRIVVYEKNIYFNPNTGRIX
||||||| |||||:||||| |||||:||||| |||||:||||| |||||:|||||
g690      ERNPKPFLDIHFDENGKITRIVVYEKNIY
      250     260     270

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2301>

```

a690.aag
1  ATGAAAAACA AAACCTCATC ACTTCTCTTA TGGCTTGCCG CAATGATGCT
51  GACCGCGTGT TCCCGAGCA AAGAAGATAA AACGAAAGAA AACGGCGCAT
101 CCGCCGCTCT GTCCACGGCA TCCGCGCTT CGTCTTCCGC GCCCAAAACC
151 GATTTGCAAC CGGCCGCATC CGCCCTGAT AACGTCAGC AGGCAGAAAG
201 CGTGCCGCGC TCAAATTGCA CCGACCTGCA CCCC GCCACC GGCATTGACG
251 ATCTCATGCA GCAAATCGCC GAACACATTG ACTCGGACTG TCTGTTTGCC
301 CTTTCCCATC ACGAACTGGA AACCCGTTTC GGCTTACCCG GCGGCGGCTA
351 TGACAACATA CAGCGGCTGC TGTTCCTCGA CATCCGCCCT GAAGATCCCG
401 ACTACCATCA GAAAATCATA CTGGCAATG AAGACTTGC GTTACGGAAAG
451 CGCACGATCA GCGGCGAGGC ACAAGATGCC TTGATGGAAC AGGAACGCCG
501 CCTCCGAGAA GCGACGCTGT TGCTGATACA GGGCAGTCAA GAAACCCGCG
551 GACAAAGCGA GGAGCCGAAA CGCAGCGCTT ATTTGAAAG TTCCGCAACC
601 CTGCGCTATT CGAGCCGGCA CAACAACGGA CTGGCGGCA ATTTCCAATA
651 CATCGGCCAA TTGCCCGGCT ATCTGAAAT ACACGGAGAA ATGCTTGAAA

```

1111

701 ACCAATCACT CTTCCGGCTG TCCAACCGTG AACGCAATCC CGACAAACCG
 751 TTTTGTAGACA TCCATTTTGA CGAAATGGC AAAATCACGC GTATTGTCST
 801 TTACGAAAA AACATCTACT TCAATCCAAA CTTGGGCGA AGATAA

This corresponds to the amino acid sequence <SEQ ID 2302; ORF 690.a>:

a690.pep
 1 MKNKTSLLLL WLAAMMLTAC SPSKEDKKE NGASAASSTA SAASSAPQT
 51 DLQPAASAPD NVKQAESVFP SNCTDLHPAT GIDDLMOQIA EHIDSDCLFA
 101 LSHHELETRF GLPGGGYDNI QRLLFPDIRP EDPDYHQKII LAIEDLRYGK
 151 RTISRQAQDA LMEQERRLRE ATLLLIQGSQ ETRGQGEPEK RTRYFEVSAT
 201 PAYSSRHNNG LGGNFQYIGQ LPGYLKHGE MLENQSLFRL SNRERNPDKP
 251 FLDIHFDENG KITRIVVYEK NIYFNENLGR R*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 690 shows 93.9% identity over a 280 aa overlap with a predicted ORF (ORF 690) from *N. meningitidis*:

m690/a690 93.9% identity in 280 aa overlap

m690.pep	10	20	30	40	50
a690	10	20	30	40	50
m690.pep	60	70	80	90	100
a690	60	70	80	90	100
m690.pep	120	130	140	150	160
a690	120	130	140	150	160
m690.pep	180	190	200	210	220
a690	180	190	200	210	220
m690.pep	240	250	260	270	279
a690	240	250	260	270	279

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2303>

g691.seq
 1 GTGCCGCTGC CTGCTCCCTG CCGTTTTGCC AACCTGCCG CCTCTTTTT
 51 AAGTATGGCT TTGCTTTCTT GCCAGCTTTC CCACGCCGCC ACGGCTTATA
 101 TCCCCCGGAA CGATTTTCAA CCGAAGTGGC ACATACGCCG GUTCGGGCTG
 151 ACACAGGGTC AGCACAATGA GCTGCGTAAA ATCCGCCGCC CCTTCAAAAT
 201 GGCGGGCGAC AGGCGCGGTT TGAAGGTTAT GCATTCCGAA CACAGCCGCC
 251 GCCGCTCTGT CGTCGAAATC ATTTCTTCGG ATGTTTTTAA TCAGAACGAG
 301 GCGCGCGATT ATGTCGAAAG CCGTACCAC TCCAGCATGG ATTTGCGGT
 351 GGACGAATTG GAAATCCAAC ACCGCTTCTT CCATATTCTC ACACCGCAAC
 401 AGCAGCAAA GTGGCTTTCT TCCTGCCTCA AATAA

This corresponds to the amino acid sequence <SEQ ID 2304; ORF 691 >:

g691.pep
 1 VPLPAPCRFA KPAASFLSMA LLSCQLSHAA TAYIPPNDFO PNCDIRRLGL
 51 TQGGHNELRK IRAAFKMGD RARLKVHSE HSRRSVVEI ISSDVFNRE
 101 ARDYVESRYH SSMDFAVDEL EIQRFFHIL TPOQQOMWLS SCLK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2305>:

```
m691.seq
1  GTGCCACTGC CTGCTCCCTG CCGTTTGGCC AAACCTGCCG CCTCTTTTTT
51  AAGTATGGCT TTGCTTTCCT GTCAGCTTTC CCACGCCGCC ACGGCTTATA
101 TCCCCCGGAA CGATTTTCAA CCGAACTGCG ACATACGCCG ACTCGGGCTG
151 ACCCAAAGTC AGCACAATGA GCTGCGTAAA ATCCGCACCG CCTTCAAAT
201 GCGGGGCGAC AGGGCGCGTT TGAAGTTAT GCATTCCGAA CACAGCCGCC
251 GCCGCTCTGT CGTCGAAATC ATTCCTCGG ATGTTTTTAA TCGGAACGAG
301 GCGCGCGATT ATGTCGAAAG CCGCTATTG TCCGGTATGG ATTTGCGGT
351 GGACGAATTG GAAATCCAAC ACCGGTTCTT CCATATCTC ACACCGCAAC
401 AGCAGCAAAT GTGGCTTTCT TCCTGCCTCA AATAA
```

This corresponds to the amino acid sequence <SEQ ID 2306; ORF 691>:

```
m691.pep
1  VPLPAPCRFA KPAASFLSMA LLSCQLSHAA TAYIPPNDFO PNCDIRRLGL
51  TQSQHNELRK IRTAFKMGD RARLKMVHSE HSRRSVVEI ISSDVFNRE
101 ARDYVESRYL SGMDFAVDEL EIQRFFHIL TPQQQMWLS SCLK*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 691 shows 97.2% identity over a 144 aa overlap with a predicted ORF (ORF 691) from *N. gonorrhoeae*:

```
m691/g691 97.2% identity in 144 aa overlap

      10      20      30      40      50      60
m691.pep VPLPAPCRFAKPAASFLSMALLSCQLSHAATAYIPPNDFOPNCDIRRLGLTQSQHNELRK
      |||
g691      VPLPAPCRFAKPAASFLSMALLSCQLSHAATAYIPPNDFOPNCDIRRLGLTQSQHNELRK
      |||

      10      20      30      40      50      60

      70      80      90     100     110     120
m691.pep IRTAFKMGADRARLKMVHSEHSRRSVVEIISSDVFNREARDYVESRYLSGMDFAVDEL
      |||
g691      IRTAFKMGADRARLKMVHSEHSRRSVVEIISSDVFNREARDYVESRYLSGMDFAVDEL
      |||

      70      80      90     100     110     120

      130     140
m691.pep EIQRFFHILTPQQQMWLSSCLKX
      |||
g691      EIQRFFHILTPQQQMWLSSCLKX
      |||

      130     140
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2307>

```
a691.seq
1  GTGCCACTGC NTGCTCCCTG CCGTTTGGCC AAACCTGCCG CCTCTTTTTT
51  AAGTATGGCT TTGCTTTCCT GCCAGCTTTC CCACGCCGCC ACGGCTTATA
101 TCCCCCTGAA CGATTTTCAA CCGAACTGCG ACATACGCCG GCTCGGACTG
151 ACACAGGGTC AGCACAATGA ACTGCGTAAA ATCCGCACCG CCTTCAAAT
201 GCGGGGCGAC AGGGCGCGTT TGAAGTTAT GCATTCCGAA CACAGCCGCC
251 GTCGGTCTGT CGTCGAAATC ATTCCTCGG ATGTTTTTAA TCGGAACGAG
301 GCGCGCGATT ATGTCGAAAG CCGCTATTG TCCGGTATGG ATTTGCGGT
351 GGACGAATTG GAAATCCAAC ACCGGTTCTT CCATATCTC ACACCGCAAC
401 AGCAGCAAAT GTGGCTTTCT TCCTGCCTCA AATAA
```

This corresponds to the amino acid sequence <SEQ ID 2308; ORF 691.a>:

```
a691.pep
1  VPLXAPCRFA KPAASFLSMA LLSCQLSHAA TAYIPLNDFQ PNCDIRRLGL
51  TQSQHNELRK IRTAFKMGD RARLKMVHSE HSRRSVVEI ISSDVFNRE
101 ARDYVESRYL SGMDFAVDEL EIQRFFHIL TPQQQMWLS SCLK*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 691 shows 97.2% identity over a 144 aa overlap with a predicted ORF (ORF 691) from *N. meningitidis*:

m691/a691 97.2% identity in 144 aa overlap

	10	20	30	40	50	60
m691.pep	VPLPAPCRFAKPAASFLSMALLSCQLSHAATAYIPNDPQNCIDIRRLGLTQSQHNELRK					
a691	VPLXAPCRFAKPAASFLSMALLSCQLSHAATAYIPNDPQNCIDIRRLGLTQSQHNELRK					
	10	20	30	40	50	60
	70	80	90	100	110	120
m691.pep	IRTAFKMAGDRARLKVMHSEHSRRRSVVEIISSDVFNREARDYVESRYLSGMDFAVDEL					
a691	IRAAFKMAGDRARLKVMHSEHSRRRSVVEIISSDVFNREARDYVESRYLSGMDFAVDEL					
	70	80	90	100	110	120
	130	140				
m691.pep	EIOHRFFHILTPQQQOMWLSSCLKX					
a691	EIOHRFFHILTPQQQOMWLSSCLKX					
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2309>

g692.seq

```

1  GTATCGCACA CACGCTGTCG CTGTTTCGGAA TCGATACGCC GGATTTCGGCG
51  GAATGGCAGG GAATGGCGGA TTAAAGGACA AAAATGCCGT CTGAACACGG
101 ATGCGGTTCA GACGGCATCA TTTTATACGA CTGCCTTATT TGCGTCGCGC
151 TTCATTCCAT GCGGCAGGGT ATTTGTAGCC CTCGAAGCGT TTGTGCGCGT
201 AGGCTTTGAA CGCGTCGGAG TTATAGGCCT CGGTTACGTC TTTAAGCCAT
251 TGGCTGTCTT TGTGCGCGGT TTTGACGCCA GACCAGTTGA CATAGGCAAA
301 GCTCGGTTCT TGGACAGGG CTTCGGTCAG CTTTATGCGG CTGCTTATGG
351 CGTAGTTGCC GTTGACGACG GCAAAATCCA CGTCGGCGCG GCTACGCGGC
401 AGTTGTGCGG CTCAAGCTC GACGATTTTG ATGTTTTTCA GGTTTTCCGC
451 GATGTCGGCT TTGGATGCGG TCAGCGGATT GATGCGCTCT TTGAGTTTGA
501 TCCAACCCAG TTCGTTACG ATCACCAGG CGCGTGCAGG GTTGGACggG
551 TegtTGGCGG CGGATACGGT GCTGCCCTCT TTGACTTCTT CCAGCGATT
601 CAGTTTGGCC GGATACAGTC CCAAGCGCGC GGTCGGCACT TGAAGGCTT
651 CGGTGATGTC CAGGTTGTGT TCTTTTTTGA AATCGTCAAG ATAGGGTTT
701 TGTGGAAGA CGTTGATGTC CAACTCGCCC TCCGCCAATG CCAGATTTCG
751 GCGCACAATG TCggTAAATT cgaccaatTT gacgGTGTay cCTTTTTTCT
801 CCAGCTCGgc tTGGATTTGT TCTTTGACCA TATcgccgaa gtcgcccacg
851 gTCGTGCGCG agacgaTTTC TTTTTCGCGc GcgcCGTTAT CGGCAGAAGG
901 GCGGCGGgca gaggctgCGG GCGCGCTGTC TTTTtgaccG ccgCAGGCTG
951 CGAGGATGAG CGCGAGtgcg gcggcggaaa ggGTTTGA GAAGGTTTTc
1001 atATTTTCTc ctga

```

This corresponds to the amino acid sequence <SEQ ID 2310; ORF 692 >:

g692.pep

```

1  VSHTRCRCSE SIRRIWRNGR EWRIGQKCR LNTDAVQTAS FYTTALFGCA
51  FIPCGRVFVA LEAFVRVCFE RVGVIGLVV FKPLAVFVGG FDGRFPVDIGK
101 ARLLEQFGQ LHAAAYGVVA VDDGKIHVGA AARQLCGFKL DDFDVQVQFR
151 DVGFGCGQRI DAVFEFDPTQ FVQHHQGACE VGRVVGGRYG AAVFDFFQRF
201 QFARIQSQR GRHLEGFGDV QVVFEEIVK IGFVLEDVDV QLALRQCQIR
251 AHIVGRFDQF DGVAFFLQLG LDLFDDHIAE VAHGRAEDDF FFRKAVIGRR
301 GGGRGCGRAV FLTAAGCEDE RECGGKGFE EGFHIFS*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2311>:

m692.seq

```

1  GTGTTGCACA CGCTTTGTCG CTGTTTCGGAA TCGATACGCC GGATTTCGGCG
51  GAATGGCAGG GAATGGCGGA TTAAAGGACA AAAATGCCGT CTGAACACGG
101 ATACAGTTCA GACGGCATCA TTTTATACGA CTGCCTTATT TGCGTCGCGC
151 TTCATTCCAT GCGGCAGGGG ATTTGTAGCC CTCGAAGCGT TTGTGCGCGT
201 AGGCTTTGAA CGCGTCGGAG TTATAGGCCT CGGTTACGTC TTTAAGCCAT
251 TGGCTGTCTT TGTGCGCGGT TTTGACGCCA GACCAGTTGA CATAGGCAAA
301 GCTCGGTTCT TGGACAGGG CTTCGGTCAG CTTTATGCGG CTGCTTATGG
351 CGTAGTTGCC GTTGACGACG GCAAAATCCA CGTCGGCGCG GCTACGCGGC

```

1114

```

401 AGTTGCGCGG CTTCAAGCTC GACGATTTTG ATGTTTTTCA GGTTCCTCGGC
451 GATGTCGCGT TTGGATGCGG TCAACGGATT GATGCCGCTT TTGAGTTTGA
501 TCCAACCCAG TTCGTCGAGC ATCACCAGA CGCGGGCGAA GTTGGACGGG
551 TCGTTGGGCG CGGATACGGT GCTGCCGTCT TTGACTTCTT CCAGCGATT
601 CAGCTTGCCC GGGTACAGTC CCAAAGCGCG GGTCCGCACT TGAAGACTT
651 CGGTGATGTC CAGATTGTGT TCTTTTTTGA AGTCGTCAG ATAGGGTTTG
701 TGTGGAAGA CGTTGATGTC CAACTCGCCC TCAGCCAATG CCAGATTCTG
751 GCGTACATAG TCGGTAAACT CGACCAGTTT GACGGTGTAG CCTTTTTTCT
801 CCAGCTCGGC TTGGATTGT TCTTTGACCA TATCGCCGAA GTCGCCGACG
851 GTCGTGCCGA AGACGATTTC TTTTTCGCC GCGCCGTTGT CGGCGGCGGC
901 AGAAGCGGAT GCGGCGGGCG CGCTGTCTTT TTGACCGCCG CAGGCGGCGA
951 GGATGAGCGC GAGTGGCGCG GCGGAAAGGG TTTGAAGAA GGTTCCTATA
1001 TTTTCTCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2312; ORF 692>:

m692.pep

```

1 VLHTLCRCSE SIRRIIRNGR EWRIKQKCR LNTDTVQTAS FYTTALFGCA
51 FIPCGRGFVA LEAFVRVGF EYGVIGLVY FKPLAVFVG FDGRPVDIGK
101 ARFLEQGFQ LHAAYGVVA VDDGKIHVGA ATRQLRGFKL DDFDVFGVLG
151 DVFRCGQRI DAVFEFPTQ FVEHHQDAGE VGRVVGRCY AAVFDFQRF
201 QLARVQSRR GRHLEDFGDV QIVFFEYVK IGFVLEDVDV QLALSQQIR
251 AYIVGKLDQF DGVAFFLQLG LDLFFDHIAE VADGRAEDDF FFRRAVVG
301 RSGCGGRAVF LTAAGGEDER ECGGKGFEF GFHIFS*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 692 shows 91.1% identity over a 338 aa overlap with a predicted ORF (ORF 692) from *N. gonorrhoeae*:

m692/g692 51.1% identity in 338 aa overlap

m692.pep	10	20	30	40	50	60
	VLHTLCRCSESIRRIIRNGREWRIKQKCR LNTDTVQTASFYTTALFGCAFIPCGRGFVA					
g692	VSHTRCRCSESIRRIWRNGREWRIKQKCR LNTDAVQTASFYTTALFGCAFIPCGRVFVA					
m692.pep	70	80	90	100	110	120
	LEAFVRVGFERYGVIGLVYFKPLAVFVGFDGRPVDIGKARFLEQGFQ LHAAYGVVA					
g692	LEAFVRVGFERYGVIGLVYFKPLAVFVGFDGRPVDIGKARLLEQGFQ LHAAYGVVA					
m692.pep	130	140	150	160	170	180
	VDDGKIHVGAATRLRGFKLDDFDVFGVLEVRFGCGQRI DAVFEFPTQFVEHHQDAGE					
g692	VDDGKIHVGAARQLCGFKLDDFDVFGVFRVFGCGQRI DAVFEFPTQFVOHHQGAGE					
m692.pep	190	200	210	220	230	240
	VGRVVGRCYGAAVDFDFQRFQLARVQSRRGRHLEDFGDVQIVFFEYVKIGFVLEDVDV					
g692	VGRVVGRCYGAAVDFDFQRFQFARIQSRRGRHLEFGDVQVVFVEYVKIGFVLEDVDV					
m692.pep	250	260	270	280	290	
	QLALSQQIRAYIVGKLDQFDGVAFFLQLGLDLFFDHIAEVADGRAEDDF FFRRAVVG--					
g692	QLALSQQIRAHIVGKFDQFDGVAFFLQLGLDLFFDHIAEVAGRAEDDF FFRRAVIGRR					
m692.pep	300	310	320	330		
	GGRSGCGGRAVELTAAGGEDERECGGGKGFEEGFHIFSX					
g692	GGGRCG-RAVELTAAGCEDERECGGGKGFEEGFHIFSX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2313>

a692.seq

```

1 GTGTTGCACA CGCTTTGTCG CTGTTCCGAA TCGATACGCC GGATTCGGCG

```

```

51 GAATGGCAGG GAATGGCGGA TTAAAGGACA AAAATGCCGT CTGAACACGG
101 ATACGGTTCA GACGGCATCA TTTTATACGA CTGCCTTATT TGGCTGCGCC
151 TTCATTCCAT CCGGCAGGGG ATTTGTAGCC CTCGAAGCGT TTGTGCGCGT
201 AGGCTTTGAA CGCGTCGGAG TTATAGGCCT CGGTTACGTC TTTAAGCCAT
251 TGGCTGTCTT TGTCGGCGGT TTTGACGGCA GACCAGTTGA CATAGGCAAA
301 GCTCGGTTCT TGGAACAGGG CTTGGGTCAG CTTTCATGCCG CTGCTTATGG
351 CGTAGTTGCC GTTGACGACG GCAAAATCCA CGTCGGCGCG GCTACGCGGC
401 AGTTGCGCGG CTTCAAGCTC GACGATTTTG ATGTTTTTCA GGTTTTCGGC
451 AATGTCCGCT TTGGATGCGG TCAGCGGATT GATGCCGTCT TTGAGTTTGA
501 TCCAACCCAG TTCGTCGAGC ATCACCAGA CGCGGGCGAA GTTCGACGGG
551 TCCTTGGCGC CGGATACGGT GCTGCCGTCT TTGACTTCTT CCAGCGATT
601 CAGCTTGCCC GGTACAGTC CCAAAGCGC GGTCCGCACT TGGAGACTT
651 CGGTGATGTC CAGATTGTGT TCTTTTTTGA AGTCGTCAAG ATAGGGTTTG
701 TGTGGAAGA CGTTGATGTC CAACTCGCCC TCAGCCAATG CCAGATTCGG
751 CGGCACATAG TCGGTAAACT CGACCAAGTT GACGGTGTAG CCTTTTTTCT
801 CCAGCTCGGG TTGGATTGTG TCTTTGACCA TATCGCCGAA GTGCGCGACG
851 GTCGTGCCGA AGACGATTTC TTTTTCGCC GCGCCGTGTG CGGCGGCGGC
901 AGAAGCGGAT GCGGCGGGCG CGCTATCTTT TTGACCGCCG CAGGCGCGCA
951 GGATGAGCGG GAGTGCGGCG GCGGAAAGGG TTTTGAAGAA GGTTTTCATA
1001 TTTTCTCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2314; ORF 692.a>:

a692.pep

```

1: VLHTLCRCSE SIRRIIRNGR EWRIKQKCR LNTDTVQTAS FYTTALFGCA
51: FIPCGRGFVA LEAFVRVGF E RVGVLGLGYV FKPLAVFVCG FDRPVDIGK
101: ARFLEQGFQ LHAAAYGVVA VDDGKIHVGA ATRQLRGFKL DDFDVQVFG
151: NVRFQCGQRI DAVFEEDPTQ FVEHHQDAGE VGRVVGGRYG AAVFDFQRF
201: QLARVQSQR GRHLEDFGDV QIVFFFEVVK IGFVLEDVDV QLALSQCQIR
251: AHIVGKLDQF DGVAFFLQLG LDLFFDHIAE VADGRAEDDF FFRRAVVGGG
301: RSGCGGRAIF LTAAGGEDER ECGGGKGFEE GFHIFS*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 692 shows 98.8% identity over a 336 aa overlap with a predicted ORF (ORF 692) from *N. meningitidis*:

m692/a692 98.8% identity in 336 aa overlap

	10	20	30	40	50	60
m692.pep	VLHTLCRCSE	SIRRIIRNGR	EWRIKQKCR	LNTDTVQTAS	FYTTALFGCA	FIPCGRGFVA
a692	VLHTLCRCSE	SIRRIIRNGR	EWRIKQKCR	LNTDTVQTAS	FYTTALFGCA	FIPCGRGFVA
	70	80	90	100	110	120
m692.pep	LEAFVRVGF	ERVGVGLGYV	FKPLAVFV	GGFDRPVD	IGKARFLE	QGFQGLHAAAYGVVA
a692	LEAFVRVGF	ERVGVGLGYV	FKPLAVFV	GGFDRPVD	IGKARFLE	QGFQGLHAAAYGVVA
	130	140	150	160	170	180
m692.pep	VDDGKIHVGA	ATRQLRGFKL	DDFDVFOVL	GDVRFQCG	QRI	DAVFEEDPTQFVEHHQDAGE
a692	VDDGKIHVGA	ATRQLRGFKL	DDFDVFOVL	GDVRFQCG	QRI	DAVFEEDPTQFVEHHQDAGE
	190	200	210	220	230	240
m692.pep	VGRVVGGRYG	AAVDFDFQRF	QLARVQSQR	GRHLEDFGDV	QIVFFFEVVK	IGFVLEDVDV
a692	VGRVVGGRYG	AAVDFDFQRF	QLARVQSQR	GRHLEDFGDV	QIVFFFEVVK	IGFVLEDVDV
	250	260	270	280	290	300
m692.pep	QLALSQCQIR	AHIVGKLDQF	DGVAFFLQLG	LDLFFDHIAE	VADGRAEDDF	FFRRAVVGGG
a692	QLALSQCQIR	AHIVGKLDQF	DGVAFFLQLG	LDLFFDHIAE	VADGRAEDDF	FFRRAVVGGG
	310	320	330			
m692.pep	RSGCGGRAIF	LTAAGGEDER	ECGGGKGFEE	GFHIFS		
a692	RSGCGGRAIF	LTAAGGEDER	ECGGGKGFEE	GFHIFS		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2315>:

```
g694.seq
1   TCGGCATTG TGTGCCCCA ACATCCGATG CCTGCGTTAA CGCCTGCGTC
51  AACGTTTGCA CAAATCGGGT TTGGTTTCGC CCTCGCGGCG CAGCTCCTTG
101 GGCAGGACGA ACACGATGCT TTCTTCCGCG CCCCCCCTT CGCGCACGGT
151 TTCATGCCCC CATCCGCGTA TGGTTGCCAA TACTTCCCGC ACCAACACTT
201 CGGGCGCGGA CGCGCTGCC GTTACGCCGA CTTTGTCTTT GCCTTCAAAC
251 CACGTGCGTT GCaggTAGGA CGCGTTGTCC ACCATATACG CATCGATTCC
301 CGCGGATGCC GCCACTTCGC GCAGGCGGTT GCTGTGGAC GAATTGGGCG
351 AACCGACCAC AATCAGGATG TCGCACTGTT CCGCCAGCTC TTTGACGGCG
401 GTTTGCCGGT TGGTCGTCGC ATAGCAGATG TCTTCTTGT GCGGATTGCG
451 GATATTGGGG AAACGCGCGT TCAGCGCGCG GATGATGTCT TTGGTTTCAT
501 CGACCGAGAG CGTGGTTTGG CTGACATAGG CGAGTTTGTG GGGGTTTCTG
551 ACTTCGAGTT TTGCCACATC TCCGACCGTT TCGACCAAAA GCATTTTGCC
601 CGGTGCAAGC TGCCCCATCG TGCTTCGAC CTCGGCGTGC CCCTTATGCC
651 CGATCATGAT GATTTCACAG TCTTGGSCAT CCAGTCGGGC GACTTCCTTA
701 TGCACTTTTG TCACACGCGG GCAAGTCGCA TCAATAACCC GGAACCCGCG
751 CTCCGCGCGT TCCTGCTGCA CGGCCTCGA TACGCCGTGT GCCGAATAAA
801 CCACTGTGCG GCCCGGCGGC ACTTCCGCCA AGTCTTCGAT AAACACCGCG
851 CTTTTTTGCG GCAGGTTGTC CACGACGAAT TTGTTGTGGA CGACTTCGTG
901 GCGCACATAA ACCGGCGCGC CGAATTCCTC CAAAGCACGT TCGACAATAC
951 TGATTGCCCG ATCCACACCG GCGCAGAAGC CGCGCGGATT GGCAAGGATG
1001 ATGGTTTTTC CGTTCATAAG TTTTGCATTG CGTGTTCAGA CGGCATTAC
1051 GTTTTTTTGC TNNATCTTG CGATGGACGA TATTGTCAA GACCGCCAAC
1101 ACCGCACCGA CGCAGATAA
```

This corresponds to the amino acid sequence <SEQ ID 2316; ORF 694>:

```
g694.pep (partial)
1   SAFVLPKHEM FALTPASTFA QIGGFALAA QLLGQDEHDA FFRAPPPAHG
51  FMPPSAYGCQ YFPHQHFRG RACRYADFAF AFKPRALQVG RVVHHIRIDS
101 ARCRHFAQAV AVGRIGRTDH NHDVALFRQL EDGLPVGRR IADVFLVRIA
151 DIGETRVQRG DDVFGFIDRE RSLADIGFV GVSDFEFCHI SDREFQKHFA
201 RCKLPHRAFD LGVPLMPDHD DFTVLGIQSG DFLMHFRHOR ASRIKYPETA
251 LRRFLHLRLR YAVCRINOCR ARRHFRQVFD KHRAFFAQV HDEFVVDDEV
301 AHINRRAEFF QSTFDNTDCP IHTGAEAARI GKDDGFSVHK FCIPCSGDIH
351 VFLLXLCDDR YQAPPTPHR RR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2317>:

```
m694.seq
1   TTGGTTTCCG CATCCGGCAC ACGGCAAAAA TGCCGTCTGA AGCCTGTTC
51  GACGGCATTG GTGTTGCCCA AACATTCAAC GCCTGCGTCA ACGTTTGAC
101 AAATCGGGTT TGGTTTCGCC CTCGCGGCGC AACTCTTTGG GCAGGACGAA
151 CACAATGCTT TCTTCCGCAC CCTCGCCTTC CGGTACGGTT TCGTGCCCCC
201 ATCCGCGTAT GGTGCCAGT ACTTCCCGCA CCAACACTTC GGGCGCGGAC
251 GCGCCTGCCG TTACGCCGAC TTTGTTTTTG CCCTCAAACC ATGCGCGTTG
301 CAGGTAGCCT GCATTATCCA CCATATACGC ATCGATTCCG CGCGATGCCG
351 CCACCTTCGG CAAGCGGTTG CTGTTGGACG AATTGGGCGA ACCGACCACA
401 ATCACGATGT CGCACTGTTT TGCCAACTCT TTGACGGCGG TTTGCCGGTT
451 GGTCTGTCGA TAGCAGATAT CTTCTTGTG CGGATTGCGG ATATTGGGGA
501 AACGCGCGT CAGCGCGGCG ATGATGTCTT TGGTTTCATC GACCGAGAGC
551 GTGGTTTGGC TGACATAGGC GAGTTTGTG GGGTTTCTGA CTTCGAGTTT
601 TGCCACATCT CCGACCGTTT CGACCAAAAG CATTTTGCCC GGCACAAAGT
651 GCCCCATCGT TCCTTCGACC TCGACGTGCC CCTTATGCCC GATCATGATG
701 ATTTACAGT CTTGGGCATC CAGTCGGGCG ACTTCCTTAT GCACTTTCGT
751 CACGAGCGGG CAAGTCGCAT CAAACACGCG GAACCGGCGC TCCGCGGCTT
801 CTTGCCGCAC CGCCTTCGAT ACGCCGTGTG CCGAATAAAC CAGTGTGCGG
851 CCCGGCGGCA CTTCCGCCAA GTCTTCAATA AACACCGCAC CTTTTTCACG
901 CAGGTGTGCC ACGACGAATT TGTTGTGAAC GACTTCGTGG CGCACATAAA
951 TCGGCGCGCC GAACTCTTCC AAAGCAGGTT CGACAATACT GATT GCCCGA
1001 TCCACACCA GCGAGAAGCC GCGCGGATTG GCAAGGATGA TGGTTTCTC
1051 GTTCATAAGC CCGGTATITC GTTTTCAGAC GGCATCAATA TTTTCTTCT
1101 TGGGTTTTAC GGTGGACGAT GTTGTCACAC ACCGCCAACA CCGCACCGAC
1151 GCAGATAA
```

This corresponds to the amino acid sequence <SEQ ID 2318; ORF 694>:

```
m694.pep
1   LVSASGRQK CRLKPVQTA VLPKHSTPAS TFAQIGFGA LAAQLFGQDE
51  HNAFFRTLAF AYGFVPPSAY GCQYFPHQHF GRGRACRYAD FVFALKPCAL
101 QVACIIHHIR IDSARCRHFA QAVAVGRIGR TDHNDVALF COLFDGGLPV
```

1117

```

151 GRIADIFLV RIADIGETRV QRGDDVFGFI DRERGLADIG EFVGVSDFEF
201 CHISDRFDQK HFARRKLPHR SFOLDVPLMP DHDDFTVLGI QSGDFLMHFR
251 HQRASRIKHA ETALRRFLPH RLRYAVCRIN QCRARRHFRO VFNKHRTFFT
301 QVHDEFVFN DFVAHINRRA ELFQSTFDNT DCPIHTSAEA ARIGKDDGFL
351 VHKPGISFSD GINIFLLGFY GGRCCPTPPT PHRRR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 694 shows 86.8% identity over a 372 aa overlap with a predicted ORF (ORF 694) from *N. gonorrhoeae*:

m694/g694 86.8% identity in 372 aa overlap

```

              10      20      30      40      50
m694.pep      LVSASGTRQKCRCLKPVQTAFLPKHS---TPASTFAQIGFGFALAAQLFGQDEHNAFFR
              :||||| :||||| :||||| :||||| :|||||
g694           SAFVLPKHPMPALTTPASTFAQIGFGFALAAQLLGQDEHDAFFR
              10      20      30      40

              60      70      80      90      100     110
m694.pep      TLAFAYGFVPFSAYGCGYFPFHOFGRGRACRYADVFALKPCALQVACIIHHIRIDSARC
              : |||:||||| :||||| :||||| :||||| :|||||
g694           APPFAHGFMPSAYGCGYFPFHOFGRGRACRYADFAFAKPRALQVGRVHHIRIDSARC
              50      60      70      80      90      100

              120     130     140     150     160     170
m694.pep      RHFAQAVAVGRIGRTDHNHDVALFCQLFDGGLPVGRRRIADIFLVRIADIGETRVQRGDDV
              :||||| :||||| :||||| :||||| :||||| :|||||
g694           RHFAQAVAVGRIGRTDHNHDVALFRQLFDGGLPVGRRRIADVFLVRIADIGETRVQRGDDV
              110     120     130     140     150     160

              180     190     200     210     220     230
m694.pep      FGFIDRERGLADIGEFVGVSDFEFCHISDRFDQKHFAARRKLPHRSFDLDVPLMPDHDDFT
              :||||| :||||| :||||| :||||| :||||| :|||||
g694           FGFIDRERGLADIGEFVGVSDFEFCHISDRFDQKHFAARCKLPHRAFDLGVPLMPDHDDFT
              170     180     190     200     210     220

              240     250     260     270     280     290
m694.pep      VLGIQSGDFLMHFRHQRASRIKHAETALRRFLPHRLRYAVCRINQCRARRHFROVFNKHR
              :||||| :||||| :||||| :||||| :||||| :|||||
g694           VLGIQSGDFLMHFRHQRASRIKYPETALRRFLHRLRYAVCRINQCRARRHFROVFNKHR
              230     240     250     260     270     280

              300     310     320     330     340     350
m694.pep      TFFTQVVHDEFVNDDFVAHINRRAELFQSTFDNTDCPIHTSAEAARIGKDDGFLVHKPGI
              :||||| :||||| :||||| :||||| :||||| :|||||
g694           AFFAQVVHDEFVNDDFVAHINRRAELFQSTFDNTDCPIHTGAEAARIGKDDGFSVHKFCI
              290     300     310     320     330     340

              360     370     380
m694.pep      SFSDGINIFLLGFYGGRCCTPPTPHRRRX
              :||||| :||||| :|||||
g694           PCSDGIHVFLXXLCDGRYCQAPPTPHRRRX
              350     360     370

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2319>:

```

a694.seq
1  TTGGTTTCCG CATCCGGCAC ACGGCAAAAA TGCCGTCTGA AGCCTGTTCA
51  GACGGCATIT GTGTTGCCCA AACATTCAAC GCCTGCGTCA ACGTTGCAC
101 AAATCGGGTT TGGTTTCGCC CTCGCGGCGC AACTCTTTGG GCAGGACGAA
151 CACRATGCTT TCTTCCGCAC CCTCGCCTTC GCGTACGGTT TCGTGCCCCC
201 ATCCGCGTAT GGTTCGCCAGT ACTTCCGCGA CCAACACTTC GGGCGCGGAC
251 GCGCCTGCGC TTACGCGGAC TTTGTTTTTG CCCTCAAACC ATGCGCGTTG
301 CAGGTAGCCT GCATTATCCA CCATATACGC ATCGATTCCG CGCGATGCCG
351 CCACTTCGCG CAAGCGGTTG CTGTTGGACG AATTGGGCGA ACCGACCACA
401 ATCAGCATGT CGCACTGTTT TGCCAACTCT TTGACGGCGG TTTGCCGGTT
451 GGTCTGTCGA TAGCAGATAT CTTCTTTGTG CGGATTGCGG ATATTGGGGA
501 AACGCGCGTT CAGCGCGGCG ATGATGTCTT TGGTTTCATC GACCGAGAGC
551 GTGGTTTGGC TGACATAGGC GAGTTTGTCT GGGTTTCTGA CTTGAGTTT
601 TGCCACATCT CCGACCGTTT CGACCAAAAG CATTTTGCCG GCGCAAGCT
651 GCCCCATCGT TCCTTCGACC TCGACGTGCC CCTTATGCCG GATCATGATG

```

```

701 ATTTCACAGT CTTGGGCATC CAGTCGGGCG ACTTCCTTAT GCACCTTTCGT
751 CACCAGCGGG CAAGTCGCAT CAAACACGCG GAAACCGCGC TCCGCCGCTT
801 CTTGCCGCAC CGCCTTCGAT ACGCCGTGTG CCGAATAAAC CAGTGTGCGG
851 CCGGGCGGCA CTTCCGCCAA GTCTTCAATA AACACCGCAC CTTTTTCACG
901 CAGGTTGTCC ACGACGAATT TGTGTGAAC GACTTCGTGG CGCACATAAA
951 TCGGGCGGCC GAACTCTTCC AAAGCACGTT CGACAATACT GATTGCCCGA
1001 TCCACACCAG CGCAGAAGCC GCGCGGATTG GCAAGGATGA TGGTTTTCTC
1051 GTTCATAAGC CCGGTATTTC GTTTTCAGAC GGCATCAATA TTTTCTTCT
1101 TGGGTTTAC GGTGGACGAT GTTGTCACAC ACCGCCAACA CCGCACCGAC
1151 GCAGATAA

```

This corresponds to the amino acid sequence <SEQ ID 2320; ORF 694.a>:

```

a694.pep
1  LVSASGTRQK CRLKPVQTAF VLPKHSTPAS TFAQIGFGFA LAAQLFGQDE
51  HNAFFRTLAF AYGFVPPSAY GCQYFPQHFF GRGRACRYAD FVFALKPCAL
101 QVACIIHHIR IDSARCRHFA QAVAVGRIGR TDHNDVALF CQLFDGGLPV
151 GRIADIFLV RIADIGETRV QRGDDVFGFI DRERGLADIG EFVGVSDFEF
201 CHISDRFDQK HFARRKLPHR SFDLDVPLMP DHDDFTVLGI QSGDFLMHFR
251 HQRASRIKHA ETALRRFLPH RLYAVCRIN QCRARRHFRQ VFNKHRTFFT
301 QVVHDEFVFN DVAHINRRA ELFOSTFDNT DCPHTSAEA ARIGKDDGFL
351 VHKPGISFSD GINIFLLGFY GGRCCPTPPT PHRRR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 694 shows 100% identity over a 385 aa overlap with a predicted ORF (ORF 694) from *N. meningitidis*:

```

m694/a694 100.0% identity in 385 aa overlap

      10      20      30      40      50      60
m694.pep LVSASGTRQKRLKPVQTAFVLPKHSTPASTFAQIGFGFALAAQLFGQDEHNAFFRTLAF
a694      LVSASGTRQKRLKPVQTAFVLPKHSTPASTFAQIGFGFALAAQLFGQDEHNAFFRTLAF
      10      20      30      40      50      60

      70      80      90     100     110     120
m694.pep AYGFVPPSAYGCQYFPQHFGGRGRACRYADFVFAKPCALQVACIIHHIRIDSARCRHFA
a694      AYGFVPPSAYGCQYFPQHFGGRGRACRYADFVFAKPCALQVACIIHHIRIDSARCRHFA
      70      80      90     100     110     120

      130     140     150     160     170     180
m694.pep QAVAVGRIGRTDHNHDVALFCQLFDGGLPVGRRRIADIFLVRIADIGETRVQRGDDVFGFI
a694      QAVAVGRIGRTDHNHDVALFCQLFDGGLPVGRRRIADIFLVRIADIGETRVQRGDDVFGFI
      130     140     150     160     170     180

      190     200     210     220     230     240
m694.pep DRERGLADIGEFVGVSDFEFCHISDRFDQKHFAARRKLPHRSFDLDVPLMPDHDDFTVLGI
a694      DRERGLADIGEFVGVSDFEFCHISDRFDQKHFAARRKLPHRSFDLDVPLMPDHDDFTVLGI
      190     200     210     220     230     240

      250     260     270     280     290     300
m694.pep QSGDFLMHFRHQRASRIKHAETALRRFLPHRLRYAVCRINQCRARRHFRQVFNKHRTFFT
a694      QSGDFLMHFRHQRASRIKHAETALRRFLPHRLRYAVCRINQCRARRHFRQVFNKHRTFFT
      250     260     270     280     290     300

      310     320     330     340     350     360
m694.pep QVVHDEFVFNDFVAHINRRAELFQSTFDNTDCPIHTSAEAARIGKDDGFLVHKPGISFSD
a694      QVVHDEFVFNDFVAHINRRAELFQSTFDNTDCPIHTSAEAARIGKDDGFLVHKPGISFSD
      310     320     330     340     350     360

      370     380
m694.pep GINIFLLGFYGGRCCTPPTPHRRRX
a694      GINIFLLGFYGGRCCTPPTPHRRRX
      370     380

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2321>:

```
g695.seq
1  TTGCTCAAA CTCGTCCGGC AAGGCGGCAT CATCGCCATC GACAATATTT
51  TGTGAACGG AAGGGTGATG CGCGAAGCGG CTTTGTATGC GCCGCCCAGT
101 GTCAAAATTC TCAAAGATTT CAATCAAAC CTGCCGAACG ATACGCGGAT
151 TGTCCCATC ACCCTGCCCG TCGGCGACGG TTTGACCTG CTTCTGAAAA
201 AATAATGAAG ACCAAATTAC CGCTTTTAT CATTGGCTG TCTGTGTCTG
251 CCTCCTGTGC TTCCGTTTCA CCCGTTCCGG AGGGCAGCGG AACCGAAATG
301 CCGACACAGG AAAATGCTTC AGACGGCATT CCCTATCCCG TTCCCACTCT
351 GCAAGACCGT TTGGACTATC TGGAAGGCAA AATCGTCCGG CTGTCGAACG
401 AAGTGGAAAT GTTAAACGGG AAAGTCAAAG CATTGGAGCA TACGAAAATA
451 CACCCTTCG GCAGGACATA CGTCCAAAA CTCGACGACC GCAAATTGAA
501 AGAGCATTAC CTCAATACCG AAGGCGGCAG CGCATCCGCA CATACCGTCG
551 AAACCGCACA AAACCTCTAC AATCAGGCAC TCAAACACTA TCAAACGGC
601 AGGTTTCTG CCGCAGCCGC CTTGTTSAAG GGGCGGACG GCGGAGACGG
651 CGGCAGCATC GCGCAACGCA GTATGTACCT GTTGCTGCAA AGCAGGGCGC
701 GTATGGGGA CTGTGAATCT GTCATCGAAA TCGGAGGGCG TTACGCCAAC
751 CGTTTCAAAG ACAGCCCAAC CGCGCCGAA GTCATATTCA AAATCGGCGA
801 ATGCCAATAC AGGCTTCAGC AAAAAGACAT TGCAAGGGCG ACTTGGCGCA
851 GCCTGATACA GACCTATCCC GGCAGCCCGG CGGCAAAACG CGCCGCCGCA
901 GCCGTACGCA AACGATAG
```

This corresponds to the amino acid sequence <SEQ ID 2322; ORF 695>:

```
g695.pep
1  LPQTRPARRH HRHRQYFVER KGDARSGF*C AAQCQNSQRF QSKPAERYAD
51  CPHHPARRRR FDPASEKIMK TKLPLFIWL SVSASCASVL PVPEGSRTM
101 PTQENASDGI PYPVPTLQDR LDYLEGKIVR LSNEVEMLNG KVKALEHTKI
151 HPSGRITYVQK LDDRKLKEHY LNTGGGSASA HTVETAQNLY NQALKHYQNG
201 RFSAAAALLK GADGGDGGSI AQRSMYLLQ SRARMGNCS VIEIGGRYAN
251 RFKDSPTAPE VIFKIGECQY RLQOKDIARA TWRSLIQTYP GSPAARKRAA
301 AVRKR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2323>:

```
m695.seq
1  TTGCTCAAA CTCGTCCGTC AAGGCGGCAT CATCGCCATC GACAATATTT
51  TGTGAACGG AAGGGTGATG CGCGAAGCGG CTTCCGATGC GCCGCCCAGC
101 GTCGGCATCC TCAAAGATTT CAATCAAAC CTGCCGAACG ACCCGCGCAT
151 CGTCCCATC ACCCTGCCCG TCGGCGACGG CTTGACCTG CTTCTGAAAA
201 AATAATGAAG ATCAAATTAC CGCTTTTAT CATTGGCTG TCTGTGTCCG
251 CCTCCTGTGC TTCCGTTTCA CCCGTTCCGG CAGGCAGCCA AACCGAAATG
301 TCGACACGGG AAAATGCTTC AGACGGCATT CCCTATCCCG TTCCGACCTT
351 GCAAGACCGT TTGGACTATC TGGAAGGCAA AATCGTCCGG CTGTCGAACG
401 AAGTGGAAAC CTTAAACGGC AAAGTCAAAG CACTGGAACA CGCAAAAACA
451 CATTCTTCCG GCAGGGCATA CGTCCAAAA CTCGACGACC GCAAGTTGAA
501 AGAGCATTAC CTCAATACCG AAGGCGGCAG CGCATCCGCA CATACTGTCT
551 AAACCGCACA AAACCTCTAC AATCAGGCAC TCAAACACTA TAAAAGCGGC
601 AAGTTTCTG CCGCTGCCTC CTTGTTGAAA GCGCGGACG GAGGCGACGG
651 CGGCAGCATC GCGCAACGCA GTATGTACCT GTTGCTGCAA AGCAGGGCGC
701 GTATGGGCAA CTGCGAATCC GTCATCGAAA TCGGAGGGCG TTACGCCAAC
751 CGTTTCAAAG ACAGCCCAAC CGCGCCTGAA GCCATGTTCA AAATCGGCGA
801 ATGCCAATAC AGGCTTCAGC AAAAAGACAT TGCAAGGGCG ACTTGGCGCA
851 GCCTGATACA GACCTATCCC GGCAGCCCGG CGGCAAAACG CGCCGCCGCA
901 GCCGTGCGCA AACGATAG
```

This corresponds to the amino acid sequence <SEQ ID 2324; ORF 695>:

```
m695.pep
1  LPQTRPSRRH HRHRQYFAER KGDARSGFRC AAQRRHPQRF QSKPAERPAH
51  RPHHPARRRR LDPASEKIMK IKLPLFIWL SVSASCASVS PVPAGSOTEM
101 STRENASDGI PYPVPTLQDR LDYLEGKIVR LSNEVETLNG KVKALEHAKT
151 HSSGRAYVQK LDDRKLKEHY LNTGGGSASA HTVETAQNLY NQALKHYKSG
201 KFSAAASLLK GADGGDGGSI AQRSMYLLQ SRARMGNCS VIEIGGRYAN
251 RFKDSPTAPE AMFKIGECQY RLOQKDIARA TWRSLIQTYP GSPAARKRAA
301 AVRKR*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 694 shows 90.8% identity over a 305 aa overlap with a predicted ORF (ORF 695) from *N. gonorrhoeae*:

m695/g695 90.8% identity in 305 aa overlap

m695.pep	10	20	30	40	50	60
	LPQTRPSRRHHRQYFAERKGDARSGFRCAAQRRHPQRFQSKPAERPAPHRPHHPARRRR					
g695	10	20	30	40	50	60
	LPQTRPARRHHRQYFVERKGDARSGFXCAAQCONSQRFSKPAERYADCPHHPARRRR					
m695.pep	70	80	90	100	110	120
	LDPASEKIMKIKLPLFIWLVSASCSVSPVPAGSQTEMSTRENASDGIPYPVPTLQDR					
g695	70	80	90	100	110	120
	FDPASEKIMKTKLPLFIWLVSASCSVLPVPEGSRTMPTQENASDGIYPYPVPTLQDR					
m695.pep	130	140	150	160	170	180
	LDYLEGKIVRLSNEVELNGKVKALEHAKTHSSGRAYVQKLDLDRKLKEHYLNTEGGSASA					
g695	130	140	150	160	170	180
	LDYLEGKIVRLSNEVELNGKVKALEHTXIHPSGRTYVQKLDLDRKLKEHYLNTEGGSASA					
m695.pep	190	200	210	220	230	240
	HTVETAQNLYNQALKHYKSGKFSAAASLLKGADGGDGGGSAQSRMYLLLSRARMGNCS					
g695	190	200	210	220	230	240
	HTVETAQNLYNQALKHYQNGRFSAAAALLKGADGGDGGGSAQSRMYLLLSRARMGNCS					
m695.pep	250	260	270	280	290	300
	VIEIGGRYANRFKDSPTAPEAMFKIGECQYRLQKDIARATWRSLIQTYPGSPAARKAAA					
g695	250	260	270	280	290	300
	VIEIGGRYANRFKDSPTAPEVIFKIGECQYRLQKDIARATWRSLIQTYPGSPAARKAAA					
m695.pep	AVRKRX					
g695	AVRKRX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2325>:

a695.seq

1	TTGCTCAAG	CTTGTCGGC	AAGGCGGCAT	CATTGCCATC	GACAATATTT
51	TGTTGAACGG	AAGGGTGATG	CGCGAAGCGG	CTTCGATGC	GCCGCCCAGC
101	GTCGGCATCC	TCAAAGATT	TAATCAAAC	CTGCCGAACG	ATACGCGGAT
151	TGTCCTCCATC	ACCCTGCCCG	TCGGCGACGG	TTTGACCTCG	CTTCTGAAAA
201	AATAATGAAG	ACCAAATTAC	CGCTTTTAT	CATTGGGCTG	TCCGTATCCG
251	CCGCTGTTC	TCCCTCTGT	TCCCGCAATA	TTCAGGATAT	GCGGCTCGAA
301	CCGCAGGCAG	AGGCAGGTAG	TTCCGACGCT	ATTCCCTATC	CCGTTCCAC
351	TCTGCAAGAC	CGTTTGGATT	ATCTGGAAGG	CACACTCGTC	CGCTGTCTGA
401	ACGAAGTGGA	AACCTTAAAC	GGCAAAGTCA	AAGCACTGGA	GCATGCGAAA
451	ACACACCTT	CCAGCAGGCC	ATACGTCCAA	AACTCGACG	ACCGCAAGTT
501	GAAAGAGCAT	TACCTCAATA	CCGAACGCGG	CAGCGCATCC	GCACATACCG
551	TCGAAACCGC	ACAAAACCTC	TACAATCAGG	CACTCAAACA	CTATAAAAGC
601	GGCAGGTTT	CTGCCGCTGC	CTCCTGTGT	AAAGGCGCGG	ACGGAGGCGA
651	CGGCGGCAGC	ATCGCGCAAC	GCAGTATGTA	CCTGTTGCTG	CAAAGCAGGG
701	CGCGTATGGG	CAACTGCGAA	TCCGTCATCG	AAATCGGAGG	GCGTTACGCC
751	AACCGTTTCA	AAGACAGCCC	AACCGCGCCT	GAAGCCATGT	TCAAATTCGG
801	CGAATGCCAA	TACAGGCTTC	AGCAAAAAGA	CATTGCAAGG	GCGACTTGCC
851	GCAGCCTGAT	ACAGACCTAT	CCCGGCAGCC	CGGCGGCAAA	ACGCGCCGCC
901	GCAGCCGTGC	GCAACCGATA	G		

This corresponds to the amino acid sequence <SEQ ID 2326; ORF 695.a>:

a695.pep

1	LPQACPARRH	HCHRQYFVER	KGDARSGFRC	AAQRRHPQRF	*SKPAERYAD
51	CPHHPARRRR	FDPASEKIMK	TKLPLFIWL	SVSAACSPV	SRNIQDMRLE
101	PQAEAGSSDA	IPYPVPTLQD	RLDYLEGLTV	RLSNEVELTN	GKVKALEHAK
151	THPSSRAYVQ	KLDDRKLKEH	YLNTEGGSAS	AHTVETAQNL	YNQALKHYKS
201	GRFSAAASLL	KGADGGDGGG	IAQRSMYLLL	QSRARMGNCE	SVIEIGGRYA
251	NRFKDSPTAP	EAMFKIGECQ	YRLQKDIAR	ATWRSLIQTY	PGSPAARKAA
301	AAVRRR*				

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 695 shows 88.3% identity over a 308 aa overlap with a predicted ORF (ORF 695) from *N. meningitidis*:

m695/a695 88.3% identity in 308 aa overlap

m695.pep	10	20	30	40	50	60
a695	10	20	30	40	50	60
m695.pep	70	80	90	100	110	
a695	70	80	90	100	110	
m695.pep	120	130	140	150	160	170
a695	120	130	140	150	160	170
m695.pep	180	190	200	210	220	230
a695	180	190	200	210	220	230
m695.pep	240	250	260	270	280	290
a695	240	250	260	270	280	290
m695.pep	300					
a695	300					

The following partial DNA sequence was identified in *N. gonorrhoeae*
g696.seq: not found

This corresponds to the amino acid sequence < ORF 696.ng>:
g696.pep: not found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2327>:

```
m696.seq
1  TTGGGTTGCC GGCAGGCGGC ATCCCATCAT TTTTGCCAAG GCAACAAATT
51  ATTTGGCGGC ATCTTTCATT TTGCTGCGCG CTCCTGAGT CGCGTCGGCA
101 GCTTTGTTC AAGTATCTTT AGCTGCTTCA GTTACAGCTT CTTTGGCTTC
151 AGTTACAGCT TCCTCGGCAC TTGCCTTTC ATCAGCCGCA GCATCTTTGA
201 CTTGGTCTTT CGCTTCTTCG ACGGCAGAAG CGGCAGACTC GCGCGCAGAA
251 GCCGAGTGT CTTTAACATC GGAATCAACG GCTTGAACCG CTTCTTAAAC
301 CTCCTGTTTG GCTTCTTTCG AACAAGCTGC CAAGGCAGCC GCCATCATTG
351 CGGCAATCAA TAA
```

This corresponds to the amino acid sequence <SEQ ID 2328; ORF 696>:

```
m696.pep
1  LGCROAASHH FCQGNKLFEG IFHFVCRFLS RVGSFVQSIF SCFSYSFFGF
51  SYSFLGTCLC ISRSIFDLVF RFFDGRSGRL GGRSRSVFNI GLNGLNRFLN
101 LLFGFLRTSC QGSRHHCNGQ *
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2329>:
a696.seq

1122

```

1  TTGGGTTGCC GGCAGGCGGC ATCCCATCAT TTTTGCCAAG GCAACAAATT
51  ATTTGGCGGC ATCTTTTCATT TTGTCTGCCG CTTCTGAGT CGCGTCGGCA
101 GCTTTGTTC AAGTATCTTT AGCTGCTTCA GTTACAGCTT CTTTGGCTTC
151 AGTTACAGCT TCCTCGGCAC TTGCCTTTGC ATCAGCCGCA GCATCTTTGA
201 CTTGGTCTTT CGCTTCTCG ACGGCAGAAG CGGCAGACTC GCGCGCAGAA
251 GCCGCAGTGT CTTTAACATC GGAACAACG GCTTGAACCG CTTCTTAAC
301 CTCCTGTTT GCTTCTTGGC AACAAGCTGC CAAGGCAGCC GCCATCATTG
351 CGGCAATCAA TAA

```

This corresponds to the amino acid sequence <SEQ ID 2330; ORF 696.a>:

a696.pep

```

1  LGCRQAASHH FCQGNKLFGG IFHFVCRFLS RVGSFVQSIF SCFSYSFFGF
51  SYSFLGCLC ISRSIFDLVF RFFDGRSGRL GGRSRSVFNI GLNGLNRFLN
101 LLFGFLRTSC QGSRHHCNQ *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N meningitidis*

ORF 696 shows 100.0% identity over a 120 aa overlap with a predicted ORF (ORF 696.a) from *N. meningitidis*:

m696/a696 100.0% identity in 120 aa overlap

```

          10      20      30      40      50      60
m696.pep  LGCRQAASHHFCQGNKLFGGIFHFVCRFLSRVGSFVQSIFSCFSYSFFGFYSFLGTCLC
          |||
a696      LGCRQAASHHFCQGNKLFGGIFHFVCRFLSRVGSFVQSIFSCFSYSFFGFYSFLGTCLC
          10      20      30      40      50      60

          70      80      90      100     110     120
m696.pep  ISRSIFDLVFRFFDGRSGRLGGRSRSVFNI GLNGLNRFLNLLFGFLRTSCQGSRHHCNQ
          |||
a696      ISRSIFDLVFRFFDGRSGRLGGRSRSVFNI GLNGLNRFLNLLFGFLRTSCQGSRHHCNQ
          70      80      90      100     110     120

```

```

m696.pep  X
          |
a696      X

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2331>:

g700.seq

```

1  ATGAGCAGCC TGATGACGTT GTTTTCGGTA TTGGTACCGA TGTTTGCCGG
51  ATTTTTTATC CGTGTTCCCA AGCCTTACCT GCCCGCTTCG GACAAGGTGC
101 TGTCGGTTTT GGTGTATGCC GTGCTGCTGC TGATCGGCGT ATCGTTGTCTG
151 CGCGTGAGG AATTGGGTTT GCGGTTGGGC GATATGGCGT TGACGGTTCT
201 GTGGCTGTTT GTTTGTACGG TAGGGGCGAA CCTGCTTGCC TTGGCAGTGT
251 TGGGAAAGTT GTCCCGTGG CGGATAGGGG GAAAAGGGAA GGGCGTTTCG
301 GTCGGCGTGT CGGGCAGTGT GAGGCAGCTC GGATGCGTAC TGCTCGGTTT
351 TGTGTCCGGC AAATTGATGT GCGATATTG GATGCCGTCT GAAAACGCGG
401 GTATGTACTG CCTGATGCTG CTGGTGTTCC TCATCGGCGT ACAGCTCAAA
451 AGTAGCGGCG TATCGTTGCG GCAGGTTTTG CTTAACCGGC GGGGCATCCG
501 GCTGTCGGTT TGGTTTATAT TGTCTCTCT TTCAGGCGGG CTGCTGTTTG
551 CCGCATCGGC AGATGGTGTG TCGTGACGA AAGGTTTGGC GATGGCTTCC
601 GGCTTCGGTT GGTATTCCCT CTCGGGTTTG GTAATGACCG AGGCTTACGG
651 GCGGATATGG GGCAGCATCA TGCTGCTGAA CGATTGGCA CGAGAGCTGT
701 TTGACTGGC ATTTATPCCG CTGCTGATGA AGCGTTTTCC GGATGCGGCG
751 GTGGGGGTTC GCGGCGCGAC CAGTATGGAT TTCACATTGC CCGTAATTCA
801 GGGTGCGGCG GGTTTGGAAG TCGTGCCGGT AGCGGTGAGC TTCGCGGTGG
851 TGGTCAATAT GCCTGCCCCG TTTCTGATGG TGGTGTTC CACGCTGGGC
901 TGA

```

This corresponds to the amino acid sequence <SEQ ID 2332; ORF 700>:

g700.pep

```

1  MSSMLTLFSV LVPMFAGFFI RVPKPYLPAS DKVLSVLVYA VLLLIGVSL
51  RVEDLGSRLG DMALTVLWLF VCTVGANLLA LAVLGKLSPW RIGGKKGVS
101 VGVSGSVRQL GCVLLGFVSG KLMCDIWMP ENAGMYCLML LVFLIGVQLK
151 SSGVSLRQVL LNRRGIRLSV WFILSSLSGG LLFAASADGV SWTKGLAMAS

```

201 GFGWYLSGL VMTEAYGAVW GSIMLLNDLA RELFALAFIP LLMKRFPDAA
 251 VGVGGATSMD FTLPVIQAG GLEVVPVAVS FGVVVNIAAP FLVVVFSTLC
 301 *

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2333>:

m700.seq

1 ATGGACAGCC TGATGACGTT GCTTTCGGTA TTGATACCGA TGTTTGCCGG
 51 ATTTTATC CGTGTGCCCA AGCCTTACCT GCCCGCTTG GATAAGGTGC
 101 TATCGGCTCTT GGTGTATGCT GTGCTGCTGC TGATCGGCGT CTCGTTGTCTG
 151 CGCGTGGAGG ATTTGGGTTC GCGTTGGAC GATATGGCGT TGACGGTTCT
 201 GTGGCTGTTT GTTGTACGG TCGGGGCGAA CCTGCTTGCT TTGGCAGTGT
 251 TGGGAAAGTT ATTCCCGTGG CGGATAAAGG GGAAGGGAA GGGCGTTTCG
 301 GTCGGCGTGT CGGGCAGTGT GGGGCAGCTC GGATGCGTGC TGCTCGGATT
 351 TGCATTCCGC AAACGATGC GCGATATTG GATGCCGTCT GAAAGCGCGG
 401 GCATGTATTG TCTGATGCTG CTGGTGTTC TCATCGGCGT ACAGCTCAA
 451 AGCAGCGCGG TATCGTTGCG GCAGGTTTGT GTCAACCGCA GGGGTATTCTG
 501 GTTGTGCGTC TGGTTTATGC TTTCATCTCT TTCGGGCGGG CTGCTCTTGT
 551 CCGCATCGAC AGACGGTGTG TCGTGGACGA AAGGTTTGGC GATGGCTTCC
 601 GGCTTCGGTT GGTATTCCCT CTCGGGTTTG GTCATGACCG AGCCTTACGG
 651 CGCGGTATGG GGCAGCATCA TGCTGCTGAA CGATTGGCA CGAGAGCTGT
 701 TTGCACTGGC ATTTATCCCG CTGCTGATGA AGCGTTTCC AGATGCGGCG
 751 GTGGGGTTG GCGGTGCGAC CAGTATGGAT TTTACATTGC CCGTGATTCA
 801 GGTGCGGGC GGTTTGGAAG TCGTGCCGGT AGCGGTCAGC TTCGGCGTGG
 851 TGGTCAATAT CGCCGCCCGG TTTCTGATGG TGGTGTTTTC CGCTTTGGGT
 901 TGA

This corresponds to the amino acid sequence <SEQ ID 2334; ORF 700>:

m700.pep

1 MDSLMTLLSV LIPMFAGFFI RVPKPYLPAL DKVLSVLVYA VLLIGVSL
 51 RVEDLGSRD DMALTVLWLF VCTVGANLLA LAVLGKLPW RIKGKGKGV
 101 VGVSGSVQGL GCVLLGFAGF KLMRDIWMP ESAGMYCLML LVFLIGVQLK
 151 SSGVSLRQVL VNRGIRLSV WFLSSLSGG LLEAASDGV SWTKGLAMAS
 201 GFGWYLSGL VMTEAYGAVW GSIMLLNDLA RELFALAFIP LLMKRFPDAA
 251 VGVGGATSMD FTLPVIQAG GLEVVPVAVS FGVVVNIAAP FLVVVFSALG
 301 *

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae* with *menB*

ORF 700 shows 94.7% identity over a 300 aa overlap with a predicted ORF (ORF700.ng) from *N. gonorrhoeae*:

m700/g700

	10	20	30	40	50	60
m700.pep	MDSLMTLLSVLIPMFAGFFIRVPKPYLPALDKVLSVLVYAVLLIGVSLSRVEDLGSRD					
g700	MSSLMTLFSVLVPMFAGFFIRVPKPYLPASDKVLSVLVYAVLLIGVSLSRVEDLGSRD					
	10	20	30	40	50	60
m700.pep	DMALTVLWLFVCTVGANLLALAVLGKLPWRIKGKGKGVSVGVSGSVQGLGCVLLGFAGF					
g700	DMALTVLWLFVCTVGANLLALAVLGKLPWRIKGKGKGVSVGVSGSVRQLGCVLLGFVSG					
	70	80	90	100	110	120
m700.pep	KLMRDIWMPSESAGMYCLMLLVFLIGVQLKSSGVSLRQVLVNRGIRLSVWFLSSLSGG					
g700	KLMCDIWMPSENAGMYCLMLLVFLIGVQLKSSGVSLRQVLVNRGIRLSVWFLSSLSGG					
	130	140	150	160	170	180
m700.pep	LLFAASDGVSWTKGLAMASGFGWYLSGLVMTEAYGAVWGSIMLLNDLARELFALAFIP					
g700	LLFAASDGVSWTKGLAMASGFGWYLSGLVMTEAYGAVWGSIMLLNDLARELFALAFIP					
	190	200	210	220	230	240

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	190	200	210	220	230	240
	250	260	270	280	290	300
m700.pep	LLMKRFPDAAVGVGGATSMDFTLFVIQAGGLEVPVAVSFGVVVNIAAPFLMVVFSALG					
g700	LLMKRFPDAAVGVGGATSMDFTLFVIQAGGLEVPVAVSFGVVVNIAAPFLMVVFSALG					
	250	260	270	280	290	300
m700.pep	x					
g700	x					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2335>:

```

a700.seq
1  ATGGACAGCC  TGATGACGTT  GCTTTCGGTA  TTGATACCGA  TGTTGCCGG
51  ATTTTTTATC  CGTGTGCCCA  AGCCTTACCT  GCCCGCTTTG  GATAAGGTGC
101  TATCGGTCTT  GGTGTATGCT  GTGCTGCTGC  TGATCGGCGT  CTCGTTGTCG
151  CGCGTGGAGG  ATTTGGGTTT  GCGGTGGGAC  GATATGGCGT  TGACGGTTCT
201  GTGGCTGTTT  GTTTGTACGG  TCGGGGCGAA  CCGCTTGCT  TTGGCAGTGT
251  TGGGAAAGTT  ATTCCCGTGG  CGGATAAAGG  GGAAAGGGAA  GGGCGTTTCG
301  GTCGGTGTGT  CGGGCAGTGT  GGGGCAGCTC  GGATGCGTGC  TGCTCGGATT
351  TGCATCCGGC  AAAGTGAATC  GCGATATTTC  GATGCCGTCT  GAAAACGCGG
401  GTATGTATTG  TCTGATGCTG  CTGGTGCTCN  TCATCGGCGT  ACAGCTCAAA
451  AGCAGCGGCG  TATCGTTGCG  GCAGGTTTTC  GTCAACCGCA  GGGGTATTTC
501  GTTGTGCGTC  TGGTTTATGC  TTTCATCTCT  TTCAGGCGGG  CTGCTGTTTG
551  CCGCATCGGC  AGACGGTGTG  TCGTGGGTGA  AAGGTTTGGC  GATGGCTTCC
601  GGCTTCGGTT  GGTATTCCCT  CTCGGGTTTC  GTGATGACCG  AGGCTTACGG
651  CGCGGTATGG  GGCAGTATCC  CGCTTTTGAA  CGATTGGGCA  CGAGAGCTGT
701  TCGCGCTGGC  ATTTATTCCG  CTGCTGATGA  AGCGTTTTC  CGATGCGGCA
751  GTGGGGGTCG  GCGGCGCGAC  CAGTATGGAT  TTCACATTGC  CCGTGATTTC
801  GGGTGCAGGC  GGCTTGAAG  CCGTACCGGT  AGCGGTCAGC  TTCGGCGTGG
851  TGGTCAATAT  CGCCGCTCCG  TTCTGATGG  TGGTGTTTTC  CGCTTTGGGC
901  TGA
  
```

This corresponds to the amino acid sequence <SEQ ID 2336; ORF 700.a>:

```

a700.pep
1  MDSLMTLLSV  LIPMFAGFFI  RVPKPYLPAL  DKVLSVLVYA  VLLLIGVSL
51  RVEDLGSRLD  DMALTVLWLF  VCTVGANLLA  LAVLGKLFPP  RIKGKGKGV
101  VGVSGSVGQL  GCVLLGFASG  KLMRDIWMP  ENAGMYCLML  LVLXIGVQL
151  SSGVSLRQVL  VNRRGIRLSV  WFMLSSLSGG  LLFAASADGV  SWVKGLAMAS
201  GFGWYSLSG  VMTEAYGAVW  GSIALNDLA  RELFALAFIP  LLMKRFPDAA
251  VGVGGATSM  DFTLPVIRGAG  GLEAVPVAVS  FGVVNIAAP  FLMVVFSA
301  *
  
```

m700/a700 97.0% identity in 300 aa overlap

	10	20	30	40	50	60
m700.pep	MDSLMTLLSVLIPMFAGFFIRVPKPYLPALDKVLSVLVYAVLLLIGVSLSRVEDLGSRLD					
a700	MDSLMTLLSVLIPMFAGFFIRVPKPYLPALDKVLSVLVYAVLLLIGVSLSRVEDLGSRLD					
	10	20	30	40	50	60
m700.pep	DMALTVLWLFVCTVGANLLALAVLGKLFPPRIKKGKGVSVGVSGSVGQLGCVLLGFASG					
a700	DMALTVLWLFVCTVGANLLALAVLGKLFPPRIKKGKGVSVGVSGSVGQLGCVLLGFASG					
	70	80	90	100	110	120
m700.pep	KLMRDIWMPSESAGMYCLMLLVFLIGVQLKSSGVSLRQVLVNRRGIRLSVWFMLSSLSGG					
a700	KLMRDIWMPSENAGMYCLMLLVXIGVQLKSSGVSLRQVLVNRRGIRLSVWFMLSSLSGG					
	130	140	150	160	170	180
m700.pep	KLMRDIWMPSESAGMYCLMLLVFLIGVQLKSSGVSLRQVLVNRRGIRLSVWFMLSSLSGG					
a700	KLMRDIWMPSENAGMYCLMLLVXIGVQLKSSGVSLRQVLVNRRGIRLSVWFMLSSLSGG					
	130	140	150	160	170	180

q701.seq

1	ATGTCCTTGGC	ACATATTCCA	AGTTGCAGGG	ATACCGACCG	CTTCGATGGC
51	ACAATCTACG	CCGTCCTCG	CGACGATGC	GAAAACTTGT	TTGGAGACGT
101	CGCCGGAAGC	GGGGTCGATC	GATCGGGTCG	CGCCCAACTC	TTTCGCCGGT
151	TTCAAACGGT	TTTCGTCCAT	ATCGCACACG	ATAATGGCGG	CAGGGCTATA
201	CAGTTGGGCG	GTCAACAAGG	CGGACATACC	GACAGGGCCG	GCACCTGCGA
251	TGAATACGGT	ATCGCCGGGT	TTCACATCGC	CGTATTGCAC	GCCGATTTCG
301	TGGGCGGCTG	GTAAGACGTC	GTCACCAACG	AGGGCGGATT	CTTCGTTGAC
351	GTGTGCTGCG	GGCGGCACGA	GGCTGTTTGC	GGCATAA	

q701.pep

1 MSWHIFQVAG IPTASMAQST PSSPTMAKTC LETSPEAGLM VVWVAPNSFAG
51 FKRFSISHT IMAAGLYSWA VNKADIPTGP APAMNTVSPG FTSPYCTPIS
101 WAVGKASLNS RAISSLTLSG GGTLLLSA*

m701.seq

1	ATGTCCTTGGC	ACATATTCCA	TGTAGCAGGG	ATACCGACGG	CTTCGATGGC
51	GCAATCCACG	CCGTCCTCGC	CGACGATGCG	AAAGACTTGT	TTGGATACTT
101	CGCCGGAAGC	AGGGTTAATG	GTCATGGGTGC	CACCCAATTG	TTTCGCCGAT
151	TTCAAAACGGT	TTTCGTCAT	ATCCGAAACG	ATGATGGCGG	CGGGGACTGA
201	CAGTTGGGCG	GTCAACAGGG	CGGACATACC	GACAGGGCCT	GCCCCAGCGA
251	TGAATACGGT	GTCCGCCGGT	TTGACAACCG	CGTATTGCAC	GCCGATTTCG
301	TGGGCGGTGC	GCAAAGCGTC	GCTCAACAC	AGGGCGATT	CTTCGTTGAC
351	ATTATCGGGC	AGCGGAACGA	GGCTGTTGTC	GGCATAA	

m701.pap

1 MSWHIFHVAG IPTASMAQST PSSPTMAKTC LOTSPEAGLM VVAPNSFAS
51 FKRFSISQST MMAAGLYSWA VNRAIDIPTGP APAMNTVSPG LTSPYCTPIS
101 WAVGKASLNN RAISSLTLSG SCTRLLSA*

Homology with a predicted ORF from *N. gonorrhoeae* with *menB*

m701/g701

```

              10      20      30      40      50      60
m701.pep      MSWHIFHVAGIPTASMAQSTPSSPTMAKTCLDTSPEAGLMVWVAPNSFASFKRFSISQ
               |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g701          MSWHIFQVAGIPTASMAQSTPSSPTMAKTCLETSP EAGLMVWVAPNSFAGEKRFSSISHT

```

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	10	20	30	40	50	60
	70	80	90	100	110	120
m701.pep	MMAAGLYSWAVNRADIP TGPAPAMNTVSPGLTSPYCTPISWAVGKASLNNRAISSLTLSG					
	: : : : : : :					
g701	IMAAGLYSWAVNKADIP TGPAPAMNTVSPGFTSPYCTPISWAVGKASLNSRAISSLTLSG					
	70	80	90	100	110	120
	129					
m701.pep	SGTRLLSAX					
	:					
g701	GGTRLLSAX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2341>:

```
a701.seq
1  ATGTCTTGGC ACATATTCCA AGTTGCAGGG ATACCGACGG CTTGATCGC
51  GCAGTCCACG CCGTCTTCGC CGACGATAGC GGCAACTTGC TTGCTTACAT
101 CGCCGGAAGC AGGGTTAATG GTATGGGTG CGCCCAACTC TTTCGCCAGT
151 TTCAAACGGT TTCGTCCAT ATCGCAAACA ATGATGGCGG CGGGGCTGTA
201 CAGTTGGGCG GTCGGCAAGG CGGACATACC GACAGGAGCG GCACCTGCGA
251 TGAATACGGT GTCGCCGGT TTGACATCGC CGTATTGCAC GCCGATTTCG
301 TGTGCGGTCG GCAAAGCGTC GCTCAACAAC AGGGCGACTT CTTGTTGAC
351 GTTGTGCGGC AGCGGCACGA GGCTGTTGTC GGCATAA
```

This corresponds to the amino acid sequence <SEQ ID 2342; ORF 701.a>:

```
a701.pep
1  MSWHIFQVAG IPTASIAQST PSSPTIAATC LLTSPEAGLM VWVAPNSFAS
51  FKRFSSISQT MMAAGLYSWA VGKADIPTGA APAMNTVSPG LTSPYCTPIS
101 CAVGKASLNN RATSSLTSLG SGTRLLSA*
```

m701/a701 92.2% identity in 128 aa overlap

	10	20	30	40	50	60
m701.pep	MSWHIFHVAGIPTASMAQSTPSSPTMAKTCLDTSPEAGLMVWVAPNSFASFKRFSSISQT					
	: : : : : :					
a701	MSWHIFQVAGIPTASIAQSTPSSPTIAATCLLTSPPEAGLMVWVAPNSFASFKRFSSISQT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m701.pep	MMAAGLYSWAVNRADIP TGPAPAMNTVSPGLTSPYCTPISWAVGKASLNNRAISSLTLSG					
	: : : : : :					
a701	MMAAGLYSWAVGKADIPTGAAPAMNTVSPGLTSPYCTPISCAVGKASLNNRATSSLTSLG					
	70	80	90	100	110	120
	129					
m701.pep	SGTRLLSAX					
a701	SGTRLLSAX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2343>:

```
g702.seq
1  ATGCCGTGTT ccaAAGCCAG TTGGACTTCG CCCGGAGtgg cAACGCCGGG
51  AATCAGGGGA ATGCCGCTGT TGCGGCCGGC TCTGGCGAGG GATTCGTGCA
101 AACCCGGGCT GATGGCGAAA ACCGCGCCTG CGTCTTCGAC GGCTTTGAGC
151 TGTTCCGGAT TGGTTACCGT ACCTGCGCCG ATGATGGCGT TGGGCATTTC
201 TTTGGCAATC AGGCGGATGG CCTCGAGTCC GACGGGGGTG CGCAAGGTAA
251 TTTCCGAGGT GGGGATGCCG CCTTCGACAA GGGCGCGGGA CAAATCGACG
301 GCGGTGCTTA AGTCGTCAAt cgCCATCACA GGCACAAC TG CGCCGGCGGT
351 CAGGATTTCG cgggggggtca gttga
```

This corresponds to the amino acid sequence <SEQ ID 2344; ORF 702>:

g702.pep

m702.seq

m702.pgp

m702/q702

a702.seq

a702.pep

10 20 30 40 50 60

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```

m702.pep    MPCSKASWISPGVATPGIRGMPLLWPALARDSCSPGLMAKTAPASSTALSCSGLVTPAP
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a702         MPCSKASWISPGVATPGIRGMPLLWPALARDSCSPGLMAKTAPASSTALSCSGLVTPAP
             10      20      30      40      50      60

             70      80      90      100     110     120
m702.pep    TMALGTSLAIRRMASRPTGVRVRVISRVGMPPSTRAWDKSMAVLKSSIAITGTTAPAVKIS
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a702         TMALGTSLAIRRMASRPTGVRVRVISRVGMPPSTRAWDKSMAVLKSSIAITGTTAPAVKIS
             70      80      90      100     110     120

             130     140
m702.pep    RGVSLDISVLRVEWGILLRWDR LX
             ||||||||||||||||||
a702         RGVSLDISVLRVEWGILLRWDR LX
             130     140

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2349>:

g703.seq

```

1  ATGAAAGCAA AAATCCTGAC TTCCGTTGCG CTGCTTGCCT GTTCCGGCAG
51 CCTGTTTGCC CAAACGCTGG CAACCGTTAA CGGTCAGAAA ATCGACAGTT
101 CCGTCATCGA TGCGCAGGTT GCCGCATTCC GTGCGGAAAA CAGCCGTGCC
151 GAAGACACGC CGCAACTGCG CCAATCCCTG CTGGAACACG AAGTGGTCAA
201 CACCGTGGTC GCACAGGAAG TGAAACGCCT GAAACTCGAC CGGTCGGCAG
251 AGTTTAAAGA TGCGCTTGCC AAATTGCGTG CCGAAGCGAA AAAGTCGGGC
301 GACGACAAGA AACCGTCCTT CAAAACCGTT TGGCAGGCGG TAAAATATGG
351 CTTGAACGGC GAGGCATACG CACTGCATAT CGCCAAAACC CAACCGTTT
401 CCGAGCAGGA AGTAAAAGCC GTTTACGACA ATATCAGCGG TTTTATAAAA
451 GGCACGCAGG AAGTCCAGTT GGGCGAAATC CTGACCGACA AGGAAGAAAA
501 TCGCAAAAAA GCGGTTGCCG ATTTGAAGGC GAAAAAAGGT TTTGATGCCG
551 TTTTGAACA ATACTCGCTC AACGACCGCA CCAAACGGAC CGGCGCGCCG
601 GACGGATATG TGCCGCTGAA AGATTGGAA CAGGGTGTTT CGCCGCTTTA
651 TCAGGCAATT AAGGACTTGA AAAAAGGCGA ATTTACGGCA ACGCCGCTGA
701 AAAACGGCGC TTTCTACGGC GTTTATTATG TCAACGACAG CCGcgaggTG
751 AAAGTGCTT CTTTGGACGA AATGAAAGGA CAGATTGCCG GCAACCTTCA
801 GCGGGAACGG ATTGACCGTG CCGTctgTGc gcTGTtggtt aaggCAAACA
851 TCAAACCTGC AAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2350; ORF 703>:

g703.pep

```

1  MKAKILTSVA LLACSGSLFA QTLATVNGQK IDSSVIDAQV AAFRAENSRA
51 EDTPQLRQSL LENEVNTTVV AOEVKRLKLD RSAEFKDALA KLRAEAKKSG
101 DDKKPSFKTV WQAVKYGLNG EAYALHIAKT QPVSEQEVKA VYDNISGFYK
151 GTQEVQLGEI LTDKEENAKK AVADLKAKKG FDAVLKQYSL NDRTKRTGAP
201 DGYVPLKDLE QGVPPYQAI KDLKKGEFTA TPLKNGDFYG VYYVNSREV
251 KVPSFDEMKG QIAGNLQAER IDRAVCALLG KANIKPAK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2351>:

m703.seq

```

1  ATGAAAGCAA AAATCCTGAC TTCCGTTGCA CTGCTTGCCT GTTCCGGCAG
51 CCTGTTTGCC CAAACGCTGG CAACCGTCAA CGGTCAGAAA ATCGACAGTT
101 CCGTCATCGA TGCGCAGGTT GCCGCATTCC GTGCGGAAAA CAGCCGTGCC
151 GAAGACACGC CGCAACTGCG CCAATCCCTG CTGGAACACG AAGTGGTCAA
201 TACCGTGGTC GCACAGGAAG TGAAACGCCT GAAACTCGAC CGGTCGGCAG
251 AGTTTAAAAA TGCGCTTGCC AAATTGCGTG CCGAAGCGAA AAAGTCGGGC
301 GACGACAAGA AACCGTCCTT CAAAACCGTT TGGCAGGCGG TAAAATATGG
351 CTTGAACGGC GAGGCATACG CATTGCATAT CGCCAAAACC CAACCGTTT
401 CCGAGCAGGA AGTAAAAGCC GCATATGACA ATATCAGCGG TTTTACAAA
451 GGTACGCAGG AAGTCCAGTT GGGCGAAATC CTGACCGACA AGGAAGAAAA
501 TGCAAAAAA GCGGTTGCCG ACTTGAAGGC GAAAAAAGGT TTTGATGCCG
551 TCTTGAACA ATATTCCCTC AACGACCGTA CCAAACAGAC CGGTGCGCCG
601 TGCGGATATG TGCCGCTGAA AGATTGGAA CAGGGTGTTT CGCCGCTTTA
651 TCAGGCAATT AAGGACTTGA AAAAAGGCGA ATTTACGGCA ACGCCGCTGA

```

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701 AAAACGGCGA TTTCTACGGC GTTTATTATG TCAACGACAG CCGCGAGGTA
 751 AAAGTGCCTT CTTTGTATGA AATGAAAGGA CAGATTGCGG GCAACCTTCA
 801 GCGGAACGG ATTGACCGTG CCGTCGGTGC ACTGTGGGC AAGGCAAACA
 851 TCAACCTGC AAAATAA

This corresponds to the amino acid sequence <SEQ ID 2352; ORF 703>:

m703.pep

1 MKAKILTSVA LLACSGSLFA QTLATVNGQK IDSSVIDAQV AAFRAENSRA
 51 EDTPQLRQSL LENEVNTVV AQEVKRLKLD RSAEFKNALA KLRAEAKKSG
 101 DDKKPSFKTV WQAVKYGLNG EAYALHIAKT QPVSEQEVKA AYDNISGFYK
 151 GTQEVQLGEI LTDKEENAKK AVADLKAKKG FDAVLKQYSL NDRTKQTGAP
 201 VGYVPLKDLE QGVPLYQAI KDLKKGEFTA TPLKNGDFYG VYYVNSREV
 251 KVPFSDEMKG QIAGNLQAER IDRAVGALLG KANIKPAK*

ORF 703 shows 98.3% identity over a 288 aa overlap with a predicted ORF (ORF703.ng) from *N. gonorrhoeae*:

m703/g703

	10	20	30	40	50	60
m703.pep	MKAKILTSVALLACSGSLFAQTLATVNGQKIDSSVIDAQVAAFRAENSRAEDTPQLRQSL					
g703	MKAKILTSVALLACSGSLFAQTLATVNGQKIDSSVIDAQVAAFRAENSRAEDTPQLRQSL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m703.pep	LENEVNTVVVAQEVKRLKLDRAEFKNALAKLRAEAKKSGDDKKPSFKTVWQAVKYGLNG					
g703	LENEVNTVVVAQEVKRLKLDRAEFKDALAKLRAEAKKSGDDKKPSFKTVWQAVKYGLNG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m703.pep	EAYALHIAKTQPVSEQEVKAAYDNISGFYKGTQEVQLGEILTQKEENAKKAVADLKAKKG					
g703	EAYALHIAKTQPVSEQEVKAVYDNISGFYKGTQEVQLGEILTQKEENAKKAVADLKAKKG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m703.pep	FDAVLKQYSLNDRTKQTGAPVGYVPLKDLEQGVPLYQAIKDLKKGEFTATPLKNGDFYG					
g703	FDAVLKQYSLNDRTKRTGAPDGYVPLKDLEQGVPLYQAIKDLKKGEFTATPLKNGDFYG					
	190	200	210	220	230	240
	250	260	270	280	289	
m703.pep	VYYVNSREVKVPFSDEMKGQIAGNLQAERIDRAVGALLGKANIKPAKX					
g703	VYYVNSREVKVPFSDEMKGQIAGNLQAERIDRAVCALLGKANIKPAKX					
	250	260	270	280		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2353>:

a703.seq

1 ATGAAAGCAA AAATCCTGAC TTCCGTTGCA CTGCTTGCCT GTTCCGGCAG
 51 CCTGTTTGCC CAAACGCTGG CAACCGTCAA CGGTCAGAAA ATCGACAGTT
 101 CCGTCATTGA TGCGCAGGTT GCCGCATTCC GTGCGGAAAA CAGCCGTGCC
 151 GAAGACACGC CGCAACTGCG CCAATCCCTG CTGGAACGAC AAGTGGTCAA
 201 CACCGTGGTC GCACAGGAAG TGAACGCCT GAAACTCGAC CGGTCGGCAG
 251 AGTTTAAAAA TGCGTTGCC AAATGCGTG CCGAAGCGAA AAAGTCGGGC
 301 GACGACAAGA AACCGTCCTT CAAAACCGTT TGGCAGGCGG TAAAAATATG
 351 CTTGAACGGC GAGGCATACG CGCTGCATAT CGCCAAAACC CAACCGGTTT
 401 CCGAGCAGGA AGTAAAAGCC GCATATGACA ATATCAGCGG TTTTACAAA
 451 GGTACGCAGG AAGTCCAGT GGGCGAAATC CTGACCGACA AGGAAGAAAA
 501 TGCAAAAAAA GCGGTTGCCG ACTTGAAGGC GAAAAAGGT TTCGATGCCG
 551 TCTTGAAACA ATATTCCCTC AACGACCGTA CCAACAGAC CGGTGCGCCG
 601 GTCGGATATG TGCCGCTGAA AGATTTGGAA CAGGGTGTTC CGCCGCTTA
 651 TCAGGCAATT AAGGACTTGA AAAAAGCGCA ATTTACGGCA ACGCCGCTGA

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701 AAAACGGCGA TTTCTACGGC GTTTATTATG TCAACGACAG CCGCGAGGTA
 751 AAAGTGCCTT CTTTGTGATGA AATGAAAGGA CAGATTGCGG GCAACCTTCA
 801 GGCGGAACGG ATTGACCGTG CCGTCGGTGC ACTGTTGGGC AAGGCAAAACA
 851 TCAAACCTGC AAAATAA

This corresponds to the amino acid sequence <SEQ ID 2354; ORF 703.a>:

a703.pep

1 MKAKILTSVA LLACSGSLFA QTLATVNGQK IDSSVIDAQV AAFRAENSRA
 51 EDTPQLRQSL LENEVVNTVV AQEVKRLKLD RSAEFKNALA KLRAEAKKSG
 101 DDKKPSFKTV WQAVKYGLNG EAYALHIAKT QPVSEQEVKA AYDNISGFYK
 151 GTQEVQLGEI LTDKEENAKK AVADLKAKKG FDAVLKQYSL NDRTKQTGAP
 201 VGVVPLKDLE QGVPPLYQAI KDLKKGEFTA TPLKNGDFYG VYYVNSREV
 251 KVPSFDEMKG QIAGNLQAER IDRAVGALLG KANIKPAK*

m703/a703 100.0% identity in 288 aa overlap

m703.pep	10	20	30	40	50	60
	MKAKILTSVALLACSGSLFAQTLATVNGQKIDSSVIDAQVAAFRAENSRAEDTPQLRQSL					
a703	MKAKILTSVALLACSGSLFAQTLATVNGQKIDSSVIDAQVAAFRAENSRAEDTPQLRQSL					
	10	20	30	40	50	60
m703.pep	70	80	90	100	110	120
	LENEVVNTVVAQEVKRLKLDRSAEFKNALAKLRAEAKKSGDDKKPSFKTVWQAVKYGLNG					
a703	LENEVVNTVVAQEVKRLKLDRSAEFKNALAKLRAEAKKSGDDKKPSFKTVWQAVKYGLNG					
	70	80	90	100	110	120
m703.pep	130	140	150	160	170	180
	EAYALHIAKTQPVSEQEVKAAYDNISGFYKGTQEVQLGEILTQKEENAKKAVADLKAKKG					
a703	EAYALHIAKTQPVSEQEVKAAYDNISGFYKGTQEVQLGEILTQKEENAKKAVADLKAKKG					
	130	140	150	160	170	180
m703.pep	190	200	210	220	230	240
	FDAVLKQYSLNDRTKQTGAPVGVVPLKDLEQGVPPLYQAIKDLKKGEFTATPLKNGDFYG					
a703	FDAVLKQYSLNDRTKQTGAPVGVVPLKDLEQGVPPLYQAIKDLKKGEFTATPLKNGDFYG					
	190	200	210	220	230	240
m703.pep	250	260	270	280	289	
	VYYVNSREVKVPSFDEMKGQIAGNLQAERIDRAVGALLGKANIKPAKX					
a703	VYYVNSREVKVPSFDEMKGQIAGNLQAERIDRAVGALLGKANIKPAKX					
	250	260	270	280		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2355>:

a704.seq

1 ATGAAAAAAA CCTGTTTCCA CTGCGGGCTG GACGTTCCCG AAAACCTGCA
 51 TCTGACCGTC CGTTACGAAA ACGAAGACCG CGAAACCTGC TGCGCCGGTT
 101 GTCAGGCAGT CGCACAAAGC ATTATTGACG CGGGCTTGGG CAGTTATTAC
 151 AAACAACGCA CCGCCGACGC GCAAAAAACC GAGCTGCCCG CCCAAGAAAT
 201 CCTCGACCAA ATCCGCCTGT ACGACCTGCC CGAAGTCCAG TCCGACTTTG
 251 TGGAAACCCA CGCGGGCACG CGCGAGGCGG TTTTATGCT CGGCGGCATC
 301 ACCTGCGCCG CTGCGTCTG GCTGATCGAA CAGCAGCTTT TGCCTACAGA
 351 CGGCATCGTC CGCATCGACC TCAATTACAG CACGCACCGC TGCCGCGTCG
 401 TCTGGGACGA CGGCAAAATC CGCCTTCCG ACATTCTGTT GAAAAACAGG
 451 CAGATAGGCT ACACCGCCGC ACCCTATGAC GCGCAAAAAA TCGAAGCCCG
 501 CAACCAAAAA GAACGCAAAC AATACATCGT CCGCCTCGCC GTTGCCGGGC
 551 TGGGGATGAT GCAGACGATG ATGTTGCGCG TGCCGACCTA CCTTTACGGC
 601 GGCACATCG AACCCGATTT CCTGCAAATC CTCCATTGGG GCGGCTTTTT
 651 AATGGTGCTG CCCGTCGTAT TCTATGCGCG CGTCCGTTT TATCAAGCGC
 701 CGCTGCGCGA CTTGAAAAAC CGCCGCGTCG GCATGGATAC GCCGATTACC
 751 GTCGCCATCA TCATGACCTT TATCGCCGGC GTTTACAGCC TTGCGACAAA

```

801 TCGGGGGCAG GGGATGTATT TCGAATCCAT CGCGATGCTG CTGTTTTC
851 TGCTGGGCGG ACGCTTTATG GAACACATTG CCCGCCGTAA GGCAGGCGAT
901 GCGGCCGAGA GGCTGGTGAA GCTGATTCCT GCGTTTGGCC ATCATATGCC
951 CGATTACCCC GATACGCAGC AAACCTGCGA GGCAGCTGTC STCAAATTGA
1001 AGGCGGGCGA TATCGTGCTG GTCAAACCGG GCGAAACCAT CCCCCTTGAC
1051 GGCACGGTGC TGGAAGGAAG CAGTGCCGTC AACGAATCTA TGCTGACCGG
1101 CGAGAGCCTG CCCGTCGCCA AAATGCCGTC TGAAAAAGTA ACCGCCGGCA
1151 CACTCAACAC GCAAAGCCCC CTGATTATAC GCACCGACCG CACCGCGCGC
1201 GGCACGCGAC TGTCGCACAT CGTCCGCTG CTCGACCGCG CCTTAGCGCA
1251 AAAACCGCGC ACTGCCGAGT TGGCGGAACA ATACGCCTCG TCTTTCATAT
1301 TCGGGCAACT CCTGTGTGCC GTCCCGCTCT TCATCGGCTG GACGCTGTAC
1351 GCGGACGCGC ACACCGCATT GTGGATTACC GTCGCCCTGC TGGTCATTAC
1401 CTGCCCCCTG GCCTTATCGC TTGCCACGCC GACCGCGCTG GCAGCTTCTA
1451 CCGGTACGCT GCGCGCGCAA GGTATTTTAA TCGGCGGAAA GCAGGCAATC
1501 GAAACCCTCG CCCAAACCAC CGACATCATC TTCGACAAAA CCGGCACGCT
1551 GACCCAAGGC AAACCCGCGC TCCGCCGTAT CTCATTGTTG AGAGGCACAG
1601 ACGAAGCCTT TGTTCGCG GTGGCGCAGG CTTTAGAACA ACAGTCCGAA
1651 CATCCCTTGG CCCGCCCAT CCTCAACTGC CGCATTTCAG ACGGCAGCGT
1701 CCGGACATC GCTATTAAAC AACGCCTCAA CCGCATCGGC GAAGGCGTGG
1751 GCGCGCAACT GACCGTCAAC GCGGAAACAC AGGTTTGGGC ATTGGGCAGG
1801 GCATCCTATG TCGCCGAAAT TTCAGGTAAG GAACCGCAA CAGAAGGCGG
1851 CCGCAGCGCG GTTACCTCG GCAGTCAAAG CGGTTTCAA GCCGTGTTCT
1901 ACCTGCAAGA CCCGCTCAA GACAGCGCGG CGGAGGCGGT GCGGCAGTTG
1951 GCAGGCAAAA ACCTGACGCT GCACATTCTC AGCGCGGACC GTGAAACCGC
2001 CGTTGCCGAA ACCGCACGCG CCCTGGGTGT CGCGCACTAC CGCGCCCAAG
2051 CCATGCCCGA GGACAAACTG GAATACGTCA AAGCCTTGCA AAAAGAAGGG
2101 AAAAAAGTGC TGATGATAGG CGACGGCATC AACGACGCGC CCGTTTGGC
2151 GCAGGCGAGC GTATCCGCGC CCGCAGCGGG CGGACGGAT ATTGCGAGGG
2201 ACGGCGCGGA CATTGTGTTA TTGAACGAAG ATTTGCGTAC CGTCGCCCCA
2251 CTGCTCGATC AGGCGCGGCG CACCGCGCA ATTATCCGG AAAACCTGAT
2301 ATGGGCGGGC GCGTACAATA TCATTGCCGT ACCGCTTGCC GTTTTGGGCT
2351 ATGTCCAACC GTGGATAGCC GCACTGGGTA TGAGCTTCAG TTCGCTGGCG
2401 GTTTTGGGCA ACGCCCTGCG CCTTCACAAA CGGGGAAAA TGCAGTCTGA
2451 AAAAATGCCG TCCGAACAAT GA

```

This corresponds to the amino acid sequence <SEQ ID 2356; ORF 703>:

```

a704.pep
1 MKKTCFHCGL DVPENLHLTV RYENEDRET CAGCQAVAS IIDAGLSYY
51 KQRTADAQKT ELPPQEILDQ IRLYDLPEVQ SDFVETHGGT REAVLMLGGI
101 TCAACVWLIE QLLRTDGI RYENEDRET CAGCQAVAS IIDAGLSYY
151 QIGYTAAPYD AQKIEAANQK ERKQYIVRLA VAGLGMQTM MFALEPTYLYG
201 GDIEPDLQI LHWGGFLMVL FVVFYCAVPF YQALRLDLKN RRVGMDTPIT
251 VAIIMTFIAG VYSLATNAGQ GMYFESIAML LFFLLGGRFM EHIARRKAGD
301 AAERLVKLIP AFCHHMPDYP DTQETCEAAV VKLKAGDIVL VKPGETIPVD
351 GTVLEGSSAV NESMLTGESL FVAKMPSEKV TAGTLNTQSP LIIRTDRTGG
401 GTRLSHIVRL LDRALAQKPR TAEALAEQYAS SFIFGELLVA VPVFIGWTLY
451 ADAHTALWIT VALLVITCPC ALSLATPTAL AASTGTLARE GILIGGKQAI
501 ETLAQTDDII FDKTGTLTQG KPAVRRISLL RGTDEAFVLA VAQALEQQSE
551 HPLARAILNC RISDGSVPDI AIKQRLNRIG EGVGAQLTVN GETQVWALGR
601 ASYVAEISGK EPQTEGGGSA VYLSQSGFQ AVFYLDPLK DSAAEAVRQL
651 AGKNLTLHLI SGDRETAVAE TARALGVAHY RAQAMPEDKL EYVKALQKEG
701 KKVLMIGDGI NDAPVLAQAD VSAAGAGTD IARDGADIVL LNEDLRTVAH
751 LLDQARRTRH IIRQNLIWAG AYNIIAVPLA VLGYPQWIA AIGMSFSSLA
801 VLGNALRLHK RGKMQSEKMP SEQ*

```

m704/a704 99.8% identity in 823 aa overlap

```

          10      20      30      40      50      60
m704.pep MKKTCFHCGLDVPENLHLTVRYENEDRETCCAGCQAVASIIDAGLSYYKQRTADAQKT
          |||
a704      MKKTCFHCGLDVPENLHLTVRYENEDRETCCAGCQAVASIIDAGLSYYKQRTADAQKT
          |||
          10      20      30      40      50      60

          70      80      90     100     110     120
m704.pep ELPPQEILDQIRLYDLPEVQSDFVETHGGTREAVLMLGGITCAACVWLIEQQLRTDGI
          |||
a704      ELPPQEILDQIRLYDLPEVQSDFVETHGGTREAVLMLGGITCAACVWLIEQQLRTDGI
          |||

```

1132

	70	80	90	100	110	120
m704.pep	130	140	150	160	170	180
a704	130	140	150	160	170	180
m704.pep	190	200	210	220	230	240
a704	190	200	210	220	230	240
m704.pep	250	260	270	280	290	300
a704	250	260	270	280	290	300
m704.pep	310	320	330	340	350	360
a704	310	320	330	340	350	360
m704.pep	370	380	390	400	410	420
a704	370	380	390	400	410	420
m704.pep	430	440	450	460	470	480
a704	430	440	450	460	470	480
m704.pep	490	500	510	520	530	540
a704	490	500	510	520	530	540
m704.pep	550	560	570	580	590	600
a704	550	560	570	580	590	600
m704.pep	610	620	630	640	650	660
a704	610	620	630	640	650	660
m704.pep	670	680	690	700	710	720
a704	670	680	690	700	710	720
m704.pep	730	740	750	760	770	780
a704	730	740	750	760	770	780
m704.pep	790	800	810	820		
a704	790	800	810	820		

RIDLNYSTHRCRVVWDDGKIRLS DILLKIRQIGYTAAPYDAQKIEAANQKERKQYIVRLA
|||||
RIDLNYSTHRCRVVWDDGKIRLS DILLKIRQIGYTAAPYDAQKIEAANQKERKQYIVRLA
|||||
VAGLGMMQTMFALPTYLYGGDIEPDFLQILHWGGFLMVLPPVVFYCAVPFFYQGALRDLKN
|||||
VAGLGMMQTMFALPTYLYGGDIEPDFLQILHWGGFLMVLPPVVFYCAVPFFYQGALRDLKN
|||||
RRVGMDTPITVAIIMTFIAGVYSLATNAGQGMFYFESIAMLLFFLLGGRFMEHIARRKAGD
|||||
RRVGMDTPITVAIIMTFIAGVYSLATNAGQGMFYFESIAMLLFFLLGGRFMEHIARRKAGD
|||||
AAERLVKLI PAFCHHMPDYPDTQETCEAAVVKLRAGDIVLKPGETIPVDGTVLEGSSAV
|||||
AAERLVKLI PAFCHHMPDYPDTQETCEAAVVKLRAGDIVLKPGETIPVDGTVLEGSSAV
|||||
NESMLTGESLPVAKMPSEKVTAGTLNTQSPLIIRTDRTGGGTRL SHIVRLLDRALAQKPR
|||||
NESMLTGESLPVAKMPSEKVTAGTLNTQSPLIIRTDRTGGGTRL SHIVRLLDRALAQKPR
|||||
TAE LAEQYASSFI FGELLAVPVFIGWTL YADAHTALWITVALLVITCPCALSLATPTAL
|||||
TAE LAEQYASSFI FGELLAVPVFIGWTL YADAHTALWITVALLVITCPCALSLATPTAL
|||||
AASGTGLAREGILIGGKQAIETLAQTDDIIFDKTGTLTQGGKPAVRRISLLRGTD EAFVLA
|||||
AASGTGLAREGILIGGKQAIETLAQTDDIIFDKTGTLTQGGKPAVRRISLLRGTD EAFVLA
|||||
VAQALEQQSEHPLARAILNCRISDGSVPDIAIKQRLNRIGEGVGAQLTVNGETQVWALGR
|||||
VAQALEQQSEHPLARAILNCRISDGSVPDIAIKQRLNRIGEGVGAQLTVNGETQVWALGR
|||||
ASYVAEISGKEPQTEGGGS AVYLGSGFQAVFYLTDP LKDSAAEAVRQLAGKNLTLHIL
|||||
ASYVAEISGKEPQTEGGGS AVYLGSGFQAVFYLTDP LKDSAAEAVRQLAGKNLTLHIL
|||||
SGDRETAVAETARALGV AHYRAQAMPEDKLEYVKALQKEGKKVLMIGDGIN DAPVLAQAD
|||||
SGDRETAVAETARALGV AHYRAQAMPEDKLEYVKALQKEGKKVLMIGDGIN DAPVLAQAD
|||||
VSAAAAGGTDIARDGADIVLLNEDLRTVAHLLDQARRTRHII RQNLIWAGAYNIIAVPLA
|||||
VSAAAAGGTDIARDGADIVLLNEDLRTVAHLLDQARRTRHII RQNLIWAGAYNIIAVPLA
|||||
VLGYVQPWIAALGMSFSS LAVLGNALRLHKRGKMQSEKMPSEQX
|||||
VLGYVQPWIAALGMSFSS LAVLGNALRLHKRGKMQSEKMPSEQX
|||||

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2357>:

```
g705.seq
1  GTGTTCAATA ATTCCTtgc CTCTCIGCCG TTTATGACGG AAACACGCGC
51  TGATATGCTC ATCAGCGCGT TTTGGCCCAT GGTAAAGCC GGCTTTACAG
101 TGCTCTtgc TTTGGCGATC GCTTCITTCG TTATCGGCAT GATTATTGCC
151 GTAGCCGTTG CTTTGGTAAG AATCATGCCT TCCGGCGGTA TTTCCAAAA
201 ATGCTTGTtG AAGCTGGTGG AATTTTATAT TTCCGTCGTT CGCGGTACGC
251 CGCTGTtGGT TCAGCTTGTG ATTGTGTTTT ACGGGCTGCC GTCCGTCGGC
301 ATCTATATCA ATCCGATTCC CGCCGCCATC ATCGGCTTTT CGCTCAATGT
351 CGCGGCATAC GCTTCCGAAA CCATACGCGC GCGGATTTTG TCCGTGCCGA
401 AAGGGCAGTG GGAAGCAGGT TTCTCCATCG GTATGACCTA TATGCAGACG
451 TTCCGCGGCA TCGTCGCACC GCAGGCATTC CGCGTCGCCG TTCCGCCGTT
501 GAGCAACGAG TTTATCGGCT TGTCAAAAA CACCTCGCTT GCCGCCGTGG
551 TAACGGTAAC GGAGCTTTTC CGTGTCCGAC AGGAAACGGC AAACCGCACT
601 TATGACTTTT TGCCTGTCTA TATCGAAGCT GCATTGTTTT ATTGGTGTtT
651 CTGTAAGTG CTGTTTTTGA TTCAGGCGCG TTTGAAAAA CGTTTCGACC
701 GTTATGTCGC CAAATAA
```

This corresponds to the amino acid sequence <SEQ ID 2358; ORF 705>:

```
g705.pep
1  VFNNFLASLP FMTETRADML ISAFWPMVKA GFTVSLPLAI ASFVIGMIIA
51  VAVALVRIMP SGGIFQKCLL KLVEFYISVV RGTPLLVLV IVFYGLPSVG
101 IYINPIPAAI IGFSNLVGAY ASETIRAAIL SVPKGQWEAG FSIGMTYMQT
151 FRRIVAPQAF RVAVPPLSNE FIGLFKNTSL AAVVTVTELF RVAQETANRT
201 YDFLPVYIEA ALVYWCFCKV LFLIQARLEK RFDYVAK*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2359>:

```
m705.seq
1  GTGTTCAATA ATTCCTTGC TTCGCTGCCG TTTATGACGG AAACACGCGC
51  CGATATGATT GTCAGCGCGT TTTTGCCATAT GGTCAAAGCC GGCTTCGCGG
101 TCTCTCTGCC TTTGGCGGCA GCTTCITTCG TTATCGGTAT GATGATTGCG
151 GTAGCCGTTG CTTTGGTGGC GATTATGCCG GCCGGCGGCA TCGTCGGGAA
201 AATCTCTGCTG AAATTGGTGG AATTTTATAT TTCCGTCATT CGCGGTACGC
251 CGCTGTtGGT TCAGCTTGTG ATTGTGTTTT ACGGGCTGCC TTCCGTCGGC
301 ATCTATATCG ACCCGATTCC TGCCGCCATC ATCGGCTTTT CGCTCAATGT
351 CGCGGCATAC GCTTCCGAAA CCATACGCGC GGCAATTTTG TCCGTACCTA
401 AAGGCCAATG GGAAGCAGGT TTCTCCATCG GCATGACCTA TATGCAGACG
451 TTCCGCGCGCA TTGTGCGGCC GCAGGCATTC CGCGTTGCCG TGCCGCTTT
501 GAGCAACGAG TTTATCGGTT TGTTAAAAA CACCTCGCTC GCGGCAGTCG
551 TGACGGTAAC GGAATTATTC CGCGTCGCGC AGGAAACGGC AAACCGCACT
601 TATGACTTTT TGCCCGTCTA TATCGAAGCT GCTTTGTTT ACTGGTGTtT
651 TTGTAAGTG CTGTTCTTGA TTCAGGCGCG TTTGAAAAA CGTTTCGACC
701 GCTACGTCGC CAAATAA
```

This corresponds to the amino acid sequence <SEQ ID 2360; ORF 705>:

```
m705.pep
1  VFNNFLASLP FMTETRADMI VSAFLPMVKA GFAVSLPLAA ASFVIGMMIA
51  VAVALVRIMP AGGIVRKILL KLVEFYISVI RGTPLLVLV IVFYGLPSVG
101 IYIDPIPAAI IGFSNLVGAY ASETIRAAIL SVPKGQWEAG FSIGMTYMQT
151 FRRIVAPQAF RVAVPPLSNE FIGLFKNTSL AAVVTVTELF RVAQETANRT
201 YDFLPVYIEA ALVYWCFCKV LFLIQARLEK RFDYVAK*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 705 shows 95.0% identity over a 238 aa overlap with a predicted ORF (ORF 705) from *N. gonorrhoeae*:

```
m705/g705 95.0% identity in 238 aa overlap

          10      20      30      40      50      60
m705.pep  VFNNFLASLPFMTETRADMIVSAFLPMVKAGFAVSLPLAAASFVIGMMIAVAVALVRIMP
          |||::||| |||||:|||| |||||:||||| |||||:|||||
g705       VFNNFLASLPFMTETRADMLISAFWPMVKAFTVSLPLAIASFVIGMIIAVALVRIMP
          10      20      30      40      50      60

          70      80      90     100     110     120
m705.pep  AGGIVRKILLKLVEFYISVIRGTPLLVLVIVFYGLPSVGIYIDPIPAAIIGFSNLVGAY
          |||:| |||||:|||||:|||||:|||||:|||||:|||||:|||||
```

```

g705      SGGIFQKCLKLVEFYISVVRGTPLLVQLVVFYGLPSVGIYINPIAAIIGFSLNVGAY
           70      80      90      100     110     120

           130     140     150     160     170     180
m705.pep  ASETIRAAILSVPKQWEAGFSIGMTYMQTFRRIVAPQAFRVAVPPLSNEFIGLFKNTSL
           |||
g705      ASETIRAAILSVPKQWEAGFSIGMTYMQTFRRIVAPQAFRVAVPPLSNEFIGLFKNTSL
           130     140     150     160     170     180

           190     200     210     220     230     239
m705.pep  AAVVTVTELFRAVQETANRTYDFLPVYIEAALVYWCFCVKVFLIARLEKRFDRYVAKX
           |||
g705      AAVVTVTELFRAVQETANRTYDFLPVYIEAALVYWCFCVKVFLIARLEKRFDRYVAKX
           190     200     210     220     230

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2361>:

```

a705.seq
1  GTGTTCATAA ATTCCTTGC TTCGCTGCCG TTTATGACGG AACACGCGC
51  CGATATGATT GTCAGCGCGT TTTGCTTAT GGTCAAAGCC GGCTTCGCGG
101 TCTCTCTGCC TTTGGCGGCA GCTTCTTTCG TTATCGGTAT GATGATTGCG
151 GTAGCCGTGG CTTTGGTGGC GATTATGCCC GCCGGCGGCA TCGTGCGGAA
201 AATCCTGCTG AAATGGTGG AAATTTATAT TTCCGTCATT CGCGGTACGC
251 CGCTGTTGGT TCAGCTTGTG ATTGTGTTT ACGGGCTGCC TTCCGTCGGC
301 TTCCGCTATCG ACCCGATTCC TGCCGCCATC ATCGGCTTT CGCTCAATGT
351 CGGCGCATAT GCTTCCGAAA CCATACGCGC GGCAATTTG TCCGTACCGA
401 AAGGCCAATG GGAAGCAGGT TTCTCCATCG GCATGACCTA TATGCAGACG
451 TTCCGCGCGCA TCGTCGCGCC GCAGGCATTT CGCGTTGCCG TGCCGCTTT
501 GAGCAACGAG TTTATCGGTT TGTTTAAAAA CACCTCGCTC GCGGCAGTCG
551 TGACGGTAAC GGAATTATTC CGCGTCGCGC AGGAAACGCG AAACCGCACT
601 TATGACTTTT TGCCCGTCTA TATCGAAGCC GCTTTGGTTT ACTGGTGT
651 TTGTAAAGTG CTGTCTCTGA TTCAGGCGCG TTTGAAAAA CGTTTCGACC
701 GCTACGTCGC CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2362; ORF 705.a>:

```

a705.pep
1  VFNNFLASLP FMTETRADMI VSAFLPNVKA GFAVSLPLAA ASFVIGMMIA
51  VAVALVRMP AGGIVRKILL KLVEFYISVI RGTPLLVLV IVFYGLPSVG
101 IYIDPIAAI IGFSNLVGAY ASETIRAAIL SVPKQWEAG FSIGMTYMQT
151 FRRIVAPQAF RVAVPPLSNE FIGLFKNTSL AAVVTVTELF RVAQETANRT
201 YDFLPVYIEA ALVYWCFCVK LFLIARLEK RFDRYVAK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N meningitidis*

ORF 705 shows 100.0% identity over a 238 aa overlap with a predicted ORF (ORF 705) from *N. meningitidis*:

a705/m705 100.0% identity in 238 aa overlap

```

a705.pep      10      20      30      40      50      60
VFNNFLASLPFMTETRADMIVSAFLPMVKAGFAVSLPLAAASFVIGMMIAVAVALVRIMP
|||||
m705          10      20      30      40      50      60
VFNNFLASLPFMTETRADMIVSAFLPMVKAGFAVSLPLAAASFVIGMMIAVAVALVRIMP

a705.pep      70      80      90      100     110     120
AGGIVRKILLKLVEFYISVIRGTPLLVQLVIVFYGLPSVGIYIDPIAAIIGFSLNVGAY
|||||
m705          70      80      90      100     110     120
AGGIVRKILLKLVEFYISVIRGTPLLVQLVIVFYGLPSVGIYIDPIAAIIGFSLNVGAY

a705.pep      130     140     150     160     170     180
ASETIRAAILSVPKQWEAGFSIGMTYMQTFRRIVAPQAFRVAVPPLSNEFIGLFKNTSL
|||||
m705          130     140     150     160     170     180
ASETIRAAILSVPKQWEAGFSIGMTYMQTFRRIVAPQAFRVAVPPLSNEFIGLFKNTSL

a705.pep      190     200     210     220     230     239
AAVVTVTELFRAVQETANRTYDFLPVYIEAALVYWCFCVKVFLIARLEKRFDRYVAKX
|||||
m705          190     200     210     220     230
AAVVTVTELFRAVQETANRTYDFLPVYIEAALVYWCFCVKVFLIARLEKRFDRYVAKX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2363>:

g706.seq

```

1  ATGAACTCCT CGCAACGCAA ACGCCTTTCC GgccGCTGGC TCAACTCCTA
51  CGAACGCTAc cGCCaccGCC GCCTCATACA TGCCGTGCGG CTCGGCggaa
101 cctgCCTGTT CGCCACCGCA CTCGCCCGgc tACTCCACCT CCAacacggc
151 gAATGGATAG GGatgaCCGT CTTGTCGTC CTCGGCATGC TCCAGTTCCA
201 AGGCgcgatt tActccaacg cgggtgGAacg taTGctcggg acggtcatcg
251 ggcctgGGCGC GGGTTTGGgc gTTTATGGC TGAACCAGCA TTattccac
301 ggcaacCTcc tctttacct gaccatcggc acggcaacg cactggccgg
351 ctGGGCGGCG GTCGGCAAAA acggctacgt ccctatgctg GCGGGGctgA
401 CGATGTGCAT gctcatcggc gACAAcGGCA GCGAATGGCT CGACAGCGGC
451 CTGATGCGCG CGATGAACGT CCTCATCGGC GCCGCCATCG CCATTGCCGC
501 CGCCAAACTG CTGCCGCTGA AATCCACACT GATGTGGCGT TTCATGCTTG
551 CGCACAACTT GGCCGACTGC AGCAAAATGA TTGCCGAAAT CAGCAACGGC
601 AGGCGTATGA CGCGCGAACG TTTGGAGCAG AATATGGTCA AAATGCGCCA
651 AATCAACGCA CGCATGGTCA AAAGCCGCAG CCACCTCGCC GCCACATCGG
701 GCGAAAGCCG CATCAGCCCC TCCATGATGG AAGCCATGCA GCACGCCAC
751 CGCAAAATCG TCAACACCAC CGAGCTGCTC CTGACCACCG CCGCCAAGCT
801 GCAATCTCCC AAACCTCAACG GCAGCGAAAT CCGGCTGCTC GACCGCCACT
851 TCACACTGCT CCAAACCGAC CTGCAACAAA CCGCGCCCT CATCAACGGC
901 AGACACGCCC GCCGCATCCG CATCGACACC GCCATCAACC CCGAACTGGA
951 AGCCCTCGCC GAACACCTCC ACTACCAATG GCAGGGCTTC CTCTGGCTCA
1001 GCACCAATAT GCGTCAGGAA ATTTCCGCCC TCGTCATCCT GCTGCAACGC
1051 ACCCGCCGCA AATGGCTGGA TGCCACGAA CGCCAACACC TGCGCCAAAG
1101 CCTGCTTGA ACACGGGAAC ACGGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2364; ORF 706.ng>:

g706.pep

```

1  MNSSQRKRLS GRWLNSYERY RHRRLIHAVR LGGTVLFAFA LARLLHLQHG
51  EWIGMTVFVV LGMLQFQGA I YSNAVERMLG TVIGLGAGLG VLWLNQHYFH
101 GNLLFYLTIG TASALAGWAA VGKNGYVPM L AGLTMCMLIG DNGSEWLDSG
151 LMRAMNVLI G AAIATAAKL LPLKSTLMWR FMLADNLADC SKMIAEISNG
201 RRMTRERLEQ NMVKMRQINA RMVKSRSHLA ATSGESRISP SMMEAMQHAH
251 RKIVNTTELL LTAAKLQSP KLNQSEIRLL DRHFTLLQTD LQQTVALING
301 RHARRIRIDT AINPELEALA EHLHYQWQGF LWLSTNMRQE ISALVILLQR
351 TRRWLDAHE RQHLRQSLLE TREHG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2365>:

m706.seq

```

1  ATGAACACCT CGCAACGCAA CCGCCTCGTC AGCCGCTGGC TCAACTCCTA
51  CGAACGCTAC CGCTACCGCC GCCTCATCCA CGCCGTCCGG CTCGGCGGGG
101 CCGTCTGTT CGCCACCGCC TCCGCCCGGC TGCTCCACCT CCAACACGGC
151 GAGTGGATAG GGATGACCGT CTTGTCGTC CTCGGCATGC TCCAGTTTCA
201 AGGGGCGATT TACTCCAAGG CGGTGGAACG TATGCTCGGC ACGGTCATCG
251 GGCTGGGCGC GGGTTTGGGC GTTTTATGGC TGAACCAGCA TTATTTCCAC
301 GGCAACCTCC TCTTCTACCT CACCGTCGGC ACGGCAAGCG CACTGGCCGG
351 CTGGGCGGCG GTCGGCAAAA ACGGCTACGT CCCTATGCTG GCAGGGCTGA
401 CGATGTGTAT GCTCATCGGC GACAACGGCA GCGAATGGCT CGACAGCGGA
451 CTCATGCGCG CCATGAACGT CCTCATCGGC GCGCCATCG CCATCGCCGC
501 CGCCAACTG CTGCCGCTGA AATCCACACT GATGTGGCGT TTCATGCTTG
551 CCGCAACCTT GGCCGACTGC AGCAAAATGA TTGCCGAAAT CAGCAACGGC
601 AGGCGCATGA CCCGCGAACG CCTCGAGGAG AACATGGCGA AAATGCGCCA
651 AATCAACGCA CGCATGGTCA AAAGCCGCAG CCATCTCGCC GCCACATCGG
701 GCGAAAGCCG CATCAGCCCC GCCATGATGG AAGCCATGCA GCACGCCAC
751 CGTAAATCG TCAACACCAC CGAGCTGCTC CTGACCACCG CCGCCAAGCT
801 GCAATCTCCC AAACCTCAACG GCAGCGAAAT CCGGCTGCTT GACCGCCACT
851 TCACACTGCT CCAAACCGAC CTGCAACAAA CCGTCGCCCT TATCAACGGC
901 AGACACGCCC GCCGCATCCG CATCGACACC GCCATCAACC CCGAACTGGA
951 AGCCCTCGCC GAACACCTCC ACTACCAATG GCAGGGCTTC CTCTGGCTCA
1001 GCACCAATAT GCGTCAGGAA ATTTCCGCCC TCGTCATCCT GCTGCAACGC
1051 ACCCGCCGCA AATGGCTGGA TGCCACGAA CGCCAACACC TGCGCCAAAG
1101 CCTGCTTGA ACACGGGAAC ACGGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2366; ORF 706>:

m706.pep

```

1  MNTSQRNRLV SRWLNSYERY RYRRLIHAVR LGGAFLFAFA SARLLHLQHG
51  EWIGMTVFVV LGMLQFQGA I YSKAVERMLG TVIGLGAGLG VLWLNQHYFH
101 GNLLFYLTIG TASALAGWAA VGKNGYVPM L AGLTMCMLIG DNGSEWLDSG
151 LMRAMNVLI G AAIATAAKL LPLKSTLMWR FMLADNLADC SKMIAEISNG
201 RRMTRERLEE NMAKMRQINA RMVKSRSHLA ATSGESRISP AMMEAMQHAH
251 RKIVNTTELL LTAAKLQSP KLNQSEIRLL DRHFTLLQTD LQQTVALING

```


301 RHARRIRIDT AINPELEALA EHLHYQWQGF LWLSTNMROE ISALVILLQR
 351 TRRKWLDAHE RQHLRQSLLE TREHG*

m706/g706 96.5% identity in 375 aa overlap

	10	20	30	40	50	60
m706.pep	MNTSQRNRLVSRWLNSEYERYRRLIHAVRLGGAVLFATASARLLHLQHGEWIGMTVFVV					
	: : : : : :					
g706	MNSSQRKRLSGRWLNSEYERYRRLIHAVRLGGTVLFATALARLLHLQHGEWIGMTVFVV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m706.pep	LGMLQFQGAISKAVERMLGTVIGLGAGLGVLWLNQHYFHGNLLFYLTVGTSALAGWAA					
	: : : : : :					
g706	LGMLQFQGAISNAVERMLGTVIGLGAGLGVLWLNQHYFHGNLLFYLTIGTSALAGWAA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m706.pep	VGKNGYVPMLAGLTMCLIGDNGSEWLDSEGLMRAMNVLIGAAIAIAAKLLPLKSTLMWR					
	: : : : : :					
g706	VGKNGYVPMLAGLTMCLIGDNGSEWLDSEGLMRAMNVLIGAAIAIAAKLLPLKSTLMWR					
	130	140	150	160	170	180
	190	200	210	220	230	240
m706.pep	FMLADNLADCSKMAEISNGRRMTRERLEENMAKMRQINARMVKSRSHLAATSGESRISP					
	: : : : : :					
g706	FMLADNLADCSKMAEISNGRRMTRERLEQNVMKMRQINARMVKSRSHLAATSGESRISP					
	190	200	210	220	230	240
	250	260	270	280	290	300
m706.pep	AMMEAMQHAHRKIVNTTELLTTAAKLQSPKXNGSEIRLLDRHFTLLQTDLOQTVALING					
	: : : : : :					
g706	SMMEAMQHAHRKIVNTTELLTTAAKLQSPKXNGSEIRLLDRHFTLLQTDLOQTAALING					
	250	260	270	280	290	300
	310	320	330	340	350	360
m706.pep	RHARRIRIDTAINPELEALAEHLHYQWQGF LWLSTNMROEISALVILLQTRRKWLDAHE					
	: : : : : :					
g706	RHARRIRIDTAINPELEALAEHLHYQWQGF LWLSTNMROEISALVILLQTRRKWLDAHE					
	310	320	330	340	350	360
	370					
m706.pep	RQHLRQSLLETREHGX					
	: : : : :					
g706	RQHLRQSLLETREHGX					
	370					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2367>:

a706.seq

1	ATGAACACCT	CGCAACGCAA	CGGCCTCGTC	AGCCGCTGGC	TCAACTCCTA
51	CGAACGCTAC	CGCTACCGCC	GCCTCATCCA	CGCCGTCCGG	CTCGGCGGGG
101	CCGTCCTGTT	CGCCACCGCC	TCCGCCCGGC	TGCTCCACCT	CCAACACGGC
151	GAGTGGATAG	GGATGACCGT	CTTCGTCGTC	CTCGGCATGC	TCCAGTTTCA
201	AGGGGCGATT	TACTCCAAGG	CGGTGGAACG	TATGCTCGGC	ACGGTCATCG
251	GGCTGGGCGC	GGTTTGCGC	GTTTATGGC	TGAACCAGCA	TTATTCCAC
301	GGCAACCTCC	TCTTCTACCT	CACCGTCGGC	ACGGCAAGCG	CACTGGCCGG
351	CTGGGCGGCG	GTCGGCAAAA	ACGGCTACGT	CCCTATGCTG	GCGGGGCTGA
401	CGATGTGCAT	GCTCATCGGC	GACAACGGCA	GCGAATGGTT	CGACAGCGGC
451	CTGATGCGCG	CGATGAACGT	CCTCATCGGC	GCGGCCATCG	CCATCGCCGC
501	CGCCAAACTG	CTGCCGCTGA	AATCCAACT	GATGTGGCGT	TTATGCTTG
551	CCGACAACCT	GACCGACTGC	AGCAAAATGA	TTGCCGAAAT	CAGCAACGGC
601	AGGCGCATGA	CCCGCGAACG	CCTCGAAGAG	AACATGGCGA	AAATGCGCCA
651	AATCAACGCA	CGCATGGTCA	AAAGCCGCG	CCACCTCGCC	GCCACATCGG
701	CGGAAAGCCG	CATCAGCCCC	GCCATGATGG	AAGCCATGCA	GCACGCCAC
751	CGTAAAATTG	TCAACACCAC	CGAGCTGCTC	CTGACCACCG	CCGCCAAGCT
801	GCAATCTCCC	AAACTCAACG	GCAGCGAAAT	CCGGCTGCTT	GACCGCCACT
851	TCACACTGCT	CCAAACCGAC	CTGCAACAAA	CCGTGCGCCT	TATCAACGGC

1137

```

901 AGACACGCCC GCCGCATCCG CATCGACACC GCCATCAACC CCGAACTGGA
951 AGCCCTCGCC GAACACCTCC ACTACCAATG GCAGGGCTTC CTCTGGCTCA
1001 GCACCAATAT GCGTCAGGAA ATTTCCGCCC TCGTCATCCT GCTGCAACGC
1051 ACCCGCCGCA AATGGCTGGA TGCCACGAA CGCCAACACC TGCGCCAAAG
1101 CCTGCTGAA ACACGGGAAC ACAGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2368; ORF 706.a>:

```

a706.pep
1  MNTSQNRNLV SRWLSYERY RYRRLIHAVR LGGAVLFATA SARLLHLQHG
51 EWIGMTVFVV LGMLQFGAI YSKAVERMLG TVIGLGAGLG VLWLNQHYFH
101 GNLLFYLTVG TASALAGWAA VGKNGYVPM LAGLTMCMLIG DNGSEWFD SG
151 LMRAMNVLIG AAIAIAAAKL LPLKSTLMWR FMLADNLTDC SKMIAEISNG
201 RRMTRERLEE NMAKMRQINA RMVKSRS HLA ATSGESRISP AMMEAMQHAH
251 RKIVNTTELL LTAAKLQSP KLNSEIRLL DRHFTLLQTD LQQTVALING
301 RHARRIRIDT AINPELEALA EHLHYQWQGF LWLSTNMRQE ISALVILLQR
351 TRRKWLDAHE RQHLRQSLE TREHS*

```

a706/m706 99.5% identity in 374 aa overlap

a706.pep	10	20	30	40	50	60
	MNTSQNRNLVSRWLSYERYRYRRLIHAVRLGGAVLFATASARLLHLQHGEWIGMTVFVV					
m706	MNTSQNRNLVSRWLSYERYRYRRLIHAVRLGGAVLFATASARLLHLQHGEWIGMTVFVV					
	10	20	30	40	50	60
a706.pep	70	80	90	100	110	120
	LGMLQFGAIIYSKAVERMLGTVIGLGAGLGVLWLNQHYFHGNLLFYLTVG TASALAGWAA					
m706	LGMLQFGAIIYSKAVERMLGTVIGLGAGLGVLWLNQHYFHGNLLFYLTVG TASALAGWAA					
	70	80	90	100	110	120
a706.pep	130	140	150	160	170	180
	VGKNGYVPM LAGLTMCMLIGDNGSEWFD SGLMRAMNVLIGAAIAIAAAKLLPLKSTLMWR					
m706	VGKNGYVPM LAGLTMCMLIGDNGSEWLD SGLMRAMNVLIGAAIAIAAAKLLPLKSTLMWR					
	130	140	150	160	170	180
a706.pep	190	200	210	220	230	240
	FMLADNLTDCSKMIAEISNGRRMTRERLEENMAKMRQINARMVKSRS HLA ATSGESRISP					
m706	FMLADNLADCSKMIAEISNGRRMTRERLEENMAKMRQINARMVKSRS HLA ATSGESRISP					
	190	200	210	220	230	240
a706.pep	250	260	270	280	290	300
	AMMEAMQHAHRKIVNTTELLLTAAKLQSPKLNSEIRLLDRHFTLLQTD LQQTVALING					
m706	AMMEAMQHAHRKIVNTTELLLTAAKLQSPKLNSEIRLLDRHFTLLQTD LQQTVALING					
	250	260	270	280	290	300
a706.pep	310	320	330	340	350	360
	RHARRIRIDTAINPELEALAEHLHYQWQGF LWLSTNMRQEISALVILLQTRRKWLDAHE					
m706	RHARRIRIDTAINPELEALAEHLHYQWQGF LWLSTNMRQEISALVILLQTRRKWLDAHE					
	310	320	330	340	350	360
a706.pep	370					
	RQHLRQSLE TREHSX					
m706	RQHLRQSLE TREHGX					
	370					

g707.seq not found

g707.pep not found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2369>:

1138

m707.seq

```

1  ATGGAAATTA TTAACGATGC AGAACTTATC CGTTCATGC AGCGTCAGCA
51  GCACATAGAT GCTGAATTGT TAACTGATGC AAATGTCCGT TTCGAGCAAC
101 CATTTGGAGAA GAACAATTAT GTCTGAGTG AAGATGAAAC ACCGTGTACT
151 CGGGTAAATT ACATTAGTTT AGATGATAAG ACGGTGCGCA AATTTCTTT
201 TCTTCCCTCT GTGCTCATGA AAGAAACAGC TTTTAAACT GGGATGTGTT
251 TAGGTTCCAA TAATTTGAGC AGGCTACAAA AAGCCGCGCA ACAGATACTG
301 ATCGTGCGTG GCTACCTCAC TTCCCAAGCT ATTATCCAAC CACAGAATAT
351 GGATTCGGGA ATTCTGAAAT TACGGGTATC AGCAGGCGAA ATAGGGGATA
401 TCCGCTATGA AGAAAAACGG GATGGGAAGT CTGCCGAGGG CAGTATTAGT
451 GCATTCATAA ACAAAATTCC CTTATATAGG AACAAAATTC TCAATCTTCG
501 CGATGTAGAG CAGGGCTTGG AAAACCTGCG TCGTTTGGCG AGTGTTAAAA
551 CAGATATTCA GATTATACCG TCCGAAGAAG AAGGCAAAAG CGATTTACAG
601 ATCAAATGGC AGCAGAATAA ACCCATACGG TTCAGTATCG GTATAGATGA
651 TGCGGGCGGC AAAACGACCG GCAATATCA AGGAAATGTC GCTTTATCGT
701 TCGATAACCC TTTGGGCTTA AGCGATTGT TTTATGTTTC ATATGGACGC
751 GGTTCGCGC ACAAACGGA CTTGACTGAT GCCACCGGTA CGGAACTGA
801 AAGCGGATCC AGAAGTTACA GCGTGCATTA TTCGGTGCCC GTAAAAAAT
851 GGCTGTTTTC TTTTAATCAC AATGGACATC GTTACCAGA AGCAACCGAA
901 GGCTATTCCG TCAATTACGA TTACAACGGC AAACAATATC AGAGCAGCCT
951 GGCGCGCGAG CGCATGCTTT GCGGTAACAG ACTTCATAAA ACTTCAGTCG
1001 GAATGAAATT ATGGACACGC CAACCTATA AATACATCGA CGATGCCGAA
1051 ATCGAAGTAC AACGCCGCCG CTCGTCAGGC TGGGAAGCCG AATTGCGCCA
1101 CCGTGCTTAC CTCAACCGTT GGCAGCTTGA CGGCAAGTTG TCTTACAAAC
1151 GCGSGACCGG CATGCGCAA AGTATGCCTG CACCGAAGA AAACGGCGGC
1201 GATATTCTTC CAGGTACATC TCGTATGAAA ATCATTACTG CCAGTTTGGG
1251 CGCAGCCGCC CCATTTATTT TAGGCAACA GCAGTTTTC TACGCAACCG
1301 CCATTCAAGC TCAATGGAAC AAAACGCCGT TGGTTGCCA AGATAAATTG
1351 TCAATCGGCA GCCGCTACAC CGTTCGCGGA TTTGATGGG AGCAGAGTCT
1401 TTTGCGGAG CGAGGTTTCT ACTGGCAGAA TACTTTAACT TGGTATTTTC
1451 ATCCGAACCA TCAGTTCTAT CTCGGTGCGG ACTATGGCCG CGTATCTGSC
1501 GAAAGTGCAC AATATGTATC GGGCAAGCAG CTGATGGGTG CAGTGGTCGG
1551 CTTGAGAGGA GGGCATAAAG TAGCGGTAT GTTTGCTTAT GATCTGTTT
1601 CCGGCAAGCC GCTTCATAAA CCCAARGGCT TTCAGACGAC CAACACCGTT
1651 TACGGCTTCA ACTTGAATTA CAGTTTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 2370; ORF 707>:

m707.pep

```

1  MEIINDAELI RSMQRQQHID AELLTDANVR FEQPLEKNNY VLSEDETPCT
51  RVNYISLDDK TVRKFSFLPS VLMKETAFKT GMCLGSNNLS RLQKAAQQIL
101 IVRGYLTSA IIQPNMDSG ILKLRSVAGE IGDIREYERK DGKSAEGSIS
151 AFNNKFPLYR NKILNLRDVE QGLENLRRLP SVKTDIQUIP SEEEGKSDLQ
201 IKWQONKPIR FSIIGIDDAGG KTTGKYQGNV ALSFDNPLGL SDFYVSYGR
251 GLAHKTDLTD ATGTETESGS RSYSVHYSVP VKKWLFSFNH NGRHYHEATE
301 GYSVNYDYNG KQYQSSLAEE RMLWRNRLHK TSVGMKLWTR QYKYIDDAE
351 IEVQRRRSAG WEAE LRHRAY LNRWQLDGKL SYKRGTGMRQ SMPAPEENG
401 DILPGTSRNM IITASLDAEA PFILGRQOFF YATAIQAOWN KTLPLVAQDKL
451 SIGSRYTVRG FDGEQSLFGE RGFYQWNTLT WYFHPNHOFY LGADYGRVSG
501 ESAQYVSGEQ LMGAVVGFRC GHKVGCMFAY DLFAGKPLHK PKGFQTTNTV
551 YGFNLNYSF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2371>:

a707.seq

```

1  NTGAAAGAAA CAGCTTTTAA AACTGGGATG TGTTTAGGTT CCAATAATTT
51  GAGCAGGCTA CAAAAAGCCG CGCAACAGAT ACTGATTGTG CGTGGCTACC
101 TCACTTCCCA AGCTATTATC CAACCACAGA ATATGGATTG GGAATTCTG
151 AAATTACGGG TATCAGCAGG CGAAATAGGN GATATCCGCT ATGAAGAAAA
201 ACGGGATGNG AAGTCTGCCG AGGGCAGTAT TAGTGCATTG AATAACAAAN
251 TTCCCTTATA TAGGAACAAA ATTCTCAATC TTCGCGATGT AGAGCAGGGC
301 TTGGA AAAACC TGCGTCGTTT GCCGAGTGTT AAAACAGATA TTCAGATTAT
351 ACCGTCCGAA GAAGAAGGCA AAAGCGATT ACAGATCAAA TGGCAGCAGA
401 ATAAACCCAT ACGGTTTCA GTATCGGTATAG ATGATGCGGG CGGCAAAACG
451 ACCGGCAAAAT ATCAAGGAAA TGTCGCTTTA TCGTNCGATA ACCCTTTGGG
501 NNTAAGCGAT TNGTTTATG TTTTATATGG ACGCGGTTTG GTGCACAAAA
551 CGGACTTGAC TGNTGCCACC GGTACGAAA CTGAAAGCGG ATCCAGAAGT
601 TACAGCGTGC ATTATTCGGT GNNCGTAAAA AAATGGCTGT TTTCTTTTAA
651 TCACAAATGGA CATCGTTACC ACGAAGCAAC CGAAGGCTAT TCCGTCAATT
701 ACGATTACAA CGGCAACAAA TATCAGAGCA GCCTGGCCGC CGAGCGCATG

```

1139

```
751 CTTTGGNNNN NNAGNTTTCN TNAAACTTCA GTCNGAATGA AATTATGGAC
801 ACGCCAAACC TATAAATACA TCGACGATGC CGAAATCGAA GTGCAACGCC
851 GCCGCTCTGC AGGCTGGGAA GCCGAATTGC GCCACCGTGC TTACCTCNAC
901 CGTTGGCAGC TTGACGGCAA GTTGTCTTAC AAACGCGGGA CCGGCATGCG
951 CCAAAGTATG CCCGCACCTG AAGAAAACGG CGGCGGTACT ATTCCAGNCA
1001 NATCCCGTAT GAAAATCATA ACCGCCGGAT TGGATGCAGC GGCCCCGTNT
1051 ATGTTGGGCA AACAGCAGTT TTTCTACGCA ACCGCCATTG AAGCTCAATG
1101 GAACAAAACG CCTTTGGTTG CCCAAGACAA GTTGTCTATC GGCAGCCGCT
1151 ACACCGTTTCG CGGATTGAT GGGGAGCAGA GTCTTTTCGG AGAGCGAGGT
1201 TTCTACTGGC AGAATACTTT AACTTGGTAT TTTTCATCCGA ACCATCAGTT
1251 CTATCTCGGT GCGGACTATG GCCGCGTATC TGGCGAAAGT GCACATATG
1301 TATCGGGCAA GCAGCTGATG GGTGCAGTGG TCGGCTTCAG AGGAGGGCAT
1351 AAAGTAGGCG GTATGTTTGC TTATGATCTG TTTGCCGGCA AGCCGCTTCA
1401 TAAACCCAAA GGCTTTCAGA CGACCAACAC CGTTTACGGC TTCAACTTGA
1451 ATTACAGTTT CTAA
```

This corresponds to the amino acid sequence <SEQ ID 2372; ORF 707.a>:

```
a707.pep
1  XKETAFTKGM CLGSNNLSRL QKAAQQILIV RGYLTSQAI QPQNMDSGIL
51  KLRVSAGEIG DIRYEEKRDX KSAEGSISAF NNKXPLYRNK ILNLRDVEQG
101 LENLRLPSV KTDIQIIPSE EEGKSDLQIK WQONKPIRFS IGIDDAGGKT
151 TGKYQGNVAL SXDNPLGLSD XFYVSYGRGL VHKTDLTXAT GTETESGSR
201 YSVHYSVXVK KWLFSFNHNG HRYHEATEGY SVNYDYNKQ YQSSLAER
251 LWXXXFXXTS VXMKLWTRQT YKYIDDAEIE VQRRRSAGWE AELRHAYLX
301 RWQLDGKLSY KRGTMQRQSM PAPEENGGGT IPXXSRMKII TAGLDAAAPX
351 MLGKQQFFYA TAIQAQWNKT PLVAQDKLSI GSRYTVRGFD GEQSLFGERG
401 FYWQNTLTWY FHPNHQFYLG ADYGRVSGES AQYVSGKQLM GAVVGFRGGH
451 KVGGMFAYDL FAGKPLHKPK GFQTTNTVYG FNLNYSF*
```

a707/m707 95.3% identity in 486 aa overlap

```

                                10      20      30
a707.pep                      XKETAFTKGMCLGSNNLSRLQKAAQQILIVR
                                |||
m707      EDETPCTRVNYISLDDKTVRKFSFLPSVLMKETAFKTMCLGSNNLSRLQKAAQQILIVR
                                50      60      70      80      90     100

                                40      50      60      70      80      90
a707.pep      GYLTSQAIQPPQNMDSGILKLRVSAGEIGDIRYEEKRDXKSAEGSISAFNNKXPLYRNKI
                                |||
m707      GYLTSQAIQPPQNMDSGILKLRVSAGEIGDIRYEEKRDGKSAEGSISAFNNKFPLYRNKI
                                110     120     130     140     150     160

                                100     110     120     130     140     150
a707.pep      LNLRDVEQGLLENLRLPSVKTDIQIIPSEEEGKSDLQIKWQONKPIRFSIGIDDAGGKTT
                                |||
m707      LNLRDVEQGLLENLRLPSVKTDIQIIPSEEEGKSDLQIKWQONKPIRFSIGIDDAGGKTT
                                170     180     190     200     210     220

                                160     170     180     190     200     210
a707.pep      GK YQGNVALSXD NPLGLSDX F YVSYGRGLVHKTDLTXATGTETESGSRSYSVHYSVXVKK
                                |||
m707      GK YQGNVALSFD NPLGLSDL F YVSYGRGLAHTDLTCATGTETESGSRSYSVHYSVPVKK
                                230     240     250     260     270     280

                                220     230     240     250     260     270
a707.pep      WLFSFNHNGHRYHEATEGYSVNYDYNKQYQSSLAERMLWXXXFXXTSVXMKLWTRQTY
                                |||
m707      WLFSFNHNGHRYHEATEGYSVNYDYNKQYQSSLAERMLWRNRLHKTSGVMKLWTRQTY
                                290     300     310     320     330     340

                                280     290     300     310     320     330
a707.pep      KYIDDAEIEVQRRRSAGWEAELRHAYLXRWQLDGKLSYKRGTMQRQSM PAPEENGGGTI
                                |||
m707      KYIDDAEIEVQRRRSAGWEAELRHAYLNRWQLDGKLSYKRGTMQRQSM PAPEENGGDIL
                                350     360     370     380     390     400
```

1140

```

          340      350      360      370      380      390
a707.pep  PXXSRMKIITAGLDAAAPXMLGKQQFFYATAIQAQWNKTPLVAQDKLSIGSRYTVRGFDG
m707      PGTSRMKIITASLDAAAPFILGKQQFFYATAIQAQWNKTPLVAQDKLSIGSRYTVRGFDG
          410      420      430      440      450      460

          400      410      420      430      440      450
a707.pep  EQSLFGERGFYWQNTLTWYFHPNHQFYLGADYGRVSGESAQYVSGKQLMGAVVVGFRGGHK
m707      EQSLFGERGFYWQNTLTWYFHPNHQFYLGADYGRVSGESAQYVSGKQLMGAVVVGFRGGHK
          470      480      490      500      510      520

          460      470      480
a707.pep  VGGMFAYDLFAGKPLHKPKGFQTTNTVYGFNLNYSFX
m707      VGGMFAYDLFAGKPLHKPKGFQTTNTVYGFNLNYSFX
          530      540      550      560

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2373>:

```

g708.seq
1  ATGCCTTTTA AGCCATCCAA ACGAATCTCT TTATTACTTG TTCTTGCCTT
51  GGGCGCGTGC AGCACTTCCT ACCGCCCTC GCGGGCAGAA AAAGCCAATC
101 AGGTTTCCAA TATCAAAACC CAGTTGGCGA TGGAAATATAT GCGCGGTCAG
151 GACTACCGTC AGGCAACGGC AAGTATTGAA GATGCCTTGA AATCGAACCC
201 TAAAAACGAA CTTGCCTGGC TGGTCCGTGC CGAAATCTAT CAATACCTGA
251 AAGTTAACGA CAAGGCGCAG GAAAGTTTCC GGCAAGCCCT CTCCATCAAA
301 CCCGACAGTG CCGAAATCAA CAACAACCTAC GGCTGGTTCC TGTGCGGCAG
351 GCTCAACCGC CTTGCCGAAT CTATGGCATA TTTCGACAAA GCTCTGGCCG
401 ACCCCACCTA CCCGACCCCT TATATTGCCA ACCTGAATAA AGGTATATGC
451 AGCGCAAAAC AGGGGCAATT CGGATTGGCG GAAGCCTATT TGAACGTTT
501 CCTCGCGGCC CAGCCGCAGT TCCCACCCGC ATTTAAAGAA CTGGCGCGCA
551 CCAAAATGCT GGCCGGGCAG TTGGGCGATG CCGATTACTA CTTTAAAAAA
601 TACCAAAGCA GGGTAGAAGT CCTTCAGGCC GATGATTTCG TGCTAGGCTG
651 GAAAATTGCC AAAGCCCTCG GCAACGTGCA GGCGGCATAC GAATATGAAG
701 CACAATTGCA GGCAAAATTC CCCTACTCGG AAGAATTGCA AACCGTCTC
751 ACCGGTCAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 2374; ORF 708.ng>:

```

g708.pep
1  MPFKPSKRIS LLLVLALGAC STSYRPSRAE KANQVSNIKI QLAMEYMRGQ
51  DYRQATASIE DALKSNPKNE LAWLVRAEIY QYLKVNDAQ ESFRQALSIK
101 PDSAEINNNY GWFLCGRLNR PAESMAYFDK ALADPTYPTP YIANLNKGIC
151 SAKQGQFLA EAYLKRSIA QPQFPFAFKE LARTKMLAGQ LGDADYYFKK
201 YQSRVEVLQA DDLGLGWKIA KALGNVQAAY EYEAQLQANF PYSEELQTVL
251 TGG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2375>:

```

m708.seq
1  ATGCCTTTTA AGCCATCCAA ACGAATCTCT TTATTACTCG TTCTTGCCTT
51  GGGCGCGTGC AGCACTTCCT ACCGCCCTC GCGGGCAGAA AAAGCCAATC
101 AGGTTTCCAA TATCAAAACC CAGTTGGCAA TGGAAATATAT GCGCGGTCAG
151 GACTACCGTC AGGCGACGGC AAGTATTGAA GACGCCCTGA AATCGGACCC
201 TAAAAACGAG CTTGCCTGGC TGGTCCGTGC CGAAATCTAT CAATACCTGA
251 AAGTTAACGA CAAGGCGCAG GAAAGTTTCC GGCAAGCCCT CTCCATCAAA
301 CCCGACAGTG CCGAAATCAA CAACAACCTAC GGTGGTTTCC TATGCGGCAG
351 GCTCAACCGC CTTGCCGAAT CTATGGCATA TTTCGACAAA GCTCTGGCCG
401 ACCCCACCTA CCCGACCCCT TATATTGCCA ACCTGAATAA AGGCATATGC
451 AGCGCAAAAC AGGGGCAATT CGGATTGGCG GAAGCCTATT TGAACGTTT
501 CCTCGCGGCC CAGCCGCAGT TCCCACCCGC ATTTAAAGAA CTGGCGCGCA
551 CCAAAATGCT GGCCGGGCAG TTGGGCGATG CCGATTACTA CTTTAAAAAA
601 TACCAAAGCA GGGTAGAAGT CCTTCAGGCC GATCATTTTC TGCTAGGCTG
651 GAAAATTGCC AAAGCCCTCG GCAACGCACA GGCGGCATAC GAATATGAAG
701 CACAATTGCA GGCGAAATTC CCCTACTCGG AAGAATTGCA AACCGTCTC
751 ACCGGTCAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 2376; ORF 708>:

m708.pep

1141

```

1  MPFKPSKRIS LLLVLALGAC STSYRPSRAE KANQVSNIKT QLAMEYMRGQ
51  DYRQATASIE DALKSDPKNE LAWLVRAEIY QYLVNDKAQ ESFRQALSIK
101 PDSAEINNYY GWFLCGRLNR PAESMAYFDK ALADPTYPTP YIANLNKGIC
151 SAKQGQFGLA EAYLKRSIAA QPQFPFAFKE LARTKMLAGQ LGDADYYFKK
201 YQSRVEVLQA DDLLLGWKIA KALGNAQAAY EYEAQLQANF PYSEELQTVL
251 TGQ*

```

m708/g708 99.2% identity in 253 aa overlap

```

              10      20      30      40      50      60
m708.pep      MPFKPSKRISLLLVLALGACSTSYRPSRAEKANQVSNIKTQLAMEYMRGQDYRQATASIE
g708           MPFKPSKRISLLLVLALGACSTSYRPSRAEKANQVSNIKTQLAMEYMRGQDYRQATASIE
              10      20      30      40      50      60

              70      80      90     100     110     120
m708.pep      DALKSDPKNELAWLVRAEIYQYLVNDKAQESFRQALSIKPDSEINNYYGWFLCGRLNR
g708           DALKSNPKNELAWLVRAEIYQYLVNDKAQESFRQALSIKPDSEINNYYGWFLCGRLNR
              70      80      90     100     110     120

              130     140     150     160     170     180
m708.pep      PAESMAYFDKALADPTYPTPYIANLNKGICSAKQGQFGLAEAYLKRSIAAQPQFPFAFKE
g708           PAESMAYFDKALADPTYPTPYIANLNKGICSAKQGQFGLAEAYLKRSIAAQPQFPFAFKE
              130     140     150     160     170     180

              190     200     210     220     230     240
m708.pep      LARTKMLAGQLGDADYYFKKYQSRVEVLQADDLLGWKIAKALGNAQAAYEYEAQLQANF
g708           LARTKMLAGQLGDADYYFKKYQSRVEVLQADDLLGWKIAKALGNVQAAYEYEAQLQANF
              190     200     210     220     230     240

              250
m708.pep      PYSEELQTVLTGQX
g708           PYSEELQTVLTGQX
              250

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2377>:

```

a708.seq
1  ATGCCTTTTA AGCCATCCAA ACGAATCTCT TTATTACTTG TCCTTGCCTT
51  GGGCGCGTGC AGCACTTCCT ACCGCCCTC GCGGGCAGAA AAAGCCAATC
101 AGGTTTCCAA TATCAAAACC CAGTTGGCAA TGAATATAT GCGCGGTCAG
151 GACTACCGTC AGNGACGGC AAGTATTGAA GACGCCTTGA AATCAGACCC
201 TAAAACGAG CTTGCCTGGC TGGTCCGTGC CGAAATCTAT CAATACCTGA
251 AAGTTAACGA CAAGGCGCAG GAAAGTTTCC GGCAAGNCCT CTCCATCAAA
301 CCCGACAGTG CCGAAATCAA CAACAACACT NGCTGGTTCC TGTGCGGCAG
351 GCTCAACCGC CCTGCCGAAT CTATGGCATA TTTCGACAAA GCCCTGGCCG
401 ACCCCACNTA CCCGANCCCT TATATTGCCA ACCTGAATAA AGGCATATGC
451 AGCGCAAAAC AGGGGCAATT CGGATTGGCG GAAGCCTATT TGAAACGTTC
501 CCTCGCCGCC CAGCCGCAGT TCCCACCGCG ATTTAAAGAA CTGGCGCGCA
551 CCAAATGCT GGCCGGGCAG TTGGCGGATG CCGATTACTA CTTTAAAAAA
601 TACCAAAGCA GGGTAGAAGT CCTTCAGGCC GATGATTTCG TGCTAGGCTG
651 GAAAATTGCC AAAGCCCTCG GCAACGCACA GGCGGCATAC GAATATGAAG
701 CACAATTGCA GGCGAATTTC CCCTACTCGG AAGAATTGCA AACCGTCCTC
751 ATCGGTCAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 2378; ORF 708.a>:

```

a708.pep
1  MPFKPSKRIS LLLVLALGAC STSYRPSRAE KANQVSNIKT QLAMEYMRGQ
51  DYRQXTASIE DALKSDPKNE LAWLVRAEIY QYLVNDKAQ ESFRQXLSIK
101 PDSAEINNYY XWFLCGRLNR PAESMAYFDK ALADPTYPTP YIANLNKGIC
151 SAKQGQFGLA EAYLKRSIAA QPQFPFAFKE LARTKMLAGQ LGDADYYFKK
201 YQSRVEVLQA DDLLLGWKIA KALGNAQAAY EYEAQLQANF PYSEELQTVL
251 IQQ*

```

a708/m708 98.0% identity in 253 aa overlap

1142

	10	20	30	40	50	60
a708.pep	MPFKPSKRISLLLVLALGACSTSYRPSRAEKANQVSNIKTQLAMEYMRGQDYRQXTASIE					
m708	MPFKPSKRISLLLVLALGACSTSYRPSRAEKANQVSNIKTQLAMEYMRGQDYRQATASIE					
	10	20	30	40	50	60
	70	80	90	100	110	120
a708.pep	DALKSDPKNELAWLVRAEIQYLKVNDKAQESFRQXLSIKPDSAEINNXYWFLCGRNLNR					
m708	DALKSDPKNELAWLVRAEIQYLKVNDKAQESFRQALSIKPDSAEINNXYGWFLCGRNLNR					
	70	80	90	100	110	120
	130	140	150	160	170	180
a708.pep	PAESMAYFDKALADPTYXPYPIANLNKGICSAKQGQFGLAEAYLKRSALAAQPQFPFAFKE					
m708	PAESMAYFDKALADPTYTPYPIANLNKGICSAKQGQFGLAEAYLKRSALAAQPQFPFAFKE					
	130	140	150	160	170	180
	190	200	210	220	230	240
a708.pep	LARTKMLAGQLGDADYYFKKYQSRVEVLQADDLLLGWKIAKALGNAQAAYEYEAQLQANF					
m708	LARTKMLAGQLGDADYYFKKYQSRVEVLQADDLLLGWKIAKALGNAQAAYEYEAQLQANF					
	190	200	210	220	230	240
	250					
a708.pep	PYSEELQTVLIGQX					
m708	PYSEELQTVLTGQX					
	250					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2379>:

g709.seq

```

1  ATGTTTGCTT TCAAATCCTT ACTCGATATG CCGCGCGGTG AGGCACTTGC
51  CGTCGTCGTC GCTCTGATTG CCGCAATGGG CTATACCATC ATTTCAATTG
101 AGTGCGTCGCC GCATATGTCC ATTATTGCCG CCATCGTCGT GCTGATTTTG
151 TACGGCTTGG CGCGCGGTTT GAAATACAAC GATATGCAGG CAGGGATGAT
201 AGGCGCGTTG AATCAGGGTA TGGGCGCGGT TTACCTGTTT TTCTTCATCG
251 GGCTGATGGT CAGCGCGCTG ATGATGAGCG GCGCGATTCC GACGCTGATG
301 TATTACGGTT TCGGGCTGAT TTCCCCGACT TATTTTATTT TTTCCGCGCTT
351 CGCGCTGTGT TCCGTCATCG GCGTGTCCAT CGGCAGCAGC CTGACCGCCT
401 GCGCCACTGT CGGCGTTGCC TTTATGGGGA TGGCGCGCGC GTTTCAGGCC
451 GATATGGCGA TGACGgcggg cgcgattgTT tccggtGTGT TTTTCGCGCA
501 TAAATGTCTC CCGCTTTCCG ACACCACGGG CATTTCGCGC TCCATCGTCG
551 GTATCGACCT GTTTGAACAC ATCAAAAACA TGATGTACAC CACCATCCCT
601 CGGTGGCTTA TCAGCGCGGC ACTGATGCTT TGGCTTCTTC CCAGCGTCGC
651 CGCGCAGGAT TTGAACAGCG TCGAATCCTT CCGCAGCCAG CTTGAAGCCA
701 CGGGATTGGT GCACGGCTAT TCGCTGATTC CGTTTGCACT GTTGGTCGTT
751 TTGGCATTGA TCGCGGTCAA TGCCGTGGTC GCCATGCTCT TTACCGTCAT
801 TGCCGCCGTT GCCGTAACGT ATCTGCACAG CACGCCCGAT CTGCGTCAGC
851 TCGGCGCGTG GTTTTATGGC GGCTACAAAC TCGAAGGCGA AGCGTTTAAA
901 GACATTGCCA AACTGATTTC GCGCGGCGGC TTGGAGAGTA TGTTCCTTAC
951 GCAGACCATC GTTATCCTCG GTATGAGTTT GGGCGGGCTG CTGTTTGCGC
1001 TCGGTGTGAT TCCTTCCTTG CTGGAGGCCG TCCGTACCTT CTTGACGAAT
1051 GCGCGACGCG CGACGTTTCA GCTTGCCATG ACTTCGGTCG GGGTCAATTT
1101 CCTGATTGGA GAGCAATATT TGAGCATCCT GCTTTCGGGA GAAACGTTCA
1151 AACCCTTTTA CGACAACTC GGCTGCATT CGTGCAACCT GTCGCGGACT
1201 CTGGAAGATG CGGGGACGGT GATTAACCCG CTCGTGCCGT GGAGCGTGTG
1251 CGGCGTATTT ATCAGCCACG CCCTTGCGGT ACCCGTTTGG GAATATCTGC
1301 CTTATGCCTT TTTCTGCTAT TTGAGTTTGG CTTTAACCTT GTTATTCGGC
1351 TGGACGGGGC TGACTTTGAG CAAAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2380; ORF 709.ng>:

g709.pep

```

1  MFAFKSLDDM PRGEALAVVV ALIAAMGYTI ISLEWLPHMS IIAAIVVLIL
51  YGLARGLKYN DMQAGMIGAL NOGMGAVYLF EFIGLMVSAL MMSGAIPTLM
101 YYGFLISPT YFYFSAFALC SVIGVSIGSS LTACATVGVA FMGMAAFQA
151 DMAMTAGAIV SGVFFGDKMS PLSDTTGISA SIVGIDLFEB IKNMHTTIP
201 AWLISAALML WLLPSVAAOD LNSVESFRSQ LEATGLVHGY SLIPFALLVV
251 LALMRVNAVV ANLFTVIAAV AVTYLHSTPD LRQLGAWFYG GYKLEGEAFK
301 DIAKLISRGG LESMEFTQTI VILGMSLGLL LFLALGVPSL LEAVRTFLTN

```

1143

351 AGRATFSVAM TSVGVNFLIG EQYLSILLSG ETFKPVYDKL GLHSCNLSRT
 401 LEDAGTVINP LVPWSVCGVF ISHALGVPVW EYLPYAFFCY LSLALTLFLG
 451 WTGLTLSKK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2381>:

m709.seq
 1 ATGTTTCGCTT TCAAATCCTT ACTCGATATG CCGCGCGGTG AGGCACCTTGC
 51 CGTCGTCGTC GCTCTGATTG CCGCGATGGG CTATACCATC ATTTCAATTGG
 101 AGTGGTTGCC GCATATGTCC ATTATGCGCG CCATCGTCGT GCTGATTTTG
 151 TACGGCTTGG CCGCGGTTT GAAATACAAC GATATGCAGC AGGGCATGAT
 201 AGGCGCGTTG AATCAGGGTA TGGGCGCGAT TTACCTGTTT TTCTTCATCG
 251 GGCTGATGGT CAGCGCGCTG ATGATGAGCG GCGCGATTCC GACGCTGATG
 301 TATTACGGTT TCGGACTGAT TTCCCGGACT TATTTTATTT TTTCTCCTT
 351 CCGCTGTGTG TCCGTGTCAT GCGTGTCCAT CGGCAGCAGC CTGACCACCT
 401 GCGCCACTGT CCGCGTTGCC TTTATGGGGA TGGCGGCGGC GTTTCAGGCC
 451 GATATGGCGA TGACGGCGGG CCGGATTGTT TCGGGCGCAT TTTTGGCGA
 501 CAAAATGTCC CCGCTTTCGG ATACGACGGG TATTTCCGCG TCCATCGTCG
 551 GCATCGACTT GTTTGAGCAC ATCAAAAATA TGATGTACAC CACCATCCCC
 601 GCGTGGCTCA TTAGTGCGGC ACTGATGCTT TGGCTTTTGC CGAATGTGCG
 651 CGCGCAGGAT TTGAACAGCG TCGAATCCTT CCGCAGCCAG CTTGAAGCCA
 701 CGGGATTGGT GCACGGCTAT TCGCTGATTG CGTTTGGCGT GTTGGTCATT
 751 TTGGCATTGA TCGCATCAA CGCCGTCGTC GCCATGCTCT TTACCGTCAT
 801 GGTTCGCCGT GCTGTAACGT ATCTGCACAG CACGCCGAT CTGCGTCAGC
 851 TCGGTGCGTG GTTTTACGGC GGCTACAAAC TCGAAGGCGA AGCGTTTAAA
 901 GATGTTGTCA AACTGATTTC GCGCGCGGT TTGCAAAATA TGTTTTTCAC
 951 GCAAACCATC GTGATTCTCG GGATGAGTTT GGGCGGACTG TTGTTTGCAG
 1001 TCGGTGTGAT TCCTTCCCTG TTGGAGGCCA TCCGTACCTT CTTGACGAAT
 1051 GCCGGACGGC CGACGTTTCA CGTTGCCATG ACTTCGGTCG GGGTTAATTT
 1101 CCTGATCGGC GAGCAATATT TGAGTATTTT GTTGTGCGGT GAAACGTTCA
 1151 AAGCCGTTTA CGATAAGCTC GGTCTGCATT CGCGCAATCT GTCGCGGACG
 1201 CTGGAAGATG CGGGGACGGT GATTAAACCG CTCGTACCGT GGAGCGTATG
 1251 CCGCTGTGTC ATCAGCCACG CGCTGGGCGT GCCGTTTGG GAATATCTGC
 1301 CGTATGCCCT TTCTGCTAT TTGAGTTTGG CTTTGACCCT GTTATTCGGT
 1351 TGGACGGGCG TGACTTTGAG CAAAAAATA

This corresponds to the amino acid sequence <SEQ ID 2382; ORF 709>:

m709.pep
 1 MFAFKSLDDM PRGEALAVVV ALIAAMGYTI ISLEWLPHMS IIAAIVVLIL
 51 YGLARGLKYN DMQQGMIGAL NQGMGAIYLF FFIGLMVSAL MMSGAIPTLM
 101 VYFGFLISPT YFYFSSFALC SVIGVSIGSS LTTTCATVGA FMGMAAFQA
 151 DMAMTAGAIV SGAFFGDKMS PLSDTTGISA SIVGIDLFEB IKNNMYTTIP
 201 AWLISAALML WLLPNVAAQD LNSVESFRSQ LEATGLVHGY SLIPFALLVI
 251 IALMRINAVV AMLFTVMVAV AVTYLHSTPD LRQLGAWFYG GYKLEGEAFK
 301 DVVKLISRGG LESMFFTQTI VILGMSLGGI LFLGVIPSL LEAIRFTLN
 351 AGRATFSVAM TSVGVNFLIG EQYLSILLSG ETFKPVYDKL GLHSCNLSRT
 401 LEDAGTVINP LVPWSVCGVF ISHALGVPVW EYLPYAFFCY LSLALTLFLG
 451 WTGLTLSKK*

m709/g709 96.9% identity in 459 aa overlap

	10	20	30	40	50	60
m709.pep	MFAFKSLDDMPRGEALAVVVVALIAAMGYTIISLEWLPHMSIIAAIVVLILYGLARGLKYN					
g709	MFAFKSLDDMPRGEALAVVVVALIAAMGYTIISLEWLPHMSIIAAIVVLILYGLARGLKYN					
	10	20	30	40	50	60
m709.pep	DMQQGMIGALNQGMGAIYLFFFFIGLMVSALMMSGAIPTLMYYGFGLISPTYFYFSSFALC					
g709	DMQAGMIGALNQGMGAVYLFFFFIGLMVSALMMSGAIPTLMYYGFGLISPTYFYFSAFALC					
	70	80	90	100	110	120
m709.pep	DMQQGMIGALNQGMGAIYLFFFFIGLMVSALMMSGAIPTLMYYGFGLISPTYFYFSSFALC					
g709	DMQAGMIGALNQGMGAVYLFFFFIGLMVSALMMSGAIPTLMYYGFGLISPTYFYFSAFALC					
	70	80	90	100	110	120
m709.pep	SVIGVSIGSSLTTCATVGVAFMGMAAFQADMAMTAGAIVSGAFFGDKNSPLSDTTGISA					
g709	SVIGVSIGSSLTACATVGVAFMGMAAFQADMAMTAGAIVSGVFFGDKNSPLSDTTGISA					
	130	140	150	160	170	180
m709.pep	SVIGVSIGSSLTTCATVGVAFMGMAAFQADMAMTAGAIVSGAFFGDKNSPLSDTTGISA					
g709	SVIGVSIGSSLTACATVGVAFMGMAAFQADMAMTAGAIVSGVFFGDKNSPLSDTTGISA					
	130	140	150	160	170	180
m709.pep	SIVGIDLFEBIKNNMYTTIPAWLISAALMLWLLPNVAAQDLNSVESFRSQLEATGLVHGY					
g709	SIVGIDLFEBIKNNMYTTIPAWLISAALMLWLLPSVAAQDLNSVESFRSQLEATGLVHGY					
	190	200	210	220	230	240
m709.pep	SIVGIDLFEBIKNNMYTTIPAWLISAALMLWLLPNVAAQDLNSVESFRSQLEATGLVHGY					
g709	SIVGIDLFEBIKNNMYTTIPAWLISAALMLWLLPSVAAQDLNSVESFRSQLEATGLVHGY					
	190	200	210	220	230	240

1144

	250	260	270	280	290	300
m709.pep	SLIPFALLVILALMRINAVVAMLF	TMVAVAVTYLHSTPDLRQLGAWFYGGYKLEGEAFK				
g709	SLIPFALLVILALMRVNAVAMLF	TVIAAVAVTYLHSTPDLRQLGAWFYGGYKLEGEAFK				
	250	260	270	280	290	300
	310	320	330	340	350	360
m709.pep	DVVKLISRGGLESMTFTQ	TIVILGMSLGGLLFALGVIPSLLEAIRFTLTNAGRATFSVAM				
g709	DIAKLISRGGLESMTFTQ	TIVILGMSLGGLLFALGVIPSLLEAVRTLTNAGRATFSVAM				
	310	320	330	340	350	360
	370	380	390	400	410	420
m709.pep	TSVGVNFLIGEYLSILLSGETFKPVYDKLGLHSRNL	SRTLEDAGTVINPLVPSVCGVF				
g709	TSVGVNFLIGEYLSILLSGETFKPVYDKLGLHSCNLS	RTELEDAGTVINPLVPSVCGVF				
	370	380	390	400	410	420
	430	440	450	460		
m709.pep	ISHALGVPVWEYLPYAF	FCYLSLALTLLFGWTGLTSLKX				
g709	ISHALGVPVWEYLPYAF	FCYLSLALTLLFGWTGLTSLKX				
	430	440	450	460		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2383>:

```

a709.seq
1  ATGTTGCGCTT TCNAATCCTT ACTCGATATG CCGCGCGGTG AGGCNCTTGC
51  CGTCGTCGTC GCTCTGATTG CCGCGATGGG CTATACCATC ATTTNNTTGG
101 AGTGGCTGCC GCATATGTCC ATTATTGCCG CCATCGTNGT GCTGATTTTG
151 TACGGCTTGG CCGCGCGTTT GAAATACAAC GATATGCAGC AGGGCATGAT
201 AGGCGCGTTG AATCAGGTA TGGGCGCGAT TTACCTNTTT TTCTTCATCG
251 GGCTGATGGT CAGCGCGCTG ATGATGAGCG GCGCGATTCC GACGCTGATG
301 TATTACGGTT TCGGACTGAT TTCCCGACT TATTTTATT TTTCCGCCTT
351 CGCGCTGTGT TCGGTGATCG GCGTGCCAT CCGCAGCAGC CTGACCACCT
401 GCGCCACTGT CCGCGTTGCC TTNATGGGTA TNNNGNCGGC GTTTCNGGCC
451 NANATGGNGN NGNNGNNGN CHNGATTGTN NNGGNCGCAT TTTNGGCGN
501 CAAAATGTCN CCGCTTCCG ATACGNCGGG CATNTCCGCG TCCATTGTCG
551 GTATCGACCT GTTGAACAC ATCAAAATA TGATGTACAC NACCATTCCC
601 GCGTGGCTCA TCAGTGNNNC ACTGATGCTG TNGCTTCTT CCAGCGTCGC
651 TCGCGCAGGAT TTGAACAGCG TCGAATCCTT CCGCAGCCAG CTGAAGCCA
701 CGGGATTGGT GCACTGCTAT TCGCTGATTC CGTTTGCGCT GTTGGTCGTT
751 TTGGCATTGA TCGCGCTCAA TGCCGTGCTC GCTATGCTCT TTACCGTCAT
801 TGCCGCCGTT GCCGTAACGT ATCTGCACAG CACGCCGAT CTGCGTCAGC
851 TCGCGCGCTG GTTTACGGC GGCTACAAAC TCGAAGCGCA AGCGTNTANA
901 GACATTGCCA AACTCATTTT TCGCGGCGGT TTGGAAGTA TGTTTTTCAC
951 GCAGACCATC GTGATTCTTG GGATGAGCCT TGGCGGGCTG CTGTTTGCAC
1001 TGGGCGCGAT TCCTTCCCTG CTGGATGCCG TCCGCAGCTT TTTGACGAAT
1051 GCCGGGCGTN CCACATTCAG CGTTGCCATG ACTTCGGTCG GGGTTAATTT
1101 CCTGATCGGC GAGCAATATT TGAGTATTTT GTTGTCTNGG GAAACGTTCA
1151 AACCTGTTTA CGATAAGCTC GGTCTGCATT CGCGCAATCT GTCGCGGACG
1201 CTGGAAGATG CGGGGACCGT CATCAACCCG CTCGTACCGT GGAGCGTATG
1251 CGCGGTGTTT ATCANCCACG CGCTGGGCGT GCCGGTTTGG GAATATCTGC
1301 CGTATGCCCT TTTCTGCTAT TTGAGTTTGG CTTTGACCCT GTTATTCGGT
1351 TGGACGGGCG TGACTTTGAG CAAAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2384; ORF 709.a>:

```

a709.pep
1  MFAFXSLDM PRGEALAVVV ALIAAMGYTI IXLEWLPHMS IIAAIVVLIL
51  YGLARGLKYN DMQQGMIGAL NQGMGAIYLF FFIGLMVSAL MMSGAIPTLM
101 YYGFLISPT YFYSAFALC SVIGVSIGSS LTTCATVGVA XMGXXXAFXA
151 XMXXXXXIV XXAXXGXKMS PLSDTXGXA SIVGIDLFH IKNMYTTIP
201 AWLISXXLML XLLEPSVAAQD LNSVESFRSQ LEATGLVECY SLIPFALLVV
251 LALMRVNAV AVAMLFVIAAV AVTYLHSTPD LRQLGAWFYG GYKLEGEAXX
301 DIAKLISRGG LESMTFTQTI VILGMSLGG L FALGAIPSL L DAVRSFLT N
351 AGRXTFSVAM TSVGVNFLIG EQYLSILLSG ETFFKPVYDKL GLHSRNLST

```

1145

401 LEDAGTVINP LVPWSVCGVF IXHALGVPVW EYLPYAFFCY LSLALTLLFG
 451 WTGLTLSKK*

a709/m709 91.1% identity in 459 aa overlap

a709.pep	MFAFXSLDMPRGEALAVVVALIAAMGYTIIIXLEWLPHMSIIAAIVVLILYGLARGLKYN
m709	MFAFXSLDMPRGEALAVVVALIAAMGYTIIISLEWLPHMSIIAAIVVLILYGLARGLKYN
a709.pep	DMQQGMIGALNQGMGAIYLFFFIGLMVSALMMSGAIPITLMMYGFGLISPTYFYFSAFALC
m709	DMQQGMIGALNQGMGAIYLFFFIGLMVSALMMSGAIPITLMMYGFGLISPTYFYFSSFALC
a709.pep	SVIGVSIGSSLTTCATVGVAXMGXXXAFXAXMXXXXXIVXXAXXGXKMSPLSDTXGXSA
m709	SVIGVSIGSSLTTCATVGVAFMGMAAAFOADMAMTAGAIVSGAFFGDKMSPLSDTTGISA
a709.pep	SIVGIDLFEHIKNMYYTIPAWLISXXLMLXLLPSVAAQDLNSVESFRSQLEATGLVHCY
m709	SIVGIDLFEHIKNMYYTIPAWLISAALMLWLLPNVAAQDLNSVESFRSQLEATGLVHGY
a709.pep	SLIPFALLVILALMRVNAVVAAMLFVIAAVAVTYLHSTPDLRQLGAWFGGYKLEGEAXX
m709	SLIPFALLVILALMRINAVVAAMLFVMVAVAVTYLHSTPDLRQLGAWFGGYKLEGEAFK
a709.pep	DIAKLISRGGLESMTFTQITVILGMSLGGLLFALGAIPSLDAVRSFLTNAGRXTFSVAM
m709	DVVKLISRGGLESMTFTQITVILGMSLGGLLFALGVIPSLLEAIRFTLTNAGRATFSVAM
a709.pep	TSVGVNFLIGEQYLSILLSGETFKPVYDKLGLHSRNLSTLEDAGTVINPLVPWSVCGVF
m709	TSVGVNFLIGEQYLSILLSGETFKPVYDKLGLHSRNLSTLEDAGTVINPLVPWSVCGVF
a709.pep	IXHALGVPVWEYLPYAFFCYLSLALTLLFGWTGLTLSKKX
m709	ISHALGVPVWEYLPYAFFCYLSLALTLLFGWTGLTLSKKX

g710.seq not found

g710.pep not found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2385>:

m710.seq
 1 ATGGAAACCC ACGAAAAAT CCGCCTGATG CGCGAATTGA ATAAATGGTC
 51 CCAGGAGGAT ATGGCGGAAA AGCTGGCGAT GTCGGCAGGC GGGTATGCCA
 101 AAATCGAACG GGGCGAAACG CAGTTAAATA TCCCGGTTT GGAGCAGTTG
 151 GCTCAGATTT TCAAAATCGA TATGTGGGAC TTGCTCAAAT CGGGCGGTGG
 201 TGGGATGGTG TTTCAGATTA ATGAAGGTGA TAGTGGTGGC GATATTGCGT
 251 TGTATGCGTC GGGTGATGTT TCGATGAAA TAGAATTTT AAAAATGGAG

1146

301 TTGAAACACT GCAAAGAAAT GTTGAACAA AAAGACAAAG AAATCGAGCT
 351 GCTCCGCAAG CTGACCGAAA CCGTTTAA

This corresponds to the amino acid sequence <SEQ ID 2386; ORF 710>:

m710.pep
 1 METHEKIRLM RELNKWSQED MAEKLAMSAG GYAKIERGET QLNIPRLEQL
 51 AQIFKIDMWD LLKSGGGGMV FQINEGDSGG DIALYASGDV SMKIEFLKME
 101 LKHCKEMLEQ KDKEIELLRK LTETV*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2387>:

a710.seq
 1 ATGGAACCC ACGAAAAAT CCGCCTGATG CGCGAATTGA ATAAATGGTC
 51 CCAGGAGGAT ATGGCGGAAA AGCTGGCGAT GTCGGCAGGC GGGTATGCCA
 101 AAATCGAACG AGGCGAAACG CAGTTGAATA TCCCGCGTTT GGAGCAGTTG
 151 GCGCAGATTT TCAAAATTGA TATGTGGGAC TTGCTCAAAT CGGGCGGCGG
 201 CGGGATGGTG TTGCAGATTA ACGATGTGGA TACCAACAGC GGGGAATTG
 251 CAATCTATAC CGCTCAGGAT GCATCNGGTA AAGCTGGATT TGTTAAATG
 301 GAATTAAAC ACTGTAAAGA AATGTTGGAA CACAAAGACA AAGAAATCGA
 351 GCTGCTCCGC AAGCTGACCG AAACCGTTTA A

This corresponds to the amino acid sequence <SEQ ID 2388; ORF 710.a>:

a710.pep
 1 METHEKIRLM RELNKWSQED MAEKLAMSAG GYAKIERGET QLNIPRLEQL
 51 AQIFKIDMWD LLKSGGGGMV LQINDVDTNS GEFAIYTAQD ASGKAGFVKM
 101 ELKHCKEMLE HKDKEIELLR KLTETV*

a710/m710 85.7% identity in 126 aa overlap

	10	20	30	40	50	60
a710.pep	METHEKIRLMRELNKWSQEDMAEKLAMSAGGYAKIERGETQLNIPRLEQLAQIFKIDMWD					
m710	METHEKIRLMRELNKWSQEDMAEKLAMSAGGYAKIERGETQLNIPRLEQLAQIFKIDMWD					
	10	20	30	40	50	60
a710.pep	LLKSGGGGMVQLINDVDTNSGEFAIYTAQDASGKAGFVKMELKHCKEMLEHKDKEIELLR					
m710	LLKSGGGGMVFQINEGDSG-GDIALYASGDVSMKIEFLKMEELKHCKEMLEQKDKEIELLR					
	70	80	90	100	110	120
a710.pep	KLTETVX					
m710	KLTETVX					
	120					

g711.seq not found

g711.pep not found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2389>:

```
m711.seq
  1 ATGCCCCGCGC CTGATTGGG ATTTGCCTTA AGTCTGCCGC CAAAAAAGGC
 51 AATCGAGTGG CTGGAAGTA AAAAGGTTAC GCGGAGAGC TACCGCAATC
101 TGACAGCCTC CGAAATTGCC AAAGTCTATA CGATTGCCCG CATGACCGAC
151 TTGGATATGC TCAACGACAT CAAAACTTCG ATGGTTGAAT CGGCAAAAAG
201 TGGACAGTCG TTTGACGATT GCGGAAAAGG TATCTTGAAT CTGCTCAGCA
251 ACAAGGGCTG GCTGCATCCG AACGGGCATA ACGGTAAGGA TATCATCGAC
301 CCAGCCACCG GCGAGGTATT CGGTCGCCG CGGAGGTTGG AGACGATTTA
351 CCGTACCAAT ATGCAAACTG CCTACAACGC CGGTCAATAT CAAGGATATA
401 TGGCAAATAT TGATGCACGA CCTTATTGGA TGTATGACGC GGTAGGCGAC
451 AGCCGCACCC GTCCGCGCA TCCGCAATA GACGGGCTGG TGTACCGCTA
501 CGACGACCCG TTTTGGGCAA CGTTTACCC GCCCAACGGC TACAACTGCC
551 GCTGCTCGGT CATCGCGCTG TCGGAGCGGG ATGTGGAACG CCAGGGGCGG
601 ATTGTTGGGC AAAGCACGGC GGACAATCTG GTCGAGACCC ATAAATCTA
651 CAACAAAAAA GCGGATACTT ATCTGACCCT TGCCTATAAA GCACCGGATG
701 GCAGTCTGTA CACGACCGAT CGAGGATTTG ATTACAACGC CGGACGAATG
751 AACTACCGCC CCGATTTAGA CAAGTACGAC CGTGCGTTGG CGCATCAATT
801 TGCCAAAGCG GAAATGGGTG GTGCGGATTT TAAAACAGC TTTAAACAGC
851 TTGAAAAAGA GTTTTATGAA GTCAAGCAAC GTTTGGATAT TGATGGCAAG
901 CCCGATAAAG AGCAGAAAAA CAAAATCCGA AATGCGCTAT CAAGACAGCT
951 TAAATTGCT GCGGGTGTAT TGAGCAAGGA AACGCAAGAA TTGGCAGGTA
1001 TGACACGAGC GACGGTGTGG CTGTCTGATG ATACGTTGGT TAAACAGGTA
1051 GACAGCCGTG AGGGGCAGAA TTTCGATGAC TCCTACTATG CTTTTTTGCC
1101 GGATATGCTG CAAAACCTG AACATGTCAT CCGCGACAAT CGTGAATTGA
1151 TTTTCACAGC TCGCTATAAA GGCTCGGCAT TGTGGGCAGT TTTAAATAT
1201 ATTAAGGAGG TGGATGAGAT TTATCTACAG TCGTACCGAA TCAGTAACGA
1251 CAAAGAGATT GCCAAATTTA TGGCGAAGAA GAAAGTATTG AAATAG
```

This corresponds to the amino acid sequence <SEQ ID 2390; ORF 711>:

```
m711.pep
  1 MPAPDLGFAL SLPPKKAIEW LESKKVTAES YRNLTAIEIA KVYTIARMTD
 51 LDMLNDIKTS MVESAKSEQS FDDWRKGILN LLSNKGWLHP NGHNGKDIID
101 PATGEVFGSP RRLETIYRTN MQTAYNAGQY QGYMANIDAR PYWMYDAVGD
151 SRTRPAHSAI DGLVYRYDDP FWATFYPPNG YNCRCSVIAL SERDVERQGR
201 IVGQSTADNL VETHKIYNKK GDTYLTLAYK APDGSLYTTD RGFYDYNAGRM
251 NYRPDLDKYD RALAHQFAKA EMGGADFSTS FKQLEKEFYE VKQRLDIDGM
301 PKKEQKIKIR NALSRLKFA AGVLSKETQE LAGMTRATVW LSDDTLVKQV
351 DSREGQNFDD SYAFLPDML QNPEHVIRDN RELIFTARYK GSALWAVLKY
401 IKEVDEIYLQ SYRISNDKEI AKFMAKKKVL K*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2391>:

```
a711.seq
  1 ATGCCCCGCGC CTGATTGGG ATTTGCCTTA AGTCTGCCGC CAAAAAAGGC
 51 AATCGAGTGG CTGGAAGTA AAAAGGTTAC GCGGAGAGC TACCGCAATC
101 TGACAGCCTC CGAAATTGCC AAAGTCTATA CGATTGCCCG CATGACCGAC
151 TTGGATATGC TCAACGACAT CAAAACTTCG ATGGTTGAAT CGGCAAAAAG
201 TGGACAGTCG TTTGACGATT GCGGAAAAGG TATCTTGAAT CTGCTCAGCA
251 ACAAGGGCTG GCTGCATCCG AACGGGCATA ACGGTAAGGA TATCATCGAC
301 CCAGCCACCG GCGAGGTATT CGGTCGCCG CGGAGGTTGG AGACGATTTA
351 CCGTACCAAC ATGCAAACTG CCTACAACGC CGGTCAATAT CAAGGATATA
401 TGGCAAATAT TGATGCACGA CCTTATTGGA TGTATGACGC GGTAGGCGAC
451 AGCCGCACCC GTCCGCGCA TCCGCAATA GACGGGCTGG TGTACCGCTA
501 CGACGACCCG TTTTGGGCAA CGTTTACCC GCCCAACGGC TACAACTGCC
551 GTTGCTCGGT CATCGCGCTG TCGGAGCGGG ATGTGGAACG CCAGGGGCGG
601 ATTGTCGGGC AAAGCACGTC GGACAATCTT GTTGAGACCC ATAAATCTA
651 CAACAAAAAA GCGGATACTT ATCTGACCCT TGCCTATAAA GCACCGGATG
701 GCAGTCTGTA CACGACCGAT CGAGGATTTG ATTACAACGC CGGACGAATG
751 AACTACCGCC CCGATTTAGA CAAGTACGAC CGTGCGTTGG CGCATCAATT
801 TGCCAAAGCG GAAATGGGTG GTGCGGATTT TAAAACAGC TTTAAACAGC
851 TTGAAAAAGA GTTTTATGAA GTCAAGCAAC GTTTGGATAT TGATGGCAAG
```

1148

```

901 CCCGATAAAG AGCAGAAAAT CAAAATCCGA AATGCGCTAT CAAGACAGCT
951 TAAATTTGCT GCGGGTGTAT TGAGCAAGGA AACGCAAGAA TTGGCAGGTA
1001 TGACACGAGC GACGGTGTGG CTGTCTGATG ATACGTTGGT TAAACAGGTA
1051 GACAGCCGTG AAGGGCAGAA TTTTCATGAC TCCTACTATG CTTTTTTGCC
1101 GGATATGCTG CAAAACCCGT AACATGTCAT CCGCGACAAT CGTGAATTGA
1151 TTTTCACAGC TCGCTATAAA GGCTCGGCAT TGTGGGCAGT TTTAAATAT
1201 ATTAAGGAGG TGGATGAGAT TTATCTACAG TCGTACCGAA TCAGTAACGA
1251 CAAAGAGATT GCCAAATTTA TGGCGAAGAA GAAAGTATTG AAATAG

```

This corresponds to the amino acid sequence <SEQ ID 2392; ORF 711.a>:

a711.pep

```

1  MPAPDLGFAL SLPPKKAIEW LESKKVTAES YRNLTASEIA KVYTIARMTD
51  LDMLNDIKTS MVESAKSGQS FDDWRKGILN LLSNKGWLHP NGHNGKDIID
101 PATGEVFGSP RRLETIYRTN MQTAYNAGQY QGYMANIDAR PYWYDAVGD
151 SRTRPAHSAI DGLVYRYDDP FWATFYPPNG YNCRCSVIAL SERDVERQGR
201 IVGQSTSDNL VETHKIYNKK GDTYLTLAYK APDGSLYTTD RGFYNAGRM
251 NYRPDLKDYD RALAHQFAKA EMGGADFCTS FKQLEKEFYE VKQRLLDIDGK
301 PDKEQKIKIR NALSRQLKFA AGVLSKETQE LAGMTRATVW LSDDTLVKQV
351 DSREGQNFDD SYAFLPDML QNPEHVIRDN RELIFTARYK GSALWAVLKY
401 IKEVDEIYLQ SYRISNDKEI AKFMAKKKVL K*

```

a711/m711 99.8% identity in 431 aa overlap

a711.pep	10	20	30	40	50	60
	MPAPDLGFALSLLPPKKAIEWLESKKVTAESYRNLTASEIAKVYTIARMTDLDMLNDIKTS					
m711	MPAPDLGFALSLLPPKKAIEWLESKKVTAESYRNLTASEIAKVYTIARMTDLDMLNDIKTS					
	10	20	30	40	50	60
a711.pep	70	80	90	100	110	120
	MVESAKSGQSFDDWRKGILNLLSNKGWLHPNGHNGKDIIDPATGEVFGSPRRLETIYRTN					
m711	MVESAKSGQSFDDWRKGILNLLSNKGWLHPNGHNGKDIIDPATGEVFGSPRRLETIYRTN					
	70	80	90	100	110	120
a711.pep	130	140	150	160	170	180
	MQTAYNAGQYQGYMANIDARPYWYDAVGDSRTRPAHSAIDGLVYRYDDPFWATFYPPNG					
m711	MQTAYNAGQYQGYMANIDARPYWYDAVGDSRTRPAHSAIDGLVYRYDDPFWATFYPPNG					
	130	140	150	160	170	180
a711.pep	190	200	210	220	230	240
	YNCRCSVIALSERDVERQGRIVGQSTSDNLVETHKIYNKKGDTYLTLAYKAPDGSLYTTD					
m711	YNCRCSVIALSERDVERQGRIVGQSTADNLVETHKIYNKKGDTYLTLAYKAPDGSLYTTD					
	190	200	210	220	230	240
a711.pep	250	260	270	280	290	300
	RGFDYNAGRMNYRPDLKDYDRALAHQFAKAEMGGADFCTSFKQLEKEFYEVKQRLLDIDGK					
m711	RGFDYNAGRMNYRPDLKDYDRALAHQFAKAEMGGADFCTSFKQLEKEFYEVKQRLLDIDGK					
	250	260	270	280	290	300
a711.pep	310	320	330	340	350	360
	PDKEQKIKIRNALSRQLKFAAGVLSKETQELAGMTRATVWLSDDTLVKQVDSREGQNFDD					
m711	PDKEQKIKIRNALSRQLKFAAGVLSKETQELAGMTRATVWLSDDTLVKQVDSREGQNFDD					
	310	320	330	340	350	360
a711.pep	370	380	390	400	410	420
	SYAFLPDMLQNPEHVIRDNRELIIFTARYKGSALWAVLKYIKEVDEIYLQSYRISNDKEI					
m711	SYAFLPDMLQNPEHVIRDNRELIIFTARYKGSALWAVLKYIKEVDEIYLQSYRISNDKEI					
	370	380	390	400	410	420

430

a711.pep	AKFMAKKKVLKX
m711	AKFMAKKKVLKX
	430

g712.seq not found yet

g712.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2393>:

```
m712.seq
1  ATGATGCCCC ATATTGATTT TGACACGATT CCGGGCAGCA TCCGCGTGCC
51  CGGGCAGTAT ATTGAATTTA ACACCCGCAA TGCCGTACAA GGT'TTGCCGC
101 AAAATCCGCA AAAGGTATTG ATGGTTGCAC CCATGCTGAC CGCGGGCATA
151 CAGCCCGCCT TAGAGCCGGT GCAACTATTT AGCGATGCCG AGGCGGCCGA
201 TTTGTTCCGA CAAGGCTCGC TGGCGCATTT GATGGTGC GC CAAGCATTTG
251 CCAACAACCC TTATT'TGGAT TTGACCGTTA TCGGTATTGC CGACCACAGC
301 GCAGGCGTGC AGGCAACCGC AACCGTTACC CTTTCCGGCA CGGCCACCGC
351 CCGGGGCGTG GTGGAAATCA CGATTGGCGG CAAGCAGGTA AGCACGGCCG
401 TTAACACCGG CGAGACCGCC GCCACAGTGG CAGACCGTCT GAAAACCGCC
451 ATCACTGCCG CCGATGTAAC CGTTACCGCA TCCGGCAGCG GCGCAGCCGT
501 TACGCTGACG GCCAAACACA AAGGCGAGAT CGGCAACGAG AGCGGCTTAA
551 CCGTGAGCAC CGGCAATACC GGCCTAACTT ATCAAGCCAA TGCCTTTACC
601 GGCGGTGCCA AAAATGCGGA CATTGCCACG GCCTTGTC CA AAGTGGCGGG
651 CAAGCATTAT CACATTATTT GCAGCCCGTT TAGCGATGAC GCCAACGCCA
701 AAGCCTTGAG CAACCATATT ACCAACGTAT CCAACGCCAT CGAGCAGCGC
751 GGCTGTATCG GCGTATTGGG TATGAGTGC GCCTTGAGCA CGGCCACCAC
801 CGCTACCGGC GAAATCAACG ACGGCCGCAT GACCTGTGCT TGGTACAAAG
851 GTGCGGTAGA GCCAAACGGC ATCATCGCCG CAGGTTATGC GCGCGTGTTG
901 GCCTTTGAAG AAGACCTGCG CAAGCCGCTG AACACGCTGG AAATCAAAGG
951 GCTGGCCGTT ACACCTGATG CGCAATGGCC GCTGTTTGCA GAATGCAACA
1001 ATGCGCTGTA CAACGGCTTG ACCCGGCTCA CAGTGGTCAA CAACCGCGTG
1051 CAGATTATGC GTGCCGTATC CACCTATACC AAGTCGGCCA ACAACACCGA
1101 CGACCCGGCA CTACTCGACA TTACCACCAT CCGCACGCTG GATTATGTGC
1151 GCCGCAGCGT TAAAGAGCGC ATTGCCCTGC GTTTTCCGCG CGACAAATTG
1201 AGCGACCGCC TGCTGCCCAA GGTTAAGAGC GAGATTTTGG ACGTGCTGAT
1251 TAAGCTCGAC CAAGCCGAAA TCATCGAAAA CGCCGAGGCC AACAAAGGCA
1301 AGCTGGTGGT GCGCGGTGCG CAAAACGACC CCAACCGTGT TAATGCCATT
1351 ATCCCGCCG ATGTGGTCAA CGGCCTGCAC GTCTTTGCCG GCGCATTGA
1401 TTTGATTTTG TAA
```

This corresponds to the amino acid sequence <SEQ ID 2394; ORF 712>:

```
m712.pep
1  MMPHIDFDTI PGSIRVPGQY IEFNTRNAVQ GLPQNPKXVL MVAFMLTAGI
51  QPALEPVOLF SDAEAADLFG QGSLAHLMVR QAFANNPYLD LTVIGIADHS
101 AGVQATATVT LSGTATAPGV VEITIGGKQV STAVNTGETA ATVADRLKTA
151 ITAADVTVTA SGSGAAVTLT AKHKGEIGNE SGLTVSTGNT GLTYQANAFT
201 GGAKNADIAT ALSKVAGKHY HII CSPFSD ANAKALSNI TNVSNAIEQR
251 GCIGVLGMSA ALSTATTATG EINDGRMTCA WYKGAVEPNG IIAAGYAAVL
301 AFEEDPAKPL NTLEIKGLAV TPDAQWPLFA ECNNALYNGL TPLTVVNNRV
351 QIMRAVSTYT KSANNTDDPA LLDITTIRTL DYVRRSVKER IALRFPRDKL
401 SDRLLPKVKS EILDVLKLD QAEIENAEA NKGKLVVARA QNDENRVNAI
451 IPADVNVGLH VFAGRIDLIL *
```

a712.seq not found yet

a712.pep not found yet

g713.seq not found yet

g713.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2395>:

```
m713.seq
1  ATGCAAAATA ATTCATACGG CTATGCCGTG TCGGTGCGCG TGGGCGGTAA
51  AGAGCACCGC CACTGGGAGC GCTACGACAT CGACAGCGAC TTTTAAATCC
101 CTGCCGACAG CTTGATTTT GTCATCGGCA GGTGGGACC GGAGGCGGCC
151 ATACCCGATT TAAGCGGAGA GAGCTGCGAG GTAGTGATAG ACGGGCAAAT
201 CGTGATGACG GGCATCATCG GCAGCCAGCG CCACGGCAA AGCAAGGGCA
251 GCCGCGAGTT GAGCTTGAGC GGGCGTGATT TGGCCGTTT TTTGGTGGAT
301 TGCTCCGCGC CGCAGCTCAA TGTAAAGGGC ATGACGGTAT TGGATGCAGC
351 CAAAAGCTG GCCGCGCCGT GGCCGAGAT TAAAGCGGTG GTGCTTAAGG
401 CCGAAAACAA CCCCCTTTG GCGAAATCG ACATCGAGCC GGGCGAAACC
451 GTATGGCAGG CATTAAACCA TATTGCCAAC TCGGTCGGGC TGCATCCGTG
501 GCTGGAGCCG GACGGCACGT TGGTGGTGGG CGGTGCGGAT TACAGCAGCC
551 CGCCGCTGGC GACATTGTGT TGGAGCCGCA CCGACAGCCG CTGCAATATC
601 GAGCGCATGG ACATTGAGTG GGATACCGAC AACCGCTTTT CCGAGGTTAC
651 TTTTTTGGCG CAATCGCACG GCCGAGCGG CGACAGCGCC AAACACGATT
701 TAAAGTGGGT GTACAAAGAC CCGACGATGA CGCTGCACCG CCTTAAACG
751 GTGGTGGTGT CCGATGCCGA CAATTTGGCC GCATTGCAAA AGCAGGCTAA
801 AAAGCAGCTG GCCGACTGGC GGCTGGAGGG ATTTACTCTC ACGATAACCG
851 TGGGCGGCCA TAAACCCGCG GACGGCGTAT TGTGGCAACC TGGCCTGCGT
901 GTGCATGTGA TCGACGACGA GCACGGTATC GATGCGGTGT TTTTCTGAT
951 GGGCGCGCGG TTTATGCTAT CCCGATGGA TGGTACGCAA ACCGAGCTGC
1001 GGCTCAAAGA GGACGGTATT TGGACACCCG ACGCTTACCC CAAAAGGCC
1051 GAGGCGGCGC GCAAGCGCAA AGGCAAACGC AAAGGCGTGA GCCATAAGGG
1101 CAAAAGAGGC GCGAAAAC AAGCAGAAAC GGCGGTGTTT GAATGA
```

This corresponds to the amino acid sequence <SEQ ID 2396; ORF 713>:

```
m713.pep
1  MQNNSYGYAV SVRVGGKEHR HWERYDIDSD FLIPADSFDF VISRLGPEAA
51  IPDLSGESCE VVIDGQIVNT GIIGSQRHGK SKGSRELSLS GRDLAGFLVD
101 CSAPQLNVKG MTVLDAAKKL AAPWPQIKAV VLKAENNPAL GKIDIEFGET
151 VVQALTHIAN SVGLHPWLEP DGLTVVGGAD YSFPVATLC WSRTDSRCNI
201 ERMDIEWDTD NRFSEVTFLA QSHGRSGDSA KHDLKWVYKD PTMTLHRPKT
251 VVVSADADNLA ALQKQAKKQL ADWRLEGFTL TITVGGHKTR DGVLWQPGLR
301 VHVIDDEHGI DAVFFLMGR FMLSMDGTQ TELRLKEDI WTPDAYPKKA
351 EAARKRKGR KGVSHKGKKG GKQAEAVF E*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2397>:

```
a713.seq
1  ATGCAAAATA ATTCATACGG CTATGCCGTG TCGGTGCGCG TGGGCGGTAA
51  AGAGCACCGC CACTGGGAGC GCTACGACAT CGACAGCGAC TTTTAAATCC
101 CTGCCGACAG CTTGATTTT GTCATCGGCA GGTGGGACC GGAGGCGGCC
151 ATACCCGATT TAAGCGGAGA GAGCTGCGAG GTAGTGATAG ACGGGCAAAT
201 CGTGATGACG GGCATCATCG GCAGCCAGCG CCACGGCAA AGCAAGGGCG
251 GCCGCGAGTT GAGCTTGAGC GGGCGTGATT TGGCCGTTT TTTGGTGGAT
301 TGCTCCGCGC CGCAGCTCAA TGTAAAGGGC ATGACGGTAT TGGATGCAGC
351 CAAAAGCTG GCCGCGCCGT GGCCGAGAT TAAAGCGGTG GTGCTTAAGG
401 TCGAAAACAA CCCCCTTTG GACAAAATCG ACATCGAGCC GGGCGAAACC
451 GTATGGCAGG CATTAAACCA TATTGCCAAC TCGGTCGGGC TGCATCCGTG
501 GCTGGAGCCG GACGGCACGT TGGTGGTGGG CGGTGTGGAT TACAGCAGCC
551 CGCCGCTGGC GACATTGTGT TGGAGCCGCA CCGACAGCCG CCGCAATATC
601 GAGCGCATGG ACATTGAGTG GGATACCGAC AACCGCTTTT CTGAGGTTAC
651 TTTTTTGGCG CAATCGCACG GCCGAGCGG CGACAGCGCC AAACACGATT
701 TAAAGTGGGT GTACAAAGAC CCGACGATGA CGCTGCACCG CCTTAAACG
751 GTGGTGGTGT CCGATGCCGA CAATTTGGCC GCATTGCAAA AGCAGGCTAA
801 AAAGCAGCTG GCCGACTGGC GGCTGGAGGG ATTTACTCTC ACGATAACCG
851 TGGGCGGCCA TAAACCCGCG GACGGCGTAT TGTGGCAACC TGGCCAGCGT
901 GTGCATGTGA TCGACGACGA GCACGGTATC GATGCGGTGT TTTTCTGAT
951 GGGCGCGCGG TTTATGCTAT CTCGATGGA TGGCAGCAA ACCGAGCTGC
1001 GGCTCAAAGA GGACGGTATT TGGACACCCG ACGCTTACCC CAAAAGGCC
1051 GAGGCGGCGC GCAAGCGCAA AGGCAAACGC AAAGGCGTGA GCCATAAGGG
```


1101 CAAAAAAGGC GGCAAAAAAC AAGCAGAAAC GGCGGTGTTT GAATGA

This corresponds to the amino acid sequence <SEQ ID 2398; ORF 713.a>:

a713.pep
 1 MQNNSYGYAV SVRVGGKEHR HWERYDIDSD FLIPADSFDV VIGRLGPEAA
 51 IPDLSGESCE VVIDGQIVMT GIIGSQRHGK SKGGRELSLS GRDLAGFLVD
 101 CSAPQLNVKG MTVLDAKKL AAPWPQIKAV VLKVENNPAL DKIDIEPGET
 151 VWQALTHIAN SVGLHPWLEP DGTLLVVGVD YSSPPVATLC WSRTDSRRNI
 201 ERMDIEWDTD NRFSEVTF LA QSHGRSGDSA KHDLLKVVYKD PTMTLHRPKT
 251 VVVSADNLA ALQKQAKKQL ADWRLEGFTL TITVGGHKTR DGVWLQPGQR
 301 VHVIDDEHGI DAVFFLMGRR FMLSMDGTQ TELRLKEDGI WTPDAYPKKA
 351 EAARKRKGR KGVSHKGGKG GKKQAETAVF E*

a713/m713 98.4% identity in 381 aa overlap

a713.pep	10	20	30	40	50	60
m713	10	20	30	40	50	60
a713.pep	70	80	90	100	110	120
m713	70	80	90	100	110	120
a713.pep	130	140	150	160	170	180
m713	130	140	150	160	170	180
a713.pep	190	200	210	220	230	240
m713	190	200	210	220	230	240
a713.pep	250	260	270	280	290	300
m713	250	260	270	280	290	300
a713.pep	310	320	330	340	350	360
m713	310	320	330	340	350	360
a713.pep	370	380				
m713	370	380				

1153

g714.seq not found yet

g714.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2399>:

```
m714.seq
  1 ATGAGCTATC AAGACATCTT GCGGGGCTTG TTGCCCCCGG TGTCGTATGC
  51 CCGCAATGCC CCGCGTGTGC GGGCGCAGGC AGAAATAGAC GGCGCAGCGC
 101 TGGATGCGGT GCGGGAATCG GCTCAAAGCG TTGCCGATGC CGTCGACCCG
 151 CGCAGCGCCG GCCAAATGCT GGCCGATTGG GAGCGCGTAT TAGGTTTGA
 201 CCGTACGGGC AAAAACC GCCAATGCT GTTGGCCGTC ATGGCCAAGC
 251 TAAACGAAAC AGGCGGCTTG AGTATTCCTT ATTTTGTGCG TTTGGCCGAG
 301 GCGGCGGGCT ATCAAATCCA AATCGACGAA CCGCAGCCGT TCCGCGCCGG
 351 TGTAAACCGC GCCGCGGACC GTCTTGCGCC GCAGGAAATC ATGTGGGTGT
 401 GGCACGTTAA CGTGCGCGGC GGCAACAACC GCATTACCCG ATTCCGCGCC
 451 GGTATCTCGG CGGCGGGCGA CAGGCTGACC GATTACAGCG ATGCCGTGAT
 501 CGAGAGCCTG TTCAACCGCC TCAAGCCCGC CCACACCGCT ATCCGATTTA
 551 CCTACCGCTA A
```

This corresponds to the amino acid sequence <SEQ ID 2400; ORF 714>:

```
m714.pep
  1 MSYQDILRGL LPPVSYARNA PRVRAQAEID GAALDAVAES AQSVAADAVDP
  51 RSAGQMLADW ERVLGLDGTG KNRQHRVLAV MAKLNETGGL SIPYFVRLAE
 101 AAGYQIQIDE POPFRAGVNR AGDRLAPQEI MWVWHVNVRG GNNRITRFRA
 151 GISAAGDRLT DYSDAVIESL FNRLKPAHTA IRFTYR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2401>:

```
a714.seq
  1 ATGAGCTATC AAGACATCTT GCGGGGCTTG TTGCCCCCGG TGTCGTATGC
  51 CCGCAATGCC CCGCGTGTGC GGGCGCAGGC AGAAATAGAC GGCGCAGCGC
 101 TGGATGCGGT GCGGGAATCG GCTCAAAGCG TTGCCGATGC CGTCGACCCG
 151 AGCAGCGCCG GCCAAATGCT GGCCGATTGG GAGCGCGTAT TAGGTTTGA
 201 CCGTACGGGC AAAAACC GCCAATGCT GTTGGCCGTC ATGGCCAAGC
 251 TAAACGAAAC AGGCGGCTTG AGTATTCCTT ATTTTGTGCG TTTGGCCGAG
 301 GCGGCGGGCT ATCAAATCCA AATCGACGAA CCGCAGCCGT TCCGCGCCGG
 351 TGTAAACCGC GCCGCGGACC GTCTTGCGCC GCAGGAAATC ATGTGGGTGT
 401 GGCACGTTAA CGTGCGCGGC GGCAACAACC GCATTACCCG ATTCCGCGCC
 451 GGTATCTCGG CGGCGGGCGA CAGGCTGACC GATTACAGCG ATGCCGTGAT
 501 CGAGAGCCTG TTCAACCGCC TCAAGCCCGC CCACACCGCT ATCCGATTTA
 551 CCTACCGATA A
```

This corresponds to the amino acid sequence <SEQ ID 2402; ORF 714.a>:

```
a714.pep
  1 MSYQDILRGL LPPVSYARNA PRVRAQAEID GAALDAVAES AQSVAADAVDP
  51 SSAGQMLADW ERVLGLDGTG KNRQRRVLAV MAKLNETGGL SIPYFVRLAE
 101 AAGYQIQIDE POPFRAGVNR AGDRLAPQEI MWVWHVNVRG GNNRITRFRA
 151 GISAAGDRLT DYSDAVIESL FNRLKPAHTA IRFTYR*
```

a714/m714 98.9% identity in 186 aa overlap

	10	20	30	40	50	60
a714.pep	MSYQDILRGLLPPVSYARNAPRVRAQAEIDGAALDAVAESAQSVAADAVDPSSAGQMLADW					
m714	MSYQDILRGLLPPVSYARNAPRVRAQAEIDGAALDAVAESAQSVAADAVDPSSAGQMLADW					
	10	20	30	40	50	60
a714.pep	ERVLGLDGTGKNRQRRVLAVMAKLNETGGLSIPYFVRLAEAAAGYQIQIDEPQPFRAVNR					
m714	ERVLGLDGTGKNRQHRVLAVMAKLNETGGLSIPYFVRLAEAAAGYQIQIDEPQPFRAVNR					
	70	80	90	100	110	120
a714.pep	ERVLGLDGTGKNRQRRVLAVMAKLNETGGLSIPYFVRLAEAAAGYQIQIDEPQPFRAVNR					
m714	ERVLGLDGTGKNRQHRVLAVMAKLNETGGLSIPYFVRLAEAAAGYQIQIDEPQPFRAVNR					
	70	80	90	100	110	120
a714.pep	AGDRLAPQEIIMWVWHVNVRGNNRITRFRAGISAAGDRLTDYSDAVIESLFNRLKPAHTA					
m714	AGDRLAPQEIIMWVWHVNVRGNNRITRFRAGISAAGDRLTDYSDAVIESLFNRLKPAHTA					

1154

m714 AGDRLAPQEIMVWVHVNRGNNRITRFRAGISAAGDRLTDYSDAVIESLFNRLKPAHTA
 130 140 150 160 170 180

a714.pep IRFTYRX
 |||||
 m714 IRFTYRX

g715.seq not found yet

g715.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2403>:

m715.seq
 1 ATGATTGATG TCAAAATAGA CAATATCTTT GTCGTCCTAA ACCAAATCGA
 51 GCGGCTTGGC AACGGGATCG AAAACCGCTA CCTGCTGATG CGCCGACTGT
 101 CCGAAACCAT GCACACGGCG GTCAAGCTCA ATTTCCGCTA CGCAGGCCGT
 151 CCGAAATGGG TTGGGCTAAA ATACCGCGAC GGCAAGCCGC TTTCGGATTG
 201 GGGTCGCTG AAAGACAGTT TTTCCACACT GTCAGACAAC GATACAGCCC
 251 TTGTCGGTAC GAATATCGTC TATGCCGCCA TCCACAACCT CGGCGGTATG
 301 GCGGGGCGCA ACCGCAAAGT TCGGATTCCG CAACGGGAAT TTTTGACGCT
 351 GACGGACGAC GACAAACAGG CTTTGATGGA CGATGTGCAG GATTATTTTT
 401 CGGGTCTGAT ACCGTGA

This corresponds to the amino acid sequence <SEQ ID 2404; ORF 715>:

m715.pep
 1 MIDVKIDNIF VVLNQIERLG NGIENRYLLM RRLSETMHTA VKLNFRYAGR
 51 PKWVGLKYRD GKPLSDSGRL KDSFSTLSDN DTALVGTNIV YAAIHNFGGM
 101 AGRNRKVRIP QREFLTLTDD DKQALMDDVQ DYFSGGLIP*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2405>:

a715.seq
 1 ATGATTGATG TCAAAATAGA CAATATCTTT GTCGTCCTAA ACCAAATCGA
 51 GCGGCTTGGC AACGGGATCG AAAACCGCTA CCTGCTGATG CGCCGACTGT
 101 CCGAAACCAT GCACACGGCG GTCAAGCTCA ATTTCCGCTA CGCAGGCCGT
 151 CCGAAATGGT TGGGCTAAA ATACCGCGAC GGCAAGCCGC TTTCGGATTG
 201 GGGTCGCTG AAAGACAGTT TTTCCACACT GTCAGACAAC GATACAGCCC
 251 TTGTCGGTAC GAATATCGTC TATGCCGCCA TCCACAACCT CGGCGGTATG
 301 GCGGGGCGCA ACCGCAAAGT TCGGATTCCG CAACGGGAAT TTTTGACGCT
 351 GACGGACGAC GACAAACAGG CTTTGATGGA CGATGTGCAG GATTATTTTT
 451 CGGGTCTGAT ACCGTGA

This corresponds to the amino acid sequence <SEQ ID 2406; ORF 715.a>

a715.pep
 1 MIDVKIDNIF VVLNQIERLG NGIENRYLLM RRLSETMHTA VKLNFRYAGR
 51 PKWLGLKYRD GKPLSDSGRL KDSFSTLSDN DTALVGTNIV YAAIHNFGGM
 101 AGRNRKVRIP QREFLTLTDD DKQALMDDVQ DYFSGGLIP*

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2407>:

g716.seq
 1 ATGAACAAAA ATATTGCTGC CGCACTCGCC GGTGCTTAT CCCTGTCTCT
 51 GGCCGCCGCG GCGTTGCCG CCCACAAACC GGCAAGCAAC GCAACAGGCG
 101 TTCAAAATC CGCCCAAGGC TCTTGCGGCG CATCCAAATC TGCCGAAGGT
 151 TCGTGCGGCG CATCCAAATC TGCCGAAGGT TCGTGCGGCG CGGCTGCTTC
 201 TAAAGCAGGC GAAGGCAAAT GCGGCGAGGG CAAATGCGGT GCAACTGTAA
 251 AAAAGCCCCA CAAACACACC AAAGCATCTA AAGCCAAAGC CAAATCTGCC
 301 GAAGGCAAAT GCGGCGAAGG CAAATGCGGT TCTAAATAA

This corresponds to the amino acid sequence <SEQ ID 2408; ORF 716.ng>:

g716.pep
 1 MNKNIAAALA GALSLSLAAG AVAAHKPASN ATGVQKSAQG SCGASKSAEG
 51 SCGASKSAEG SCGAAASKAG EGKCGEGKCG ATVKRAHKHT KASKAKAKSA

1155

101 EGKCGEGKCG SK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2409>:

```
m716.seq
1  ATGAACAAAA ACATTGCTGC CGCTCTCGCC GGTGCTTTAT CCCTGTCTTT
51  GGCCGCCCGGT GCAGTTGCTG CCAACAAACC GGCAAGCAAC GCAACAGGCG
101 TTCATAAATC CGCCCATGGC TCTTGCGGCG CGTCCAAATC TGCCGAAGGT
151 TCGTGCGGCG CGGCTGGTTC TAAAGCAGGC GAAGGCAAAT GCGGCGAGGG
201 CAAATGCGGT GCGACCGTAA AAAAAACCCA CAAACACACC AAAGCATCTA
251 AAGCCAAGGC CAAATCTGCC GAAGGCAAAT GCGGCGAAGG CAAATGCGGT
301 TCTAATAAA
```

This corresponds to the amino acid sequence <SEQ ID 2410; ORF 716>:

```
m716.pep
1  MNKNIAAALA GALSLSLAAG AVAANKPASN ATGVHKSAGH SCGASKSAEG
51  SCGAAGSKAG EGKCGEGKCG ATVKKTHKHT KASKAKAKSA EGKCGEGKCG
101 SK*
```

m716/g716 86.6% identity in 112 aa overlap

	10	20	30	40	50	
m716.pep	MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHKSAGHSCGASKSAEGSCGA-----					
g716	MNKNIAAALAGALSLSLAAGAVAANKPASNATGVQKSAOGSCGASKSAEGSCGASKSAEG					
	10	20	30	40	50	60
	60	70	80	90	100	
m716.pep	---AGSKAGEGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSKX					
g716	SCGAASKAGEGKCGEGKCGATVKKAHKHTKASKAKAKSAEGKCGEGKCGSKX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2411>:

```
a716.seq
1  ATGAACAAAA ACATTGCTGC CGCACTCGCC GGTGCTTTAT CCCTGTCTTT
51  GGCCGCCCGGT GCAGTTGCTG CCAACAAACC GGCAAGCAAC GCAACAGGCG
101 TTCATAAATC CGCCCATGGC TCTTGCGGCG CGTCCAAATC TGCCGAAGGT
151 TCGTGCGGCG CGGCTGGTTC TAAAGCAGGC GAAGGCAAAT GCGGCGAGGG
201 CAAATGCGGT GCGACCGTAA AAAAAACCCA CAAACACACC AAAGCATCTA
251 AAGCCAAGGC CAAATCTGCC GAAGGCAAAT GCGGCGAAGG CAAATGCGGT
301 TCTAATAAA
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2412.a>:

```
a716.pep
1  MNKNIAAALA GALSLSLAAG AVAANKPASN ATGVHKSAGH SCGASKSAEG
51  SCGAAGSKAG EGKCGEGKCG ATVKKTHKHT KASKAKAKSA EGKCGEGKCG
101 SK*
```

a716/m716 100.0% identity in 102 aa overlap

	10	20	30	40	50	60
a716.pep	MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHKSAGHSCGASKSAEGSCGAAGSKAG					
m716	MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHKSAGHSCGASKSAEGSCGAAGSKAG					
	10	20	30	40	50	60
	70	80	90	100		
a716.pep	EGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSKX					
m716	EGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSKX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2413>:

```
g717.seq
1  ATGGACACAA AAGAAATCCT CGGCTACGCG GCAGGCTCGA TCGGCAGCGC
```

```

51  GGTTTTAGCC  GTCATCATCC  TGCCGCTGCT  GTCGTGGTAT  TTCcccgCCG
101  ACGACATCGG  GCGCATCGTG  CTGATGCAGA  CGGCGGCGGG  ACTGACGGTG
151  TCGGTATTGT  GCCTCGGGCT  GGATCAGGCA  TACGTCCGCG  AATACTATGC
201  CGCCGCCGAC  AAAGACACTT  TGTTCAAAAC  CCTGTTCTTG  CCGCCGCTGC
251  TGTTTTCGCG  CGCGATAGCC  GCCCTGCTGC  TTTCCCGCCC  GTCCCTGCCG
301  TCTGAAATCC  TGTTTTCGCT  CGACGATGCC  GCCGCCGGCA  TCGGGCTGGT
351  GCTGTTTGAA  CTGAGCTTCC  TGCCCATCCG  CTTTCTCTTA  CTGGTTTTCG
401  GTATGGAAGG  GCGCGCCCTT  GCCTTTTCGT  CCGCGCAACT  CGTGCCCAAA
451  CTCGCCATTC  TGCTGCTGTT  GCCGCTGACG  GTCGGGCTGC  TGCACTTTCC
501  GCGGAACACC  TCCGTCTGTA  CCGCCGTTTA  CGCGCTGGCA  AACCTTGCCG
551  CCGCCGCCCT  TTTGCTGTTT  CAAAACCGAT  GCCGTCTGAA  GGCGCTCCGG
601  CGCGCGCCGT  TTTGCCCGCG  CGTCTGCAC  CGGGGGCTGC  GCTACGGCAT
651  ACCGCTCGCA  CTGAGCAGCC  TTGCCTATTG  GGGGCTGGCA  TCCGCCGACC
701  GTTTGTCTCT  GAAAAATAT  GCGGGCCTGG  AACAGCTCGG  CGTTTATTCG
751  ATGGGTATTT  CGTTCGGCGG  GCGGCGATTA  TTGCTCCAAA  GCATCTTTTC
801  AACGCTCTGG  ACACCGTATA  TTTCCGCTGC  AATCGAAGAA  AACGCCACGC
851  CCGCCCGCCT  CTCGGCAACG  GCAGAATCCG  CCGCCGCCCT  GCTTGCCCTC
901  GCCCTCTGCC  TGACCGGAAT  TTTCTCGCCC  CTCGCCCTCC  TCCTGCTGCC
951  GGAAAACTAC  GCCGCCGTCC  GGTTTACCGT  CGTATCGTGT  ATGCTGccgc
1001  cgtctGTTTAA  CACGCTGACC  GAAATCAGCG  GCATCGGTTT  GAACGTCGTC
1051  CGCAAAACGC  GTCCGATCGC  GCTTGCCACC  TTGGGCGCGC  TGGCGGCAAA
1101  CCGTGTGCTG  CTGGGGCTTG  CCGTACCGTC  CGGCGGCACG  CGCGGCGCGG
1151  CGGTTGCGCT  TGCCGCCTCA  TTCTGGTTGT  TTTTGTGTTT  CAAGACAGAA
1201  AGCTCCTGCC  GCCTGTGGCA  GCCGCTCAAA  CGCCTGCCGC  TTTATATGCA
1251  CACATTGTTT  TGCTTgCCT  CCTCGGCGGC  CTACACCTGC  TTCGGCACAC
1301  CGGCAAACTA  CCGcctgttt  gccggcgat  GGGCGGCATA  TCTGGCAGGC
1351  TGCATCCTGC  GCCACCGGAA  AAATTTGCAC  AAATGTTTC  ATTATTTGAA
1401  AAAACAAGGT  TTCCATTAT  GA

```

This corresponds to the amino acid sequence <SEQ ID 2414; ORF 717.ng>:

```

g717.pep
1  MDTKEILGYA AGSIGSAVLA VIILPLLSWY FPADDIGRIV LMQTAAGLTV
51  SVLCLGLDQA YVREYYAAAD KDTLFKTLFL PPLLFSAIA ALLLSRPSLP
101  SEILFSLDDA AAGIGLVLEF LSFLPIRELL LVLRMEGRAL AFSSAQLVPR
151  LAILLLLPLT VGLLHFPAANT SVLTAVYALA NLAAAFLLF QNRCRLKAVR
201  RAFESPVLH RGLRYGIPLA LSSLAYWGLA SADRLFLKKY AGLEQLGVYS
251  MGISFSGAAL LLOSIFSTVW TPYIFRAIEE NATPARLSAT AESAAALLAS
301  ALCLTGFISE LASLLLPENY AAVRFTVVSC MLPLFYTLT EISGIGLNVV
351  RKTRPILALAT LGALAAANLLL LGLAVPSGGT RGAAVACAAS FWLFFVFKTE
401  SSCRLWQPLK RLPLYMHTLF CLASSAAYTC FGTANYPLF AGVWAAAYLAG
451  CILRHRKNLH KLFHYLKKQG FPL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2415>:

```

m717.seq
1  ATGGACACAA AAGAAATCCT CGGCTACGCG GCAGGCTCGA TCGGCAGCGC
51  GGTTTTAGCC  GTCATCATCC  TGCCGCTGCT  GTCGTGGTAT  TTCCCGCGCG
101  ACGACATCGG  GCGCATCGTG  CTGATGCAGA  CGGCGGCGGG  GCTGACGGTG
151  TCGGTGTTGT  GCCTCGGGCT  GGATCAGGCA  TACGTCCGCG  AATACTATGC
201  CACCGCCGAC  AAAGACACTT  TGTTCAAAAC  CCTGTTCTTG  CCGCCGCTGC
251  TGCTGCCGCG  CGCGATAGCC  GCCCTGCTGC  TTTCCCGCCC  GTCCCTGCCG
301  TCTGAAATCC  TGTTTCACT  CGACGATGCC  GCCGCCGGCA  TCGGGCTGGT
351  GCTGTTTGAA  CTGAGCTTCC  TGCCCATCCG  CTTTCTCTTA  CTGGTTTTCG
401  GTATGGAAGG  ACGCGCCCTT  GCCTTTTCGT  CCGCGCAACT  CGTGCCCAAG
451  CTCGCCATCC  TGCTGCTGCT  GCCGCTGACG  GTCGGGCTGC  TGCACTTTCC
501  AGCGAACACC  GCCGTCTGTA  CCGCCGTTTA  CGCGCTGGCA  AACCTTGCCG
551  CCGCCGCCCT  TTTGCTGTTT  CAAAACCGAT  GCCGTCTGAA  GGCCGTCCGG
601  CACGCACCGT  TTTGCCCGCG  CGTCTGCAC  CGGGGGCTGC  GCTACGGCAT
651  ACCGATCGCA  CTGAGCAGCA  TCGCCTATTG  GGGGCTGGCA  TCCGCCGACC
701  GTTTGTCTCT  GAAAAATAT  GCGGGCCTGG  AACAGCTCGG  CGTTTATTCG
751  ATGGGTATTT  CGTTCGGCGG  GCGGCGATTA  TTGTTCCAAA  GCATCTTTTC
801  AACGCTCTGG  ACACCGTATA  TTTCCGCGCG  AATCGAAGAA  AACGCCCCGC
851  CCGCCCGCCT  CTCGGCAACG  GCAGAATCCG  CCGCCGCCCT  GCTTGCCCTC
901  GCCCTCTGCC  TGACCGGCAT  TTTCTCGCCC  CTGCGCTCCC  TCCTGCTGCC
951  GGAAAACTAC  GCCGCCGTCC  GGTTTATCGT  CGTATCGTGT  ATGCTGCCGC
1001  CGCTGTTTTC  CACGCTGGCG  GAAATCAGCG  GCATCGGTTT  GAACGTCGTC
1051  CGCAAAACGC  GCCGATCGC  GCTCGCCACC  TTGGGCGCGC  TGGCGGCAAA
1101  CCTGCTGCTG  CTGGGGCTTG  CCGTGCCGTC  CGCGGCGCGG  CGCGGCGCGG
1151  CGGTTGCCCT  TGCCGCCTCA  TTCTGGCTGT  TTTTGCCTT  CAAGACCGAA
1201  AGCTCCTGCC  GCCTGTGGCA  GCCGCTCAAA  CGCCTGCCGC  TTTATCTGCA
1251  CACATTGTTT  TGCTTgCCT  CCTCGGCGGC  CTACACCTGC  TTCGGCACGC
1301  CGGCAAACTA  TCCCCTGTTT  GCGGCGGTAT  GGGCGGCATA  TCTGGCAGGC
1351  TGCATCCTGC  GCCACCGGAA  AGATTTGCAC  AAATGTTTC  ATTATTTGAA
1401  AAAACAAGGT  TTCCATTAT  GA

```

This corresponds to the amino acid sequence <SEQ ID 2416; ORF 717>:

m717.pep

```

1  MDTKEILGYA AGSIGSAVLA VIILPLLSWY FPADDIGRIV LMOTAAGLTV
51  SVLCLGLDQA YVREYYATAD KDTLFKTLFL PPLLSAAAIA ALLSRPSLP
101 SEILFSLDDA AAGIGLVLE LSFLPIRFL LVLMEGRAL AFSSAQLVPK
151 LAIIIIIIIT VGLLHFPANT AVLTAVYALA NLAAAFLLF QNRCRLKAVR
201 HAPFSPAVLH RGLRYGPIA LSSIAWGLA SADRLFLKKY AGLEQLGVYS
251 MGISFGGAAL LFQSFSTVW TPYIFRAIEE NAPPARLSAT AESAAALLAS
301 ALCLTGIFSP LASLLLPENY AAVRFIVVSC MLPPLFCTLA EISGIGLNVV
351 RKTRPIALAT LGALAANLLL LGLAVPSGGA RGAAVACAAS FWLFFAFKTE
401 SSCRLWQPLK RLPLYLHTLF CLTSSAAYTC FGTFANYPLF AGVWAAYLAG
451 CILRHRKDLH KLFHYLKKQG FPL*

```

m717/g717 96.4% identity in 473 aa overlap

m717.pep	10	20	30	40	50	60
	MDTKEILGYAAGSIGSAVLAVIILPLLSWYFPADDIGRIVLMQTAAGLTVSVLCLGLDQA					
g717	MDTKEILGYAAGSIGSAVLAVIILPLLSWYFPADDIGRIVLMQTAAGLTVSVLCLGLDQA					
	10	20	30	40	50	60
m717.pep	70	80	90	100	110	120
	YVREYYATADKDTLFKTLFLPPLLSAAAIAALLSRPSLPSEILFSLDDAAAGIGLVLE					
g717	YVREYYAADKDTLFKTLFLPPLLSAAAIAALLSRPSLPSEILFSLDDAAAGIGLVLE					
	70	80	90	100	110	120
m717.pep	130	140	150	160	170	180
	LSFLPIRFLLLVLRMEGRALAFSSAQLVPKLAILLLPLTVGLLHFPANTAVLTAVYALA					
g717	LSFLPIRFLLLVLRMEGRALAFSSAQLVPKLAILLLPLTVGLLHFPANTSVLTVAVYALA					
	130	140	150	160	170	180
m717.pep	190	200	210	220	230	240
	NLAAAFLLFQNRCRLKAVRHAPFSPAVLHRLRYGPIALSSIAWGLASADRLFLKKY					
g717	NLAAAFLLFQNRCRLKAVRRAPFSPAVLHRLRYGPIALSSIAWGLASADRLFLKKY					
	190	200	210	220	230	240
m717.pep	250	260	270	280	290	300
	AGLEQLGVYSMGISFGGAALLFQSFSTVWTPYIFRAIEENAPPARLSATAESAAALLAS					
g717	AGLEQLGVYSMGISFGGAALLFQSFSTVWTPYIFRAIEENAPPARLSATAESAAALLAS					
	250	260	270	280	290	300
m717.pep	310	320	330	340	350	360
	ALCLTGIFSPLASLLLPENYAAVRFIVVSCMLPPLFCTLAETISGIGLNVVRKTRPIALAT					
g717	ALCLTGIFSPLASLLLPENYAAVRFIVVSCMLPPLFYTLTISGIGLNVVRKTRPIALAT					
	310	320	330	340	350	360
m717.pep	370	380	390	400	410	420
	LGALAANLLLGLAVPSGGARGAACAASFWLFFAFKTESSCRLWQPLKRLPLYLHTLF					
g717	LGALAANLLLGLAVPSGGTRCAACAASFWLFFVFKTESSCRLWQPLKRLPLYMHTLF					
	370	380	390	400	410	420
m717.pep	430	440	450	460	470	
	CLTSSAAYTCFGTFANYPLFAGVWAAYLAGCILRHRKDLHKLPHYLKKQGFPLX					
g717	CLASSAAYTCFGTFANYPLFAGVWAAYLAGCILRHRKDLHKLPHYLKKQGFPLX					
	430	440	450	460	470	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2417>:

a717.seq

```

1  ATGGACACAA AAGAAATCCT CGGCTACGCG GCAGGCTCGA TCGGCAGCGC
51  GGTTTTAGCC GTCATCATCC TGCCGCTGCT GTCGTGGTAT TTCCCTGCCG
101 ACGACATCGG ACGCATCGTG CTGATGCAGA CGGCGGCGCG GCTGACGGTG
151 TCGGTGTTGT GCCTCGGGCT GGATCAGGCA TACGTCCGCG AATACTATGC
201 CGCCGCCGAC AAAGACACTT TGTTCAAAC CCTGTTCTGT CCGCCGCTGC

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1158

```

251 TGTCTGCCGC CGCGATAGCC GCCCTGCTGC TTTCCCGCCC ATCCCTGCCG
301 TCTGAAATCC TGTTCCTGCT CGACGATGCC GCCGCCGCCA TCGGGCTGGT
351 GCTGTTTGAA CTGAGCTTCC TGCCCATCCG CTTTCTCTTA CTGGTTTTCG
401 GTATGGAAGG ACGCGCCCTT GCCTTTTCGT CCGCGCAACT CGTGTCGAAG
451 CTCGCCATCC TGCTGCTGCT GCCGCTGACG GTCGGGCTGC TGCACCTTCC
501 GCGGAACACC GCCGTCCTGA CCGCCGTCTTA CCGCTGGCA AACCTTGCCG
551 CCGCCGCCCTT TTTGCTGTTT CAAAACCGAT GCCGTCTGAA GGCCGTCGGG
601 ACGGCACCGT TTTCATCC3C CGTCTGCAT CCGGCGCTGC GCTACGGCAT
651 ACCGATCGCA CTAAGCAGCA TCGCCTATTG GGGGCTGCGA TCCGCCGACC
701 GTTTGTTTCT GAAAAAATAT GCGGCGCTAG AACAGCTCGG CGTTTATTCG
751 ATGGGTATTT CGTTCGGCGG AGCGGCATTA TTGTTCCAAA GCATCTTTTC
801 AACGGTCTGG ACACCGTATA TTTTCGCGC AATCGAAGCA AACGCCCCGC
851 CCGCCCCCCT CTCGGCAACG GCAGAATCCG CCGCCGCCCT GCTTGCCCTCC
901 GCCCTCTGCC TGACCGGCAT TTTCTCGCCC CTCGCCCTCC TCCTGCTGCC
951 GGAAGTCTAC GCCGCCGTC GGTATTATCGT CGTATCGTGT ATGCTGCCTC
1001 CGCTGTTTTC CACGCTGGTA GAAATCAGCG GCATCGGTTT GAACGTCGTC
1051 CGAAAAACAC GCCCGATCGC GCTCGCCACC TTGGGCGCGC TGGCGGCAAA
1101 CCTGCTGCTG CTGGGGCTTG CGTACCGTC CCGCGGCGCG CGCGGCGCGG
1151 CGGTTGCCTG TGCCCGCTCA TTTTGCTGT TTTTGTGTTT CAAGACCGAA
1201 AGCTCCTGCC GCCTGTGGCA GCCGCTCAA CGCCTGCCGC TTTATATGCA
1251 CACATTGTTT TGCCTGGCCT CCGCGCGCG CTACACCTGC TTCGCACTC
1301 CGGCAACTA CCCCCTGTTT GCCGGCGTAT GGGCGGTATA TCTGGCAGGC
1351 TGCATCTGCG GCCACCGGAA AGATTGCGAC AAAGTGTTC ATTATTGAA
1401 AAAACAAGGT TTCCATTAT GA

```

This corresponds to the amino acid sequence <SEQ ID 2418; ORF 717.a>:

```

a717.pep
1 MDTKEILGYA AGSIGSAVLA VIILPLLSWY FPADDIGRIV LMQTAAGLTV
51 SVLCLGLDQA YVREYYAAAD KDTLFKTLFL PPLLSAAAIA ALLLSRPSLP
101 SEILFSLDDA AAGIGLVLE LSFPIRFL LVLMEGRAL AFSSAQLVSK
151 LAIILLPLT VGLLHFPANT AVLTAVYALA NLAAAFLLF QNRCRLKAVR
201 RAPFSSAVLH RGLRYGPIA LSSIAYWGLA SADRLFLKKY AGLEQLGVYS
251 MGISFGGAAL LFQSFSTVW TPYIFRAIEA NAPPARLSAT AESAAALLAS
301 ALCLTGIFSP LASLLLPENY AAVRFIVVSC MLPLFCTLV EISGIGLNVV
351 RKTRPIALAT LGALANLLL LGLAVPSGGA RGAUVACAAS FWLFVFKTE
401 SSCRLWQPLK RPLYMHTLF CLASSAAYTC FGTPANYPLF AGVWAVYLAG
451 CILRHRKDLH KLFHYLKKQG FPL*

```

a717/m717 97.9% identity in 473 aa overlap

	10	20	30	40	50	60
a717.pep	MDTKEILGYAAGSIGSAVLAVIILPLLSWYFPADDIGRIVLMQTAAGLTVSVLCLGLDQA					
m717	MDTKEILGYAAGSIGSAVLAVIILPLLSWYFPADDIGRIVLMQTAAGLTVSVLCLGLDQA					
	10	20	30	40	50	60
	70	80	90	100	110	120
a717.pep	YVREYYAAADKDTLFKTLFLPPLLSAAAIAALLLSRPSLPSEILFSLDDAAAGIGLVLE					
m717	YVREYYATADKDTLFKTLFLPPLLSAAAIAALLLSRPSLPSEILFSLDDAAAGIGLVLE					
	70	80	90	100	110	120
	130	140	150	160	170	180
a717.pep	LSFLPIRFLLLVLRMEGRALAFSSAQLVSKLAILLLPLTVGLLHFPANTAVLTAVYALA					
m717	LSFLPIRFLLLVLRMEGRALAFSSAQLVSKLAILLLPLTVGLLHFPANTAVLTAVYALA					
	130	140	150	160	170	180
	190	200	210	220	230	240
a717.pep	NLAAAFLLFQNRCRLKAVRRAPFSSAVLHRLRYGIPALSSIAYWGLASADRLFLKKY					
m717	NLAAAFLLFQNRCRLKAVRHAPFSPAVLHRLRYGIPALSSIAYWGLASADRLFLKKY					
	190	200	210	220	230	240
	250	260	270	280	290	300
a717.pep	AGLEQLGVYSMGISFGGAALLFQSFSTVWTPYIFRAIEANAPARLSATAESAAALLAS					

1159

```

|||||
m717  AGLEQLGVYSMGISFGGAALLFQSI FSTVWTPYIFRAIEENAPPARLSATAESAAALLAS
      250      260      270      280      290      300

      310      320      330      340      350      360
a717.ppep ALCLTGIFSEPLASLLLPENYAAVR FIVVSCMLPPLFCTLVEISGIGLNVRKTRPIALAT
|||||
m717  ALCLTGIFSEPLASLLLPENYAAVR FIVVSCMLPPLFCTLA EISGIGLNVRKTRPIALAT
      310      320      330      340      350      360

      370      380      390      400      410      420
a717.ppep LGALAANLLLGLAVPSGGARGA AVACAASF WLFVFKTESSCRLWQPLKRLPLYMHTLF
|||||
m717  LGALAANLLLGLAVPSGGARGA AVACAASF WLFVFAFKTESSCRLWQPLKRLPLYLHTLF
      370      380      390      400      410      420

      430      440      450      460      470
a717.ppep CLASSAAYTCFGTPANYPLFAGVWAVYLAGC ILRHRKDLHKL FHYLKKQGFPLX
|||||
m717  CLTSSAAYTCFGTPANYPLFAGVWAA YLAGC ILRHRKDLHKL FHYLKKQGFPLX
      430      440      450      460      470

```

g718.seq not found yet

g718.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2419>:

```

m718.seq
1   TCAGACGGCC TTTACGTACC CCGAAACTTT ATCCACCGCC CGCAAAGCTG
51  GTTCAAATGG GACAAAGACA ACGGGCTGCT GCTGCGTACC CGCGAAATC
101 CGGAAGGCGA AGCGTTGTGG CCGCTGGGCT GGGTCGTTCA TACCCAAAAA
151 TCGCGCAGCG TCCAGCAGGC GCGCAACGGG CTTTCCGCA CGCTTTCCTG
201 GCTGTATATG TTCAAACACT ACGCCGTCCA CGATTTTGCC GAGTTTGTGG
251 AGCTGTACGG CATGCCCATC CGTATCGGCA AATACGGCGC GGGCGCAACC
301 AAAGAGGAAA AAAACACCCT GCTTCGAGCG GTGGCGGAAA TCGGTCACAA
351 CGCGGCAGGC ATCATGCCAG AAGGTATGGA AATAGAGCTC CACAACGCGG
401 CAAACGGTAC GACGGCAACC AGCAATCCGT TTTTGCAGAT GGCCGACTGG
451 TGCGAAAAAT CGGCGGCGCG GCTGATTTTG GGGCAAACGC TGACCGCGG
501 TGCGGACGGA AAATCCAGCA CCAACGCGCT GGGCAATATC CACAACGAGG
551 TACGCGCGGA TTTGCTGGTG TCGGACGCAA AACAGGTGGC GCAAACCATC
601 ACAAGCCAAA TCATCGGACC GTTCTGCAA ATCAACTATC CCCATGCCGA
651 CCCAAACCGC GTGCCGAAAT TTGAATTTGA CACGCGCGAG CCGAAAGACA
701 TCGCGGTCTT TGCCGACGCT ATCCCGAAAC TGGTGGATGT CGSCGTACAA
751 ATCCCGGAAA GCTGGGTGCG CGACAACTG GTCATTCCAG ATSTGCAGGA
801 GGGTGAGGCT GTGTTGGTGC GGCAGGTACC GGACAATCCG GTAAACAGAA
851 CTGCATTGGC GGCTTTATCC GCCACACCG TACCATCTAA GGCTACGGGC
901 AGGCATCAGG AAATATTGGA CGGCGCGTTG GATGACGCGC TGSTTGAGCC
951 CGATTTCAT TCTCAGCTCA ACCCGATGGT GCGTCAGGCG GTTGCCGCAC
1001 TTAATGCTTG CAACAGCTAC GAGGAGGCAG ATGCCGCACT GAATGCGCTT
1051 TATCCGAATT TGGACAACGC GAAACTGCGT ACCTATATGC AGCAGGCCTT
1101 GTTTATCAGC GATATTTTGG GACAAGACCA TGCCGCGGCC TGA

```

This corresponds to the amino acid sequence <SEQ ID 2420; ORF 718>:

```

m718.pep
1   SDGLYVPRNF IHRPQSWFKW DKDNGLLLR T RENPEGEALW PLGWVVHTQK
51  SRSVQQARNG LFRTLSWLYM FKHYAVHDF A EFLELYGMPI RIGKYGAGAT
101 KEEKNTLLRA VAEIGHNAAG IMPEGMEIEL HNAANGTTAT SNFFLQMAW
151 CEKSAARLIL GQTLTSGADG KSSTNALGNI HNEVRRDLV SDAKQVAQTI
201 TSQIIGPFLQ INYPHADPNR VPKEFDTRE PKDIAVFADA IPKLVDVG VQ
251 IPESWVRDKL VIPDVQEGEA VLVROQVDPN VNRTALAALS AHTVPSKATG
301 RHQEILDGAL DDALVEPDFN SQLNPMVRQA VAALNACNSY EEADAALNAL
351 YPNLDNAKLR TYMQQALFIS DILGQDHARA *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2421>:

1160

a718.seq

```

1  ATGGAGCCGA TAATGGCAAA AAAGAACAAT AAAACTAAAA TCCAAAAGCC
51  CGAAGCTGCA TTGCAGACGG ACGTGGCTCA AATTACAGCG ACCGGTCGAG
101 TTATCGCCGA GCATCCATCC AATTTTATTA CGCCGCAAAA GATGCGCGCC
151 CTCTTCGAGG ACGCAGAAAG CCGTGACATC CGCGCCCAAC ACGAGCTTTT
201 CGCGGACATT GAGGAGCGCG ACAGCGACAT CGCGGCCAAT ATGGGGACGC
251 GCAAACGCGC GCTGCTGACG CTCAACTGGC GCGTCGCCCC GCCGCGAAAT
301 GCGACGCCCC AAGAAGAAAA GCTGTCCGAC CAAGCCTACG AAATGATGGA
351 CAGCCTGCCT ACCCTCGAAG ACCTGATTAT GGATTTGATG GACGCGGTAG
401 GGCACGGATT TTCTGCGTTG GAGGTGAGT GGGTATTTTC AGACGGCCTT
451 TACCTACCCC GAAACTTTAT CCACCGCCCC CAAAGCTGGT TCAAATGGGA
501 CAAAGACAAC GGGCTGCTGC TCGGTACCCG CGAAAAATCG GAAGGCGAAG
551 CGTTGTGGCC GCTGGGCTGG GTCGTTTATA CCCAAAAATC GCGCAGCGTC
601 CAGCAGGCGC GCAACGGGCT TTCCGCGACG CTTTCCTGGC TGTATATGTT
651 CAAACACTAC GCCGTCCACG ATTTTGCCGA GTTTTGGAG CTGTACGGCA
701 TGCCCATCCG TATCGGCAAA TACGGCGCGG GCGCAACCAA AGAGGAAAAA
751 AACACCCTGC TTCGAGCGGT GCGGGAATC GGTCAACAAC CGGCAGGCAT
801 CATGCCAGAA GGTATGGAAA TCGAGCTGCA CAACGCGGCA AACGGCATGA
851 CTTCCGCCGG CAATCCGTTT TTGCAGATGG CCGACTGCTG CGAAAAATCG
901 GCGGCGCGGC TGATTTTGGG GCAAACGCTA ACCAGCGGTG CGGACGGAAA
951 ATCCAGCACC AACGCGCTGG GCAATATCCA CAACGAGATA CGCCGCGATT
1001 TGCTGGTGTC GGACGCAAAA CAGGTGGCGC AAACCATCAC AAGCCAAATC
1051 ATCGGACCGT TCCTGCAAA TCACTATCCC CATGCCGACC CAAACCGCGT
1101 GCCGAAATTT GAAATTGACA CGCGCGAGCC GAAAGACATC GCGGTCTTTG
1151 CCGACGCTAT CCCGAAACTG GTGGATGTCG GCGTACAAAT CCCCAGAAAGC
1201 TGGGTGCGCG ACAAACTGST CATTCCAGAT GTGCAGGAGG GTGAGGCTGT
1251 GTTGGTGCGG CAGGTACCGG ACAATCCGGT AAACAGAACT GCATTGGCGG
1301 CTTTATCCGC CCACACCGTA CCATCTAAGG CTACGGGCAG GCATCAGGAA
1351 ATATTGGACG GCGCGTTGGA TGACGCGCTG GTTGAGCCCG ATTTCAATTC
1401 TCAGCTCAAC CCGATGGTGC GTCAGGCGGT TGCCGCACTT AATGCTTGCA
1451 ACAGCTACGA GGAGGCAGAT GCCGCACTGA ATGCGCTTTA TCCGAATTTG
1501 GACAACGCGA AACTGCGTAC CTATATGCAG CAGGCCTTGT TTATCAGCGA
1551 TATTTTGGGA CAAGACCATG CCCGCGCCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2422; ORF 718.a>:

a718.pep

```

1  MEPIMAKKNN KTKIQKPEAA LQTDVAQITA TGRVIAEHPS NFITPQKMRA
51  LFEDAESGDI RAQHELFADI EERDSIDIAAN MGTRKRALLT LNWRVAPPRN
101 ATPEEEEKLS QAYEMMDSL P TLEDLIMDLM DAVGHGFSAL EVEWVFS DGL
151 YLPRNFIHRP QSWFKWDKDN GLLLRTRNP EGEALWPLGW VVHTQKRSRV
201 QQARNGLFRT LSWLYMFKHY AVHDFAEFLE LYGMPIRISK YCAGATKEEK
251 NTLRAVAEI GHNAAGIMPE GMEIELHNA NGMTSAGNPF LQMADWCEKS
301 AARLILGQTL TSGADGKSST NALGNIHNEI RRDLLVSDAK QVAQTITSQI
351 IGPFLQINYP HADPNRVPKF EFDTREPKDI AVFADAIPKL VCVGVQIPES
401 WVRDKLVIPD VQEGEAVLYR QVPDNPVNR ALAALSHTV PSKATGRHQE
451 ILDGALDDAL VEPDFNSQLN PMVRQAAVAL NACNSYEEAD AALNALYPNL
501 DNAKLRTYMQ QALFISDILG QDHARA*

```

a718/m718 98.4% identity in 380 aa overlap

	120	130	140	150	160	170
a718.pep	DSLPTLEDLIMDLMDAVGHGFSALEVEWVFS DGLYLPRNFIHRPQSWFKWDKDNGLLLRT					
m718	: SDGLYVPRNFIHRPQSWFKWDKDNGLLLRT					
				10	20	30
	180	190	200	210	220	230
a718.pep	RENPEGEALWPLGWVVHTQKRSVQQARNGLFRTLSWLYMFKHYAVHDFAEFLELYGMPI					
m718	RENPEGEALWPLGWVVHTQKRSVQQARNGLFRTLSWLYMFKHYAVHDFAEFLELYGMPI					
	40	50	60	70	80	90
	240	250	260	270	280	290
a718.pep	RICKYGAGATKEEKNTLLRAVAEIGHNAAGIMPEGMEIELHNAANGMTSAGNPFQOMADW					
m718	RICKYGAGATKEEKNTLLRAVAEIGHNAAGIMPEGMEIELHNAANGTTATSNPFLQOMADW					

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	100	110	120	130	140	150
a718.pep	300	310	320	330	340	350
	CEKSAARLILGQTLTSGADGKSSTNALGNIHNEIRRDLLVSDAKQVAQTITSQIIGPFLQ					
m718	160	170	180	190	200	210
	CEKSAARLILGQTLTSGADGKSSTNALGNIHNEVRRDLLVSDAKQVAQTITSQIIGPFLQ					
a718.pep	360	370	380	390	400	410
	INYPHADPNRPVKFEFDTREPKDIAVFADAI PKLVDPGVQIPESWVRDKLVIPDVQEGEA					
m718	220	230	240	250	260	270
	INYPHADPNRPVKFEFDTREPKDIAVFADAI PKLVDPGVQIPESWVRDKLVIPDVQEGEA					
a718.pep	420	430	440	450	460	470
	VLVRQVPDNPVNR TALAALSAHTVPSKATGRHQEILDGALDDALVEPDFNSQLNPMVRQA					
m718	280	290	300	310	320	330
	VLVRQVPDNPVNR TALAALSAHTVPSKATGRHQEILDGALDDALVEPDFNSQLNPMVRQA					
a718.pep	480	490	500	510	520	
	VAALNACNSYEEADAALNALYPNLDNAKLRTYMQQALFISDILGQDHARAX					
m718	340	350	360	370	380	
	VAALNACNSYEEADAALNALYPNLDNAKLRTYMQQALFISDILGQDHARAX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2423>:

m718-1.seq

```

1  ATGGAGCCGA TAATGGCAAA AAGAACAAT AAAACTAAAA TCCAAAAGCC
51  CGAAGCTGCA TTGCAGACGG ACGTGGCTCA AATTACGGCG ACCGGTCGGG
101 TTATCGCCGA GCATCCGTCC AATTTTATTA CGCCGCAAAA GATGCGGGCC
151 CTCTTCGAGG ACGCAGAAAG CGCGCACATC CGCGCCCAAC ACGAGCTTTT
201 CGCGGACATT GAGGAGCGCG ACAGCGACAT CGCGGCAAAAT ATGGGGACGC
251 GCAAACGCGC GCTGCTGACG CTCAACTGGC GCGTCGCCCC GCCGCGAAAT
301 GCGACGCCCG AAGAAGAAAA GCTGTCCGAC CAAGCCTACG AAATGATGGA
351 CAGCCTGCCT ACCCTCGAAG ACCTGATTAT GGATTTGATG GACGCGGTAG
401 GGCACGGATT TTCTGCGTTG GAGGTCGAGT GGGTATTTTC AGACGCCTT
451 TACCTACCCC GAAACTTTAT CCACCGCCCG CAAAGCTGGT TCAATGGGA
501 CAAAGACAAC GGGCTGCTGC TGCGTACCCG CGAAAATCCG GAAGGCGAAG
551 CGTTGTGCCC GCTGGGCTGG GTCGTTTATA CCCAAAATC GCGCAGCGTC
601 CAGCAGCGCG GCAACGGGCT TTTCCGCACG CTTTCTTGGC TGTATATGTT
651 CATGCCAGAA GCCGTCCACG ATTTTGCCGA GTTTTGGAG CTGTACGGCA
701 TGCCCATCCG TATCGGCAAA TACGGCGCGG GCGCAACCAA AGAGGAAAAA
751 AACACCCCTG TTCGAGCGGT GCGGGAATC GGTCAACAAC CGGCAGGCAT
801 CATGCCAGAA GGTATGGAAA TAGAGCTCCA CAACGCGGCA AACGGTACGA
851 CCGCAACCGA CAATCCGTTT TTGCAGATGG CCGACTGGTG CGAAAAATCG
901 CGCGCGCGCG TGATTTTGGG GCAACGCTG ACCAGCGGTG CGGACGGAAA
951 ATCCAGCACG AACGCGCTGG GCAATATCCA CAACGAGGTA CGCCGCGATT
1001 TGCTGGTGTC GGACGCAAAA CAGGTGGCGC AAACCATCAC AAGCCAAATC
1051 ATCCGACCGT TCCTGCAAAAT CAACTATCCC CATGCCGACC CAAACGCGGT
1101 GCCGAAATTT GAATTTGACA CGCGCGAGCC GAAAGACATC GCGGCTTTTG
1151 CCGACGCTAT CCCGAAACTG GTGGATGTCG GCGTACAAAT CCCCAGAAAGC
1201 TGGGTGCGCG ACAAACCTGGT CATTCCAGAT GTGCAGGAGG GTGAGGCTGT
1251 GTTGGTGCGG CAGGTACCGG ACAATCCGGT AAACAGAACT GCATTGGCGG
1301 CTTTATCCCG CCACACCGTA CCATCTAAGG CTACGGGCAG GCATCAGGAA
1351 ATATTGGACG GCGCGTTGGA TGACGCGCTG GTTGAGCCCG ATTTCAATTTC
1401 TCAGCTCAAC CCGATGGTGC GTCAGGCGGT TGCCGCACCT AATGCTTGCA
1451 ACAGCTACGA GGAGGCAGAT GCCGCACTGA ATGCGCTTTA TCCGAATTTG
1501 GACAACGCGA AACTGCGTAC CTATATGCAG CAGGCCTTGT TTATCAGCGA
1551 TATTTTGGGA CAAGACCATG CCCGCGCCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2424; ORF 718-1>:

m718-1.pep.

```

1  MEPIMAKKNN KTKIQKPEAA LOTDVAQITA TGRVIAEHPS NFITPQKMRA
51  LFEDAESGDI RAQHFLFADI EERDS DIAAN MGRKRALLT LNRVRAPPRN
101 ATPEEKLSD QAYEMMDSLP TLEDLIMDLN DAVGHGFSAL EVENVFSDGL
151 YLPRNFIHRP QSWFKWDKDN GLLLRTRNP EGEALWPLGW VVHTQKSRV
201 QARNGLFRT LSWLYMFKHY AVHDFAEFLE LYGMPIRIGK YGAGATKEEK
251 NTLRAVAEI GHNAAGIMPE GMEIELHNAA NGTTATSNPF LQADWCEKS
301 AARLILGQTL TSGADGKSST NALGNHNEV RRDLLVSDAK QVAQTITSQI

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351 IGPFLQINYP HADPNRVPKF EFDTREPKDI AVFADAIPKL VDVGVQIPES
401 WVRDKLVIPD VQEGEAVLVR QVPDNPVNRT ALAALSAHTV PSKATGRHQE
451 ILDGALDDAL VEPDFNSQLN PMVRQVAAL NACNSYEEAD AALNALYPNL
501 DNAKLRTYMQ QALFISDILG QDHARA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2425>:

```

a718.seq
1  ATGGAGCCGA TAATGGCAAA AAAGAACAAT AAAACTAAAA TCCAAAGGCC
51  CGAAGCTGCA TTGCAGACGG ACGTGGCTCA AATTACAGCG ACCGTCGAG
101 TTATCGCCGA GCATCCATCC AATTTTATTA CGCCGCAAAA GATGCGCGCC
151 CTCTTCGAGG ACGCAGAAAG CGGTGACATC CGCGCCCAAC ACGAGCTTTT
201 CGCGGACATT GAGGAGCGCG ACAGCGACAT CGCGGCAAAAT ATGGGGACGC
251 GCAAACGCGC GCTGCTGACG CTCAACTGGC GCGTCGCCCC GCCGCGAAAT
301 CGGACGCCCG AAGAAGAAAA GCTGTCCGAC CAAGCCTACG AAATGATGGA
351 CAGCGTGCCT ACCCTCGAAG ACCTGATTAT GGATTGTATG GACGCGGTAG
401 GGCACGGATT TTCTGCGTTG GAGGTCGAGT GGTATTATTTC AGACGGCCTT
451 TACCTACCCC GAAACTTTAT CCACCGCCCG CAAAGCTGGT TCAAATGGGA
501 CAAAGACAAC GGGCTGCTGC TGGCTACCCG CGAAAATCCG GAAGGCGAAG
551 CGTTGTGGCC GCTGGGCTGG GTCGTTTATA CCAAAAATC GCGCAGCGTC
601 CAGCAGGCGC GCAACGGGCT TTTCGACACG CTTTCCTGGC TGTATATGTT
651 CAAACACTAC GCCGTCCACG ATTTTTCGCA GTTTTGGAG CTGTACGGCA
701 TGCCCATCCG TATCGGCAAA TACGGCGCGG GCGCAACCAA AGAGGAAAAA
751 AACACCCCTG TTCGAGCGGT GCGGGAATC GGTCAACACG CGGCAGGCAT
801 CATGCCAGAA GGTATGGAAT TCGAGCTGCA CAACGCGGCA AACGGCATGA
851 CTTCGCGCGG CAATCCGTTT TTGCAGATGG CCGACTGGTG CGAAAAATCG
901 GCGGCGCGGC TGATTTTGGG GCAAACGCTA ACCAGCGGTG CGGACGGAAA
951 ATCCAGCACC AACCGCTGG GCAATATCCA CAACGAGATA CGCGCGGATT
1001 TGCTGCTGTC GGACGCAAAA CAGGTGGCGC AAACCATCAC AAGCCAAATC
1051 ATCGGACCGT TCCTGCAAT CAACTATCCC CATGCCGACC CAAACCGCGT
1101 GCCGAAATTT GAATTGACA CGCGCGAGCC GAAAGACATC GCGGTCTTTG
1151 CCGACGCTAT CCCGAAATG GTGGATGTCG GCGTACAAAT CCCGAAAGC
1201 TGGGTGCGCG ACAACTGGT CATTCCAGAT GTGCAGGAGG GTGAGGCTGT
1251 GTTGGTGGCG CAGGTACCGG ACAATCCGGT AACAGAACT GCATTGGCGG
1301 CTTTATCCGC CCACACCGTA CCATCTAAGG CTACGGGACG GCATCAGGAA
1351 ATATTGGACG GCGCGTTGGA TGACGCGCTG GTTGAGCCCG ATTTCAATTC
1401 TCAGCTCAAC CCGATGGTGC GTCAGGCGGT TGCCGCACTT AATGCTTGCA
1451 ACAGCTACGA GGAGGCGAGT GCCGCACTGA ATGCGCTTTA TCCGAATTTG
1501 GACAACGCGA AACTGCGTAC CTATATGCAG CAGGCTTGTG TTATCAGCGA
1551 TATTTTGGGA CAAGACCATG CCCGCGCCTG A

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This corresponds to the amino acid sequence <SEQ ID 2426; ORF 718-1.a>:

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a718.pep
1  MEPIMAKNN KTKIQKEAA LOTDVAQITA TGRVIAEHPS NFITPQKMRA
51  LFEDAESGDI RAQHELFADI EERDSIAAN MGRKRALLT LNRVAPPNRN
101 ATPEEKLSD QAYEMMDSL TLEDLIMDL DAVGHGFSAL EWEVVFSDGL
151 YLPRNFIHRP QSWFKWDKDN GLLRLTREN EGEALWPLGW VVHTQKRSRV
201 QQARNGLFRT LSWLYMFKHY AVHDFAEFLE LYGMPIRICK YGAGATKEEK
251 NTLRAVAEI GHNAAGIMPE GMEIELHNA NGMTSAGNPF LQADWCEKS
301 AARLILGQTL TSGADGKSST NALGNIHNEI RRDLVSDAK QVAQTITSQI
351 IGPFLQINYP HADPNRVPKF EFDTREPKDI AVFADAIPKL VDVGVQIPES
401 WVRDKLVIPD VQEGEAVLVR QVPDNPVNRT ALAALSAHTV PSKATGRHQE
451 ILDGALDDAL VEPDFNSQLN PMVRQVAAL NACNSYEEAD AALNALYPNL
501 DNAKLRTYMQ QALFISDILG QDHARA*

```

a718/m718-1 99.0% identity in 526 aa overlap

	10	20	30	40	50	60
a718.pep	MEPIMAKNNKTKIQKEAALQTDVAQITATGRVIAEHPSNFITPQKMRALEDAESGDI					
m718-1	MEPIMAKNNKTKIQKEAALQTDVAQITATGRVIAEHPSNFITPQKMRALEDAESGDI					
	10	20	30	40	50	60
	70	80	90	100	110	120
a718.pep	RAQHELFADIEERDSIAANMGRKRALLTLNRVAPPNRNATPEEEKLSDQAYEMMDSL					
m718-1	RAQHELFADIEERDSIAANMGRKRALLTLNRVAPPNRNATPEEEKLSDQAYEMMDSL					
	70	80	90	100	110	120
	130	140	150	160	170	180
a718.pep	TLEDLIMDLMDAVGHGFSALEVWVFSDGLYLFRNFIHRPQSWFKWDKNGLLRLTREN					
m718-1	TLEDLIMDLMDAVGHGFSALEVWVFSDGLYLFRNFIHRPQSWFKWDKNGLLRLTREN					
	130	140	150	160	170	180

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a718.pep	190	200	210	220	230	240
	ESEALWPLGWVVHTQKSRVQQARNGLFRTLWLYMFKHYAVHDFAEFLELYGMPIRIGK					
m718-1	ESEALWPLGWVVHTQKSRVQQARNGLFRTLWLYMFKHYAVHDFAEFLELYGMPIRIGK					
	190	200	210	220	230	240
a718.pep	250	260	270	280	290	300
	YGAGATKEEKNTLLRAVAEIGHNAAGIMPEGMEIELHNAANGMTSAGNPFLQADNCEKS					
m718-1	YGAGATKEEKNTLLRAVAEIGHNAAGIMPEGMEIELHNAANGTTATSNPFLQADNCEKS					
	250	260	270	280	290	300
a718.pep	310	320	330	340	350	360
	AARLILGQTLTSGADGKSSSTNALGNIHNEIRDLVSDAKQVAQTITSQIIGPFLQINYP					
m718-1	AARLILGQTLTSGADGKSSSTNALGNIHNEVRRDLVSDAKQVAQTITSQIIGPFLQINYP					
	310	320	330	340	350	360
a718.pep	370	380	390	400	410	420
	HADPNRVPKFEFDTREPKDIAVFADAI PKLVDVGVQIPESWVRDKLVI PDVQEGEAVLVR					
m718-1	HADPNRVPKFEFDTREPKDIAVFADAI PKLVDVGVQIPESWVRDKLVI PDVQEGEAVLVR					
	370	380	390	400	410	420
a718.pep	430	440	450	460	470	480
	QVPDNPVNRTALAALSAHTVPSKATGRHQEILDGALDDALVEPDFNSQLNPMVRQAVAAAL					
m718-1	QVPDNPVNRTALAALSAHTVPSKATGRHQEILDGALDDALVEPDFNSQLNPMVRQAVAAAL					
	430	440	450	460	470	480
a718.pep	490	500	510	520		
	NACNSYEEADAALNALYPNLDNAKLRTYMQQALFISDILGQDHARAX					
m718-1	NACNSYEEADAALNALYPNLDNAKLRTYMQQALFISDILGQDHARAX					
	490	500	510	520		

g719.seq not found yet

g719.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2427>:

m719.seq

1	ATGGCAAACG	GGAACATGAA	ACTGTCGTTG	GTGTTAACCG	CCCGAGATGA
51	CGGAGCGAGA	CGGCTACTGG	CTGATACTCA	ACGACAATTA	GATCGTACCG
101	CGAAATCGCG	GGCGCAACTT	GAACGGCAAA	GCCATACTTA	TGCGTTGACC
151	GGCATCCGCT	CAGAAAAACA	GATTCAACGC	GAAATCATGC	TGACACAGGC
201	TGCGTTTAAC	CGTTTGGCGC	GCAGCGGCAA	GGCATCACAA	AATGATTTGG
251	CACGGGCGGC	GGTCGCTACG	CGTAACCGAA	TTCGCGAGCT	GAACGCGGAA
301	CTGAAACAGG	GCACGGGATT	TGCGGACAAG	ATGGGAAAAA	TCGGAAGATT
351	CGGTGCAGCT	GCGGTGGCTG	GTGGCGCGGC	AGCGTATACG	GTGCTTAAGC
401	CTGCTATGGA	CAACAGAAAG	CAGCTTGATG	AGAACATCAA	CCGCGTGTCC
451	AGACAGGCAT	TTATTGAGGA	TAACAGTAAA	TCGCGAGCGT	GGATTGCAAC
501	TGAAGGTGCG	CAACAGATCA	AGGATTGGC	ACTTGAACCT	GTCGAGAAAA
551	ATGGCGGGAC	CCACGATAAG	GCTTTGGATT	TAATCAGCGG	CATGATGACC
601	ACCGGTCTGA	ATTTTGCCCA	AACCAAGAAT	GAAGCGCAGG	CGGCATATGC
651	TTTTTGCACTT	GCCTCAGAAG	GCAGTGGCGA	GGATACGGCA	AAACTGATTA
701	AAACCTGAA	AGATGGCGGC	ATGAGCGGTA	AAGACCTGCA	ACTCGGGCTT
751	GAGCACGTCT	TGCAATCGGG	TTTAGACGGC	ACTTTCGAGG	TGCGGGATAT
801	GGTTCGGGAG	CTGCCGAGCC	TGCTCTCTGC	CGCGCAACAG	GCAGGGATGA
851	ATGGTGTCGG	CGGTTTGGAC	TACCTGCTCT	CACTCTTACA	ATCTCGGGCG
901	AATAAATCGG	GCAATCCTGC	CGAAGCGGCG	ACTAATGTGC	AAAATCTTTT
951	GAGTAAACT	CTGTCGCCTG	ACACGATAGG	TCGTCTGAAG	AAGATGGCAA
1001	ATCCGAATGA	CCCGAAGAAA	GGTGTGCGAT	GGATAGGCTC	GGTTGTGCAA
1051	GGCAAGCAAA	ACGGCGAAAA	CGCAGTGCAG	GTGTTGTCCC	GTCTTGCCGA
1101	TGCCATGCTA	GTAAGGATA	AGCAATACCA	AGATTATAAG	AAACGCGCGG
1151	CTGCAGGCGA	TAAGACGGCG	GCGGAGCAGG	CAATATGCT	TAAGGGCGCG
1201	CTTTTGGCGC	AACTGCTGCC	TGATTGTCAG	GCAAAACAAG	GTTTGTCTGGC
1251	TGCAACGGAT	ATGACGCAAA	TCCGTGAATA	TATGGCTTCG	TTGCTGCGC

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1301 TAACGTTGGA TAACGGAAAA ATTGCTAAGA ACAACGAGGC GCGAATGTTG
1351 TCGGCAGCGG CGCAACAAGA GCAACAGGAA TCGCTGGCAA TGTTGCGGGA
1401 AAGTCTGACG GGAACATTGG TGGATATGGA AACCTCGTTT AAAAAGCTGG
1451 CAGCGGAATA CCTAATGCC ACTCTAGCCC TGCAAGCATT GACGACGGCG
1501 GCAACAGCGG CGTCTGCCGC AATGTTATTA ACCGCCGGTG GCGGTAAAGG
1551 TGCAGGCTTT CTGAAAGATG TAGGTAGTAA AGCGTTGGGA TGGGGTAAGG
1601 CTTCCGCGAG CGGCGTGGCA GCAGGTGCCA CAGCGCGAGG CGGTAAGTTG
1651 CTGTCATGGG GAAAATCTGC CGGTAGCGGG CTCATGAATA ATCCAGCGTT
1701 AGTTAAACGG GCGGGTTTGT TAGGTATGTT GCTGTATTCC GAGTCTTTGG
1751 GTGACGGCAC ATTGCCAAAG GGTTCGCGTG GTACCAAGAC AACTCCTGAA
1801 ATGATTAATC GTCTGAAAAA CAACGGTATC CGATTGGAAC CTGCGCCGAA
1851 GCGGGGAACAG GCGCGGGGTG GTGTCCCTCA GTATTGGCT GCTCCGTCAG
1901 CGCAGCCTAC CGATAAGATG TTGTCTCCGT TGTTTTCAAC TCAGACGGCG
1951 GCGTATCAGG CAGCCATTCA GCAGCAGACG GCGGCGTATC AGGCAGCATT
2001 GCGCGCAGGAT ACGGCTGCAG TTACAACAGG TTTGGCACAA GTGCAAAGTG
2051 CGATGGCGTC GGCAAGTCAG ACCATCAATA CCAATGTGAG CCTGAATATC
2101 GACGGACGTG TTATCGCGAA TGAGGTATCG CGGTATCAAG TGGCCATGTT
2151 GCGCCGTGGA GCGGTCAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 2428; ORF 719>:

```

m719.pep
1  MANGNMKLSL VLTARDDGAR RLLADTORQL DRTAKSRAQL ERQSHTYALT
51  GIRSEKQIQR EIMLTQAAFN RLARSGKASQ NDLARAAVAT RNRIRELNAE
101 LKQGTGFADK MGKIGRFGAA AVAGGAAAYT VLKPMADNRK QLDENINRVS
151 RQAFIEDNSK SAAWIATEGA QQIKDLALEL VEKNGGTHDK ALDLISGMMT
201 TGLNFAQTKN EAQAAAYAFAL ASEGSGEDTA KLIKTLKDDG MSGKDLQLGL
251 EHVLSQGLDG TFEVRDMVRE LPSLLSAAQQ AGMNGVGGLD YLLSLLQSAA
301 NKSGSPAEEA TNVQNLLSKT LSPDTIGRLK KMANPNDPKK GVDWIGSVVQ
351 GKQGENAVQ VLSRLADANL VKDKQYQDYK KRAAAGDKTA AEQANMLKGA
401 LLAQLLPDLQ AKQGLLAATD MTQIREYMAS LAGVTLDNK IAKNNEARML
451 SAAAQQEQQE SLAMLRRESLT GTLVDNETSF KKLAAEYPNA TLALQALTTA
501 ATAASAAMLL TAGGGKGAGF LKDVGSKALG WGKASAGGVA AGATAAGGKL
551 LSWGKSAGSG LMNNPALVKE AGLLGMLLYS ESLDGTLPK GLRGTKTTPE
601 MINRLKNGI RFEPAPKREQ ARGGVPOYLA APSAQPTDKM LSPLFSTQTA
651 AYQAAIQQQT AAYQAALAQD TAAVTTGLAQ VQSAMASASQ TINTNVSLNI
701 DGRVIANEVS RYQVAMFGRG AGQ*

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a719.seq not found yet

a719.pep not found yet

g720.seq not found yet

g720.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2429>:

```

m720.seq
1  ATGAGCGGAT GGCATACCTT ATTGCAGGAC GCATCTTACA AGGGCGTCCG
51  CTTTGATATT GAGGTGGTGG ACGAGAGCAA CGGCAAGGCA TTGGCCGAGC
101 ATGCGCGGCC GTTGTGTCAG GGTATCGACC TTGAAGACAT GGGCATGACC
151 GGGCGGCAGG TGCAGATTAA TCGGCTGTTT TGGGCAAGG GCTATGCAGG
201 CCGTCTGAAA AAGCTGCTGG ATGCGCTGGA GCAGCCGGGC GGCGGCGTGC
251 TGGTGCACCC TGTTCGGGGG CGGATGCACA ACATGATTGC GGCATCATGG
301 AGTTACCGAC ATGAGGCCGA TTATGTGGAT TATGCGGGCA TCGATATTAC
351 TTTCGCGAG GCGGCCGAAG CGCAGGAAAT CTTGTTTTT GAAAACGCCT
401 TTTTGGTCGA GCTTGAGGCG TTGATTGCTA ATATCGACAC CTACCGCGAG
451 GCGGCTATCG GCTTGTGTTA TCGGCTGTTG GCGGTGGATG CGGGCGTATC
501 AGCTTTATGG GGCAGCGCGC TGGGCATTG GAGTGCAGCA TCGGGTACGT
551 TTGGCGCGGT GCGCCGTTTG TTGATTTGG ACAAATTCG CTTTCCCGAT
601 CCGGGCGGAT ACAGTGCAGC GCGCTTTAAA AACGGCTCGG CCAAGCTGTT
651 TGGCGATATA TCGGTCATGG TAGATACTGG CATAACCGGT GAGGCGGGTT
701 TGGCCGATAA TGCCATGCAC CATGCCGGTT GGTGCGCGCG ACAGCGGTTT
751 GACGGGGCTG CGGCTGTTGC CGACCGCGCC GCCGCTATCC CTGATAATTT
801 GCTGACCGGC CGCTTTTCAG ACGCCCTGCA AAACCGCCTG AACCGGTTAA

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1165

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851 CCGCCAAACA GGTGCAGCCG GTAGCGCAGG CGGTGCGCCT GTTATCCACG
901 TCATCGCTGT TGTCGGTGGC AACGGCATT ATCGAGGCGC ATGGCGAAGA
951 GATGACCGCG CCCGATTGTA TTGAGGTAA CCGCGCCATG CGCCGCCGTA
1001 TGCAGGCCGA GATTGCCGCC TTGCGGGCGG TGCAGACGGC TGCTGCCGAG
1051 TCTGGTGGGC TGACGGCCAA CGCCGTGTAT ACCGAGGCTT ACCAAACGGC
1101 AGAATCCCTG CGCGGGCGG CAGGCCGTCT GAATGCGTTG GTTGCGGCGG
1151 TCATCAACCA AAAGCCGCCG CTGATTGTGC GCCAAGCCCC AATCGACGGT
1201 ACGATACACC AAATCGCCCA CGAGTTTAC GGCATATAG CCCGCGCAGC
1251 AGAGCTGGTG CGGCTCAATC CCCATATCCA CCACCCCGCG TTTATCAAGC
1301 GCGGCACTTT GGTCAACAGC TATGCAAAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 2430; ORF 720>:

```

m720.pep
  1 MSGWHTLLQD ASYKGVGFDI EVVDESNGKA LAEHARPFVQ GIDLEDMGMT
  51 GRQVQINAVF WGKGYAGRLK KLLDALEQPG GGVLVHPVWG RMHNMIAASW
 101 SYRHEADYVD YAGIDITFRE AEAQEIVFV ENAFLVELEA LIANIDTYRE
 151 AAIGFVDAVL AVDAGVSALW GSALGIWSAA SGTFGAVRRL FDLDKIAFPD
 201 RGGYSAAAFK NGSAKLFADI SVMVDTGIRR EAGLADNAMH HAGWSPRQRF
 251 DGAAAVADRA AAPDNLLTG RFSGLQNLRL NRLTAKQVQP VAQAVRLLST
 301 SLLSVATAL IEAHGEEMTA PDLIEVNRAM RRRMQAEIAA LRAVQTAAAE
 351 SGGLTANAVY TEAYQTAESE RAAAGRLNAL VAAVINQKPP LIVRQAPIDG
 401 TIHQIAHEFY GDIARAALV RLNPHIHHPA FIKRGTLVNS YAK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2431>:

```

a720.seq (partial)
  1 GGCTGCAAA ACCGCCTGAA CCGTTAACC GCCAAACAGG TGCAGCCGGT
  51 AGCGCAGGCG GTGCGCCTGT TATCCACGTC ATCGCTGTTG TCGGTGGCAA
 101 CGGCATTAAT CGAGGCGCAT GCGGAAGAGA TGACCGCGCC CGATTGATT
 151 GAGGTTAACC CGCCATGCG CCGCGTATG CAGGCCGAGA TTGCCGCTT
 201 ACGGGCGGTG CAGACGGCTG CTGCCGAGTC TGGTGGGCTG ACGGCCAACG
 251 CCGTGTATAC CGAGGCTTAC CAAACGGCAG AATCCCTGCG CGCGGCGGCA
 301 GCGCGTCTGA ATGCGTTGGT TCGGCGGCTC ATCAACCAA AGCCGCGGCT
 351 GATTGTGCGC CAAGCCCCAA TCGACGGTAC GATACACCAA ATCGCCACG
 401 AGTTTACGG CGATATAGCC CGCGCAGCAG AGCTGGTGGC GCTCAATCCC
 451 CATATCCACC ACCCGCGGTT TATCAAGCGC GGCACTTTGG TCAACAGCTA
 501 TGCAAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2432; ORF 720.a>:

```

a720.pep (partial)
  1 GLQNLRLNLT AKQVQPVQA VRLSTSSLL SVATALIEAH GEEMTAPDLI
  51 EVNRRMRMRA QAEIAALRAV QTAASGGL TANAVYTEAY QTAESELRRAA
 101 RLNALVAAV INQKPLIVR QAPIDGTIHO IAHEFYGDIA RAAELVRLNP
 151 HHHHPAFIKR GTLVNSYAK*

```

m720 / a720 100.0% identity in 169 aa overlap

```

m720.pep      250      260      270      280      290      300
SPRQREFDGA   AAVADRAAAIPDNLLTGRFSDGLQNLRLNRLTAKQVQPVQAQAVRLLSTSSLL
a720          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
                GLQNLRLNRLTAKQVQPVQAQAVRLLSTSSLL
                10      20      30

m720.pep      310      320      330      340      350      360
SVATALIEAHGEEMTAPDLIEVNRAMRRRMQAEIAALRAVQTAAESGGLTANAVYTEAY
a720          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
                SVATALIEAHGEEMTAPDLIEVNRAMRRRMQAEIAALRAVQTAAESGGLTANAVYTEAY
                40      50      60      70      80      90

m720.pep      370      380      390      400      410      420
QTAESELRRAAGRLNALVAAVINQKPLIVRQAPIDGTIHQIAHEFYGDIAAAELVRLNP
a720          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
                QTAESELRRAAGRLNALVAAVINQKPLIVRQAPIDGTIHQIAHEFYGDIAAAELVRLNP
                100     110     120     130     140     150

m720.pep      430      440
HHHHPAFIKRGT   LVNSYAKX

```

1166

a720
|||||
HIIHHPAFIKRGTLVNSYAKX
160 170

g721.seq not found

g721.pep not found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2433>:

m721.seq
1 ATGTCCAAAA ATGCACAAAA AACCTACTT GCCGTGTGCA GTTTCGAGGT
51 GCAGCCAAAA GACGGGCGAA TCCAACCTGCT GCCATATGGC GAATTTTCGCG
101 CAGTAGACGG TCGTCCGACT GATGTCCCTG CGTGGTATCT GACCGAAGAA
151 AACGGTCATG ATGTGCGGTT GTTGGCCAAC AGCTCGCGCA ATCAGTTGGT
201 TGTCGATTAT GAACACCAGA CGCTCTACAA AGAGAAAAAC GGACAACCTG
251 CACCTGCCGC CGGTTGGATG CGTTGGCTGG AGTTCACGCC TAAAGGCATG
301 TTTGCCGAAG TGGAGTGGAC GGACAAGGCG GCTGCGGCAA TTGCCGCAAA
351 AGAGTATCGC TACATCTCTG CTGTGTTTTT CTATGACACA AAGGGATATG
401 TAAGCAAAAT TTTTCACGCC GCGCTGACAA ATTTCCCGCG GTTGGACGGT
451 ATGGACGAGG TGCTGGCGGC AGCGTCGGCG CAAATTTTAA AACCGGAAAC
501 GGAGCAAAAC CCTATGAAAG AGTTGTTACA GCAACTGTTC GACCTGCCTG
551 ATGCGGGCGA AGAAGAACTG AAGGCGGCAT TGTCCGCGCT CGTGAAGCC
601 AAGCCGAAAG ACGTGGCATT GTCTGCCGAC GTGTTTCGCG AGCTGGCGGA
651 AAAAGACAGC CGCATCGCGG CATTGACGGC GCAAACCGCC AAGCCTGATT
701 TGAATAAATA CGCGCCTATC TCAGTGGTTC AAGAGCTGCA AAGCAAAGTC
751 GCCGCGCTGA CTGCCAAGCA GGAAGCAGAC AAAGGCAACG AATTGATTAC
801 CGCCGCGCTG ACTTCAGGCA AATTGCTGCC TGCTCAGAAG GAGTGGGCAG
851 AAGGCGTATT GAAACAGCCG GGCGGCTTGG CATTTTTGAC CGGCTTTATT
901 GAAAACGCCC AGCCGGTTCG TGCCTGGCA GGCTCGCAAA CGGGCGGTA
951 AGCACCCGAC GAACGCGTCG CCGCACTGAC TGCGGAAGAG GCAGCCGAG
1001 CAAAATGCT GGCATGTCC GCGAAGAAT TTGTAAAAAT CAAAGAAAGC
1051 GAAGTAAGT AA

This corresponds to the amino acid sequence <SEQ ID 2434; ORF 721>:

m721.pep
1 MSKNAQKTL AVCSFEVQPK DGRIQLLPYG EFRAVDGRPT DVPAWYLTEE
51 NGHVVALLAN SSRNQLVVDY EHQTLYKEKN GQPAPAAGWM RWLEFTRPKM
101 FAEVWTDKA AAIAAKEYR YISAVFSYDT KGYVSKIFHA ALTNFPALDG
151 MDEVLAASA QILKPETEON PMKELLQQLF DLPDAGEEEL KAALSALVEA
201 KPKDVALSAD VFAQLAEKDS RIAALTAQTA KEDLTXYAPI SVVQELQSKV
251 AALTAKQEAD KGNELITAAL TSGKLLPAQK EWARGVLKQP GGLAFLTFGI
301 ENAQVVAALA GSQTGGKAPD ERVAALTAEE AAAAKMLGMS GEEFVKIKES
351 EGK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2435>:

a721.seq
1 ATGTCCAAAA ATGCACAAAA AACCTACTT GCCGTGTGCA GTTTCGAGGT
51 GCAGCCAAAA GACGGGCGAA TCCAACCTGCT GCCATATGGC GAATTTTCGCG
101 CAGTAGACGG TCGTCCGACT GATGTCCCTG CGTGGTATCT GACCGAAGAA
151 AACGGTCATG ATGTGCGGTT GTTGGCCAAC AGCTCGCGCA ATCAGTTGGT
201 TGTCGATTAT GAACACTAGA CGCTCTACAA AGAGAAAAAC GGACAACCTG
251 CACCTGCCGC CGGTTGGATG CGTTGGCTGG AGTTCACGCC TAAAGGCATG
301 TTTGCCGAAG TGGAGTGGAC GGACAAGGCG GCTGCGGCAA TTGCCGCAAA
351 AGAGTATCGC TACATCTCTG CTGTGTTTTT CTATGACACA AAGGGATATG
401 TAAGCAAAAT TTTTCACGCC GCGCTGACAA ATTTCCCGCG GTTGGACGGT
451 ATGGACGAGG TGCTGGCGGC AGCGTCGGCG CAAATTTTAA AACCGGAAAC
501 GGAGCAAAAC CCTATGAAAG AGTTGTTACA GCAACTGTTC GGTCTGCCTG
551 ATGCGGGCGA AGAAGAACTG AAGGCGGCAT TGTCCGCGCT CGTGAAGCC
601 AAGCCGAAAG ACGTGGCATT GTCTGCCGAC GTGTTTCGCG AGCTGGCGGA
651 AAAAGACAGC CGCATCGCGG CATTGACGGC GCAAACCGCC AAGCCTGATT
701 TGAATAAATA CGCGCCTATC TCAGTGGTTC AAGAGCTGCA AAGCAAAGTC
751 GCCGCGCTGA CTGCCAAGCA GGAAGCAGAC AAAGGCAACG AATTGATTAC
801 CGCCGCGCTG ACTTCAGGCA AATTGCTGCC TGCTCAGAAG GAGTGGGCAG
851 AAGGCGTATT GAAACAGCCG GGCGGCTTGG CATTTTTGAC CGGCTTTATT
901 GAAAACGCCC AGCCGGTTCG TGCCTGGCA GGCTCGCAAA CGGGCGGTAA
951 AGCACCCGAC GAACGCGTCG CCGCACTGAC TGCGGAAGAG GCAGCCGAG
1001 CAAAATGCT GGCATGTCC GCGAAGAAT TTGTAAAAAT CAAAGAAAGC

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1051 GAAGGTAAGT AA

This corresponds to the amino acid sequence <SEQ ID 2436; ORF 721.a>:

```

a721.pep
  1 MSKNAQKTLL AVCSFEVQPK DGRIQLLPYG EFRAVDGRPT DVPAWYLTEE
 51 NGHDVALLAN SSRNQLVVDY EH*TLYKEKN GQPAPAAAGWM RWLEFTPKGM
101 FAEVEWTDKA AAAIAAKEYR YISAVFSYDT KGYVSKIFHA ALTNFPALDG
151 MDEVLAASA QILKPETEON PMKELLQQLF GLPDAGEEEL KAALSALVEA
201 KPKDVALSAD VFAQLAEKDS RIAALTAQTA KPDLTKYA?I SVVQELQSKV
251 AALTAKQEAD KGNELITAAL TSGKLLPAQK EWAEGVLKQP GGLAFLTGFI
301 ENAQPVAAAL GSQTGGKAPD ERVAALTAEE AAAAKMLGMS GEEFVKIKES
351 EGK*

```

a721/m721 99.2% identity in 353 aa overlap

a721.pep	10	20	30	40	50	60
	MSKNAQKTLLAVCSFEVQPKDGRIQLLPYGEFRAVDGRPTDVPAWYLTEENGHDVALLAN					
m721	MSKNAQKTLLAVCSFEVQPKDGRIQLLPYGEFRAVDGRPTDVPAWYLTEENGHDVALLAN					
	10	20	30	40	50	60
a721.pep	70	80	90	100	110	120
	SSRNQLVVDYEHXTLYKEKNGQPAPAAAGWMRWLEFTPKGMFAEVEWTDKAAAAIAAKEYR					
m721	SSRNQLVVDYEHQTLTYKEKNGQPAPAAAGWMRWLEFTPKGMFAEVEWTDKAAAAIAAKEYR					
	70	80	90	100	110	120
a721.pep	130	140	150	160	170	180
	YISAVFSYDTKGYVSKIFHAALTNFPALDGMDEVLAASAQILKPETEONPMKELLQQLF					
m721	YISAVFSYDTKGYVSKIFHAALTNFPALDGMDEVLAASAQILKPETEONPMKELLQQLF					
	130	140	150	160	170	180
a721.pep	190	200	210	220	230	240
	GLPDAGEEELKAALSALVEAKPKDVALSADVFAQLAEKDSRIAALTAQTAKPDLTKYAPI					
m721	DLPDAGEEELKAALSALVEAKPKDVALSADVFAQLAEKDSRIAALTAQTAKPDLTKYAPI					
	190	200	210	220	230	240
a721.pep	250	260	270	280	290	300
	SVVQELQSKVAALTAKQEADKGNELITAALTSGKLLPAQKEWAKGVKQPGGLAFLTGFI					
m721	SVVQELQSKVAALTAKQEADKGNELITAALTSGKLLPAQKEWAKGVKQPGGLAFLTGFI					
	250	260	270	280	290	300
a721.pep	310	320	330	340	350	
	ENAPVAAALAGSQTGGKAPDERVAALTAEEAAAAAKMLGMSGEEFVKIKESGKX					
m721	ENAPVAAALAGSQTGGKAPDERVAALTAEEAAAAAKMLGMSGEEFVKIKESGKX					
	310	320	330	340	350	

g722.seq not found yet

g722.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2437>:

```

m722.seq
  1 GTGTTTGAAA CGCCGACATT TGAGCAAATC CGCGAGCGTA TCCTGCCGCGA
 51 TACCAAAAAGC CTGTGGCCGG ATGCCGATAT CAGCCCCGAC AGCGACCATT
101 ATGTGCACGC CAGCCGTTTG GCCAGCTGCG CCGAAGGGCA ATATGCGCAT
151 CAAAGCTGGA TTGTGCGGCA GATTTTCCTT GATACCGCCG ACCGCGAGTA
201 TTTGGAGCGG CATGCCTCCA TGC GCGGCTT GAGCCGCGC AATCCTACCA
251 CGGCCAGCGG CACGCTGACC GTAAGCGGTA TTGCGCAATC CATGCTTTCA
301 GACGACCTGC AAGTGCCTAT CGGCCAGCGT TTTTACCGCA CTACCGCCCG
351 CGCCGTTATC GGCAGCGGCG GCACGGCGGA AATACCGGCA ATCGCCGACG

```


1168

```

401 AGCCGGGCGC GCGCGCCAAT GTGGGCGACG GCGAGGCGCA ACTGATGGCC
451 GCGCCCGCCG GTGTGGCCAC CGAATGCCGC CTTACCGTAC AAGGCGGCAC
501 CGACCGAGAA AGCGATGCCT CACTGCTGGC GCGTCTGTG GAAATCATCC
551 GCGGACCGCC CGCAGGCGGC AACCCTTACG ACTATAAAAA CTGGGCGTTG
601 AGTGTGACG GCGTAACCAG CGCATATGTT TATCCGCTGC GCGCGGCTT
651 GGGTACGGTG GATATTGCCA TTACCTCCGC CGACGGTGTG TCGTCGGAAG
701 AAAGTGTGCG CCGCGTACAG GCTTATATCG ACGAGATGCG CCCGTAACG
751 GCAAAAAATG CGCTGGTACT CAAGCCAACC GTAACGGCGG TGCCTGTTAC
801 CGTGCAAGTC AAGCTCGACG GTATCGACTT GGACGAGGCC AAGCGCCGCA
851 TACGGACGGC CCTAAAAGAA TATTTGACA CCCTGATCCC CGCGACGGC
901 CTGACTGTGT CGCAAATCGA GGCTGCTATC AGCAATGTGG ATGGTGTGAT
951 CGACCGCCGT CTGACTGCGC CGACGGCCAA CCGTGCCGCC GATACGGTTA
1001 ACCGCATCGA GTGGTTTAAA GCGGGCGCGA TTAATGTAAC GGAGATGCCG
1051 TCATGA

```

This corresponds to the amino acid sequence <SEQ ID 2438; ORF 722>:

m722.pep

```

1 VFETPTFEQI RERILRDTKS LWPADISPD SDHYVHASRL ASCAEGQYAH
51 QSWIVRQIFP DTADREYLER HASMRGLSRR NPTTASGTLT VSGIAQSMLS
101 DDLQVRIGQR FYRTTARAVI GSGGTAEIPA IADEPGAAAN VGDGEAQLMA
151 APAGVATECR LTVQGGTDRE SDASLLARLL EIIRRPAGG NRYDYKNWAL
201 SVDGVTSAYV YPLRRGLGTV DIAITSADGV SSEETVRRVQ AYIDEMRPVT
251 AKNALVLKPT VTAVPVTQV KLDGIDLDEA KRRIRTALKE YFDTLIPGDG
301 LTVSQIEAAI SNVDGVIDRR LTAPTANRAA DTVNRIEWFK AGAINVTEMP
351 S*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2439>:

a722.seq

```

1 GTGTTTGAAA CCGCGACATT TGAGCAAATC GCGAGGCGTA TCCTGCGCGA
51 TACCAAAAGC CTGTGGCCGG ATGCCGATAT CAGCCCGGAC AGCGACCATT
101 ATGTGCACGC CAGCCGTTTG GCCAGCTGCG CCGAAGGGCA ATATGCGCAT
151 CAAAGCTGGA TTGTGCGGCA GATTTCCCT GATACCGCCG ACCGCGAGTA
201 TTTGGAGCGG CATGCCTCCA TCGCGGCTT GCGCGCGCGC AATCCTACCA
251 CGGCCAGCGG CACGCTGACC GTAAGCGGTA TTGCGCAATC CATGCTTTCA
301 GACGGCCTGC AAGTGCCTAT CGGCCAGCGT TTTTACCGCA CTACCGCCCG
351 CGCCGTTATC GGCAGCGGCG GCACGGCGGA AATACCGGCA ATCGCCGACG
401 AGCCGGGCGC GGCCGCCAAT GTGCGCGACG GCGAGGCGCA ACTGATGGCC
451 GCGCCCGCCG GTGTGTCCAC CGAATGCCGC CTTACCGTAC AAGGCGGCAC
501 CGACCGAGAA AGCGATGCCT CACTGCTGGC GCGTCTGTG GAAATCATCC
551 GCGGACCGCC CGCAGGCGGC AACCCTTACG ACTATAAAAA CTGGGCGTTG
601 AGTGTGACG GCGTAACCAG CGCATATGTT TATCCGCTGC GCGCGGCTT
651 GGGTACGGTG GATATTGCCA TTACCTCCGC CGACGGTGTG CCATCGGAAG
701 AAAGTGTGCG CCGCGTACAG GCTTATATCG ACGAGATGCG CCCGTAACG
751 GCAAAAAATG CGCTGGTACT CAAGCCAACC GTAACGGCGG TGCCTGTTAC
801 CGTGCAAGTC AAGCTCGACG GCATCGACTT GGACGAGGCC AAGCGCCGCA
851 TACGGACGGC CCTAAAAGAA TATTTGACA CCCTGATCCC CGCGACGGC
901 CTGACTGTGT CGCAAATCGA GGCGGCTATC AGCAATGTGG ATGGTGTGAT
951 CGACCTCCGT CTGACTGCGC CGACGGCCAA CCGTGCCGCC GATACGGTTA
1001 ACCGCATCGA GTGGTTTAAA GCGGGCGCGA TTAATGTAAC GGAGATGCCG
1051 TCATGA

```

This corresponds to the amino acid sequence <SEQ ID 2440; ORF 722.a>:

a722.pep

```

1 VFETPTFEQI RERILRDTKS LWPADISPD SDHYVHASRL ASCAEGQYAH
51 QSWIVRQIFP DTADREYLER HASMRGLRRR NPTTASGTLT VSGIAQSMLS
101 DGLQVRIGQR FYRTTARAVI GSGGTAEIPA IADEPGAAAN VRDGEAQLMA
151 APAGVSTECR LTVQGGTDRE SDASLLARLL EIIRRPAGG NRYDYKNWAL
201 SVDGVTSAYV YPLRRGLGTV DIAITSADGV PSEETVRRVQ AYIDEMRPVT
251 AKNALVLKPT VTAVPVTQV KLDGIDLDEA KRRIRTALKE YFDTLIPGDG
301 LTVSQIEAAI SNVDGVIDLR LTAPTANRAA DTVNRIEWFK AGAINVTEMP
351 S*

```

g723.seq not found yet

g723.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2441>:

```
m723.seq
1  ATGCGACCCA AGCCCCGTTT CAGACGGTCT GTTATCGCTT GCTCAATATC
51  AGTGATCACG CCCGAACACC TTATTTTAC CGTTTACAAA CACAATACCG
101 TCTTCGCCCG CGGCCACTTC TTCGCCGCTA TCATCCACGC CCAGCTGCAC
151 TTCGCCTTTG GCCATAGCAC GCAGCAGGTC GAGCACGTCG ATTTTGTAGC
201 GGTTCGGGAT TTCGTCGGTA ATCAACACGC CCTGAGCCGC CGTCAGACGG
251 TAGCGGGCAA TGTCGCAGCA AAGGCGCACC AAGATGGGCG GCAGATCCTC
301 AAAAGGTTCG CTGAACCGCC CCAGATACGC GTCGATTTCG GCAGTGGCGT
351 CCACCAGCGC GGTTCGTGCG ACCTCGCGGT CAATCAGCCC CTCGTTGTTG
401 CCGTCGGTGA GCTGCAAGAC TTCCAGCTCA CCGAAACGCG CAACCATATC
451 CTCAACCGTC GCGTATGCCA TTACTCGACC GCCTTGCCTT GCAGCATAGG
501 CTCGGCGCAG ATTGCCTTCC ACACCGCTTC GCCGACTTCG GCGCGCTTCA
551 CTTGCGGCCA GCCGCCGTC AACAGCAGGC CGCCGCGCCA AAATTCTTTG
601 CCGTCTGCGC CGGTACTGAC GAGCATCACA TCGCGGCTGT CCGCCAAAGC
651 GTCGGCGGCA CGTTGCGTAT GCTGCACCTT GAGTTCGGCA AGTTCGGCGG
701 ACAGTGCCTT TTTGTGCTCT TCGGCTTTT CCAAGGCTGT GGTCAGCATT
751 TCGACATCGT TTCGGGCGGC GGCAAGCTCT GCCTGCACGG CGTCCAATTC
801 GGCTTTGATG TCTTCAAACG ACGGGGCGGC GGTTTCGGCG GTTTCGTGGT
851 TGTGTTGGT TTTTGCCATG ATGACTCCTT GTTTCAGACG GCGGCGGATT
901 CGCATTGA
```

This corresponds to the amino acid sequence <SEQ ID 2442; ORF 723>:

```
m723.pep
1  MRPKPRFRRS VIACISIVIT PEHLIFTVYK HNTVFARGHF FAAIHAQLH
51  FAFGHSTQQV EHVDFVAVAD FVGNQHALSR RQTVAGNVAA KAHQDGRQIL
101 KRSSEPPQIR VDFGSGVHOR GLCDLAVNQP LVVAVGELQD FOLTETRNHI
151 LNRRVCHYST ALRCSIGSAQ IAFHTASPTS ARFTSRQPPS NSRPPRQNSL
201 PSAPVLTSIT SRLSAKASAA RCVCCTLSSA SSADSAFLSS SAFSKAVVSI
251 STSFRAAASS ACTASNSALM SSNDGAAVSA VSGLLLVEAM MTECFRRRRI
301 RI*
```

a723.seq not found yet

a723.pep not found yet

g724.seq not found yet

g724.pep not found yet

The following partial DNA sequence, shown with its encoded amino acid sequence, was identified in *N. meningitidis* <SEQ ID 2443>:

```
m724.map
ATGAGTTTGAGTAAATTGGCGAAAAAACGGCACAACTGCTAAAAATATCGGCGAAACC
1  -----+-----+-----+-----+-----+ 60
TACTCAAACCTCATTTAACCGCTTTTTTTGCCGTGTTTGACGATTTTTATAGCCGCTTTGG
a  M S L S K L A K K T A Q T A K N I G E T -
CTGCGCGCGGCCTTTCGGGGAAAAATCACGCTGGTGGTGTCTGCGAGCCGATACAGCGC
61  -----+-----+-----+-----+-----+ 120
GACGCGCGCCGAAAGCCCCTTTTAGTGCGACCAACACAGCAGGCTCGGCTATGTCGCG
a  L R A A F R G K I T L V V S S E P I Q R -
GTGCAGTTGAGCGGCTTGCCGACGAAACCTGCAAGACCTTGAACATTTGCAGGAATAC
121 -----+-----+-----+-----+-----+ 180
CACGTCAACTCGCCGAACCGGCTGCTTTGGGACGTTCTGGAACCTGTAAACGTCCTTATG
a  V Q L S G L A D E T L Q D L E H L Q E Y -
GGCTTTGCCAGCCATCCGCCGACGGCAGCGAAGCGGTAGTGATACCGCTGGGCGGCAAT
181 -----+-----+-----+-----+-----+ 240
CCGAAACGGTCGGTAGGCGGGCTGCCGTGCTTCGCCATCACTATGGCGACCCGCGTTA
a  G F A S H P P D G S E A V V I P L G G N -
```

1170

```

      ACTTCGCACGGTGTGATTGTGTGCAGCCAGCACGGCAGCTACCGCATCAAAAACCTTAAG
241  -----+-----+-----+-----+-----+-----+-----+ 300
      TGAAGCGTGCCACACTAACACACGTCGGTCGTGCCGTGCGATGGCGTAGTTTTTGGAATTC
a    T S H G V I V C S Q H G S Y R I K N L K -

      CCCGGCGAGACGGCGATTTTAAATCATGAGGGTGCAAAAATCGTGATTAAGCAAGGCAAA
301  -----+-----+-----+-----+-----+-----+-----+ 360
      GGGCCGCTCTGCCGCTAAAAATAGTACTCCCACGTTTTTAGCTAATTCGTTCCGTTT
a    P G E T A I F N H E G A K I V I K Q G K -

      ATCATTGAGGCCGATTGCGACGTGTACCGGGTAACTGCAAACAATACGAGGTTAATGCG
361  -----+-----+-----+-----+-----+-----+-----+ 420
      TAGTAACTCCGGCTAACGCTGCACATGGCCCAATTGACGTTTGTATGCTCCAATTACGC
a    I I E A D C D V Y R V N C K Q Y E V N A -

      GCCACGGATGCCAAATTTAACGCTCCGTTGGTGGAGACCAGTGACGTGTTGACGGCGCAA
421  -----+-----+-----+-----+-----+-----+-----+ 480
      CGGTGCCTACGGTTTAAATTGCGAGGCAACCACCTCTGGTCACGTCACAACTGCCGCGTT
a    A T D A K F N A P L V E T S A V L T A Q -

      GGCCAAATCAACGGCAACGGCGGCATGGCCGTGAGGGCGGOGACGGAGCCACCTTTAGC
481  -----+-----+-----+-----+-----+-----+-----+ 540
      CCGGTTTAGTTGCCGTTGCCGCGTACCGGCAGCTCCCGCCGCTGCCTCGGTGGAAATCG
a    G Q I N G N G G M A V E G G D G A T F S -

      GCGCATGTTAACCAAACGGCGGCAGCTTTAACACCGACGGCGACGTGGTGGCCGGCAAT
541  -----+-----+-----+-----+-----+-----+-----+ 600
      CCGCTACAATTGGTTTGCCCGCGTCGAAATTGTGGCTGCCGCTGCACCACCGCCGCTTA
a    G D V N Q T G G S F N T D G D V V A G N -

      ATATCGTTGCCGACGACCCGCATACCGACAGCATCGGCGGCAAAACCTTACCGCGGAA
601  -----+-----+-----+-----+-----+-----+-----+ 660
      TATAGCAACGCGGTGCGGGCGTATGGCTGTCTAGCCGCGCTTTGGAATGGCCGCTT
a    I S L R Q H P H T D S I G G K T L P A E -

      CCGGCATAG
661  ----- 669
      GGCCGTATC
a    P A * -

```

Enzymes that do cut: NONE

Enzymes that do not cut: BamHI BglII EcoRI HindIII KpnI NdeI NheI PstI SacI
Sali SmaI SphI XbaI XhoI

This corresponds to the amino acid sequence <SEQ ID 2444; ORF 724>:

m724.pep

```

1  MSLSKLAKKT AQTAKNIGET LRAAFRGKIT LVVSSEPIQR VQLSGLADET
51  LQDLEHLQEY GFASHPPDGS EAVVIPLGGN TSHGVIVCSQ HGSYRIKNLK
101 PGETAIFNHE GAKIVIKQ GK IIEADCDVYR VNCKQYEVNA ATDAKFNA PL
151 VETSAVLTAQ GQINGNGGMA VEGGDGATFS GDVNQTGGSF NTDGDVVAGN
201 ISLRQHPHTD SIGKTLPAE PA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2445>:

a724.seq

```

1  ATGAGTTTGA GTAAATTGGC GAAAAAACG GCACAACTG CTAAAAATAT
51  CCGCGAAACC CTGCGCGCGG CCTTTCGGGG AAAAATCACG CTGGTGGTGT
101 CGTCCGAGCC GATACAGCGC GTGCAGTTGA GCGGCTTGGC CGACGAAACC
151 CTGCAAGACC TTGAACATTT GCAGGAATAC GGCTTTGCCA GCCATCCGCC
201 CGACGGCAGC GAAGCGGTAG TGATACCGCT GGGCGGCAAT ACTTCGCACG
251 GTGTGATTGT GTGCAGCCAG CACGGCAGCT ACCGCATCAA AAACCTTAAG
301 CCCGGCGAGA CGGCATTITT TAATCATGAG GGTGCAAAAA TCSTGATTAA
351 GCAAGGCAAA ATCATTGAGG CCGATTGCCA CGTGTACCGG GTTAACTGCA
401 AACAAATACGA GGTAAATGCG GCCACGGATG CCAAATTTAA CGTCCGTTG
451 GTGGAGACCA GTGCAGTGTT GACGGCGCAA GGCCAAATCA ACGGCAACGG

```

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```

501 CGGCATGGCC GTCGAGGGCG GCGACGGAGC CACCTTTAGC GGCGATGTTA
551 ACCAAACGGG CGGCAGCTTT AACACCGACG GCGACGTGGT GGCCGCAAT
601 ATATCGTTGC GCCAGCACCC GCATACCGAC AGCATCGGCG GCAAAACCTT
651 ACCGGCGGAA CCGGCATAG

```

This corresponds to the amino acid sequence <SEQ ID 2446; ORF 724.a>:

```

a724.pep
  1  MSLSKLAKKT AQTAKNIGET LRAAFRGKIT LVVSSEPIQR VQLSGLADET
 51  LQDLEHLQEY GFASHPPDGS EAVVIPLGGN TSHGVIVCSQ HGSYRIKNLK
101  PGETAIFNHE GAKIVIKQKG IIEADCDVYR VNCKQYEVNA ATDAKFNAPL
151  VETSAVLTAQ GQINGNGGMA VEGGDGATFS GDVNQTGGSF NTDGDVVAGN
201  ISLRQHPHTD SIGGKTLPAE PA*

```

a724/m724 100.0% identity in 222 aa overlap

	10	20	30	40	50	60
a724.pep	MSLSKLAKKTAQTAKNIGETLRAAFRGKITLVVSSEPIQRVQLSGLADET					
m724	MSLSKLAKKTAQTAKNIGETLRAAFRGKITLVVSSEPIQRVQLSGLADET					
	10	20	30	40	50	60
	LQDLEHLQEY					
	70	80	90	100	110	120
a724.pep	GFASHPPDGS EAVVIPLGGNTSHGVIVCSQHGSYRIKNLKPGETAIFNHEGAKIVIKQKG					
m724	GFASHPPDGS EAVVIPLGGNTSHGVIVCSQHGSYRIKNLKPGETAIFNHEGAKIVIKQKG					
	70	80	90	100	110	120
	LQDLEHLQEY					
	130	140	150	160	170	180
a724.pep	IIEADCDVYRVNCKQYEVNAATDAKFNAPLVETSAVLTAQGQINGNGGMAVEGGDGATFS					
m724	IIEADCDVYRVNCKQYEVNAATDAKFNAPLVETSAVLTAQGQINGNGGMAVEGGDGATFS					
	130	140	150	160	170	180
	LQDLEHLQEY					
	190	200	210	220		
a724.pep	GDVNQTGGSFNTDGDVVAGNISLRQHPHTDSIGGKTLPAEPAX					
m724	GDVNQTGGSFNTDGDVVAGNISLRQHPHTDSIGGKTLPAEPAX					
	190	200	210	220		
	LQDLEHLQEY					

g725.seq not found yet

g725.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2447>:

```

m725.seq
  1  ATGGTGCGCA CGGTTAAAAG CTACAACGGC GAGGCCGACG ATTGGCGGG
 51  GCAAAATCCAT ACGCTGCCCTG CGGTTTGGGT AACGTATGGC GGCAGCAAAG
101  TTGAGCCTGC CAGCACCGGC GGCGTATGCG GACGTATATCA GGATACCGCC
151  GAATTTGTGG TGATSGTGCC GGCCCGCAAT CTGCGCAACG AGCAGGCGCA
201  GCGGCAAGGC GGATCGACA GCCGCGAAAT CGGCAGCAAC GATTTAATCC
251  GCGCTGTTGC CCGCCTGCTT GACGGCCAGC GGCTCGGTTT TGCCGATAGC
301  CGCGGCTTGG TGCCCAAAGC GGTGCGCGCG ATTGCCAATC ATGTGCTGGT
351  GCAAAACGCC GCAGTAAGCA TATATGCGGT TGAGTATGCC ATCCGCTTTA
401  ACACCTGCGG GTTGAAAAT GACCGCTACC CCGAACGCAC CGACAATCCC
451  GACGACCCCA ACCATATCTT TACCAAGTAT CAGGGTACAT TGAGCGAGCC
501  GTGGCCTGAT TTCGAGGGGT TGGACGGCAA AATTTACGAC CCGCAATCCG
551  CCGATGAAAT ACCTGTAAAC CTAACCCTTA AGGATAAGCA ATGA

```

This corresponds to the amino acid sequence <SEQ ID 2448; ORF 725>:

```

m725.pep
  1  MVRTVKSUNG EADDLAQIHL TPAVWVTYG GSKVEPASTG GVCGRYQDTA
 51  EFVVMVAARN LRNEQAQRQG GIDSREIGSN DLIRAVRRLD DGQRLGFADS
101  RGLVPKAVRA IANHVLVQNA AVSIYAVEYA IRFNTCGLEN DRYPERTONP
151  DDPNHIIFYK QGTLSEFPWD FEGLDGKIYD PQSADEIPVN LTLKDKQ*

```

a725.seq not found yet

a725.pep not found yet

g726.seq not found yet

g726.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2449>:

```
m726.seq
1  ATGACCATCT ATTTCAAAAA CGGCTTTTAC GACGACACAT TGGGCGGCAT
51  CCCCGAAGGC GCGGTTGCCG TCCGCGCCGA AGAATACGCC GCCCTTTTGG
101 CAGGACAGGC GCAGGGCGGG CAGATTGCCG CAGATTCCGA CGGCCGCCCC
151 GTTTTAACCC CGCCGCGCCC GTCCGATTAC CACGAATGGG ACGGCAAAAA
201 ATGGGAAATC AGCAAAGCCG CCGCCGCCGC CCGTTTCGCC AAACAAAAAA
251 CCGCCTTGGC ATTCCGCCTC GCGGAAAGG CCGACGAACT CAAAAACAGC
301 CTCTTGGCGG GCTATCCCA AGTGGAATC GACAGCTTTT ACAGGCAGGA
351 AAAAGAAGCC CTCGCGCGGC AGGCGGACAA CAACGCCCCG ACCCCGATGC
401 TGGCGCAAAT CGCCGCCGCA AGGGGCGTGG AATTGGACGT TTTGATTGAA
451 AAAGTTATCG AAAAATCCGC CCGCTGGCT GTTGCCGCCG GCGCGATTAT
501 CGGAAAGCGT CAGCAGCTCG AAGACAAAT GAACACCATC GAAACCGCGC
551 CCGGATTGGA CGCGCTGGAA AAGGAAATCG AAGAATGGAC GCTAAACATC
601 GGCTGA
```

This corresponds to the amino acid sequence <SEQ ID 2450; ORF 726>:

```
m726.pep
1  MTIYFKNGFY DDTLGGIPEG AVAVRAEYEA ALLAGQAQGG QIAADSDGRP
51  VLTTPRPSPDY HEWDGKKWKI SKAAAAARFA KQKTALAFRL AEKADELKNS
101 LLAGYPQVEI DSFYRQEKEA LARQADNNAP TPMLAQIAAA RGVELDLVIE
151 KVIEKSARLA VAAGAIIGKR QLEDKLNLI ETAPGLDALE KEIEEWTLNI
201 G*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2451>:

```
a726.seq
1  ATGACCATCT ATTTCAAAAA CGGCTTTTAC GACGACACCT TGGGCAGCAT
51  CCCCGAAGGC GCGGTTGCCG TCCGCGCCGA AGAATACGCC GCCCTTTTGG
101 CAGGACAGGC GCAGGGCGGG CAGATTGCCG CAGATTCCGA CGGCCGCCCC
151 GTTTTAACCC CGCCGCGCCC GTCCGAATAC CACGAATGGG ACGGCAAGAA
201 ATGGGAAATC GGCGAAGCCG CTGCCGCCGC CCGTTTCGCC GAACAAAAAA
251 CCGCCACGGC ATTCCGCCTC GCGGAAAGG CCGACGAACT CAAAAACAGC
301 CTCTTGGCGG GCTATCCCA AGTGGAATC GACAGCTTTT ACAGGCAGGA
351 AAAAGAAGCC CTCGCGCGGC AGGCGGACAA CAACGCCCCG ACCCCGATGC
401 TGGCGCAAAT CGCCGCCGCA AGGGGCGTGG AATTGGACGT TTTGATTGAA
451 AAAGTTGTCT AAAAATCCGC CCGCTGGCC GTTGCCGCCG GCGCGATTAT
501 CGGAAAGCGG CAGCAGCTCG AAGACAAAT GAACACCATC GAAACCGCGC
551 CAGGATTGGA CGCGCTGGAA AAGGAAATCG AAGAATGGAC GCTAAACATC
601 GGCTGA
```

This corresponds to the amino acid sequence <SEQ ID 2452; ORF 726.a>:

```
a726.pep
1  MTIYFKNGFY DDTLGSIEG AVAVRAEYEA ALLAGQAQGG QIAADSDGRP
51  VLTTPRPSEY HEWDGKKWEI GEAAAAARFA EQKTATAFRL AAKADELKNS
101 LLAGYPQVEI DSFYRQEKEA LARQADNNAP TPMLAQIAAA RGVELDLVIE
151 KVIEKSARLA VAAGAIIGKR QLEDKLNLI ETAPGLDALE KEIEEWTLNI
201 G*
```

a726/m726 95.5% identity in 201 aa overlap

	10	20	30	40	50	60
a726.pep	MTIYFKNGFYDDTLGSIPEGAVAVRAEYEAALLAGQAQGGQIAADSDGRPVLTTPRPSEY					
m726	MTIYFKNGFYDDTLGSIPEGAVAVRAEYEAALLAGQAQGGQIAADSDGRPVLTTPRPSPDY					
	10	20	30	40	50	60

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```

              70      80      90      100      110      120
a726.pep      HEWDGKKWEIGAAAAARFAEQKTATAFRLAAKADELKNSLLAGYPQVEIDSFYRQEKEA
              |||||:|:|||||:||||| ||||| ||||| ||||| ||||| ||||| |||||
m726          HEWDGKKWKISKAAAAARFAKQKTALAFRLAEKADELKNSLLAGYPQVEIDSFYRQEKEA
              70      80      90      100      110      120

              130      140      150      160      170      180
a726.pep      LARQADNNAPTPMLAQIAAARGVELDVLIEKVVEKSARLAVAAGAIIGKRQCLEDKLNTI
              ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
m726          LARQADNNAPTPMLAQIAAARGVELDVLIEKVIEKSARLAVAAGAIIGKRQCLEDKLNTI
              130      140      150      160      170      180

              190      200
a726.pep      ETAPGLDALEKEIEEWTLNIGX
              ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
m726          ETAPGLDALEKEIEEWTLNIGX
              190      200

g727.seq      not found yet
g727.pep      not found yet

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2453>:

```

m727.seq
1   ATGAATCTCG TGAAACTGCT GCGCAATAAC TGGCAACCGA TTGCCATTAT
51  CGCGCTTGTC GGCACGGGCT TGGCTGTGTC GCACCATCAA GGCTACAAGT
101 CGGCATTGTC GAAGCAGCAG GCGGTCATCG ACAAGATGGA GCGCGACAAG
151 GCGCAAGCCC TGCTGTTGTC GGCTCAAAAC TATGCGCGCG AACTGGAACT
201 GGCACGCGCG GAAGCTAAAA AATATGAAGT CAAGGCGCAC GCTGTCGGCA
251 TGGCTTTGGC GAAAAACAG GCGGAAGTCA GCCGTCTGAA AACGGAAAGA
301 GACCTTTGCA AAATTCCTTT CCTCCCGAC AGCCGAAACC CAAACACAGG
351 TTTTCGGCTG TTTTCGCCCC AAATACCGCC TAATTTTACC CAAATACCCC
401 CTAA

```

This corresponds to the amino acid sequence <SEQ ID 2454; ORF 727>:

```

m727.pep
1   MNLVKLLANN WOPIAIIALV GTGLAVSHHQ GYKSAFAKQQ AVIDKMERDK
51  AQALLLSAQN YARELELARA EAKKYEVKAH AVGMALAKKQ AEVSRLKTER
101 DLCKIPFPD SRNPNTGERL FSPQIPPNFT QIPP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2455>:

```

a727.seq
1   ATGAATCTCG TGAAACTGCT GCGCAATAAC TGGCAACCGA TTGCCATCAT
51  CGCGCTTGTC GGCACGGGTT TGGCGGTGTC GCACCATCAA GGCTACAAGT
101 CGGCTTTTGC GAAGCAGCAG GCGGTCATTG AGAAAATGAA GCGCGACAAG
151 GCGCAAGCCC TGCTGTTGTC GGCTCAAAAC TACGCCCGCG AACTGGAACA
201 GGCACGTCGC GAAGCTAAAA AATATGAAGT CAAGGCGCAC GCCGTGCGCA
251 TGGCTTTGGC GAAAAACAG GCGGAAGTCA GCCGTCTGAA AACGGAAAAT
301 AAAAAGGAAA TCGAAAATGT CCTTACTCAA GACCGTAAAA ATGCAGGCGG
351 CGGTTGTATT GACGGCTTTG GCCATCACGG CTTGCAGCTC TACAAGCGCG
401 CCCTCGGCTA CGGAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 2456; ORF 727.a>:

```

a727.pep
1   MNLVKLLANN WOPIAIIALV GTGLAVSHHQ GYKSAFAKQQ AVIEKMKRDK
51  AQALLLSAQN YARELEQARA EAKKYEVKAH AVGMALAKKQ AEVSRLKTEN
101 KKEIENVLTQ DRKNAGGGCI DGFHGHGLQL YKRALGYGN*

```

a727/m727 83.2% identity in 119 aa overlap

```

              10      20      30      40      50      60
a727.pep      MNLVKLLANNWQPIAIIALVGTGLAVSHHQGYKSAFAKQQAVIEKMKRDKAQALLLSAQN
              ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

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```

m727      MNLVKLLANNWQPIAIIALVGTGLAVSHHQGYKSAFAKQQAVIDKMERDKAQALLLSAQN
           10      20      30      40      50      60
           70      80      90      100     110     119
a727.pep  YARELEQARAEAKKYEVKAHAVGMALAKKQAEVSRLKTENKKEIENV-LTQDRKNAGGGC
           ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
m727      YARELELARAEAKKYEVKAHAVGMALAKKQAEVSRLKTE--RDLCKIPFPDSRNPNTGF
           70      80      90      100     110
           120     130     140
a727.pep  IDGFGHHGLQLYKRALGYGNX
m727      RLFSPIPPNFTQIPPX
           120     130

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2457>:

```

g728.seq
1  ATGTTTAAAA AATTCAAACC GGTACTGTTG TCATTTTTTG CACTTGTATT
51  TGCCTTTTGG CTGGGAACAG GTATTGCCTA TGAGATTAAT CCGCGTTGGT
101 TTTTGAGCGA TACGGCAACT GAAGTACCTG AAAATCCGAA TGCTTTTGTG
151 GCGAAACTTG CCCGCCTGTT CCGAAATGCC GACAGGGCGG TTGTCATCGT
201 GAAGGAATCG ATGAGGACGG AGGAAAGCCT TGCCGGAGCT GTGGATGACG
251 GTCCGTTGCA GTCGGAGAAG GATTATCTCG CGCTCGCTAT CCGGCTCAGT
301 CGTTTGAAAG AAAAGGCGAA ATGGTTTCAC GTAACGGAGC AGGAACATGG
351 GGAAGAGGTT TGGCTGGATT ACTATATCGG CGAGGGCGGT TTGGTTGCGG
401 TTTTCGCTTC GCAACGCTCG CCGGAAGCGT TTGTTAATGC CGAATATCTG
451 TATCGGAACG ATCGTCCGTT TTCTGTAAAT GTGTACGGCG GAACGGCTCA
501 CGGGGAATAA TATGAAACGA CAGGAGAATA TCGGGTTGTT TGGCAACCGG
551 ACGGTTCCGT ATTTGATGCG GCGGGGCGCG GGAATATCGG GGAAGATGTT
601 TATGATGCGT GCCTCGGGTG TTATCAGATG GCCCAGGTAT ATTTGGCGAA
651 ATACCGGGAT GTCGCGAATG ACGAGCAGAA GGTITGGGAC TTCCGCGAAG
701 AGAGCAACCG GATTGCATCG GACTCGCGCG ATTATGTGTT TTATCAGAAT
751 ATGCGGGAAT TGATGCCCGG GGGGATGAAG CGCAACAGTC TTGTGGTCCG
801 CTATGATGCG GACGGTCTGC CGCAAAAAGT CTATGGAGT TTTCGACAATG
851 GAAAAAACCG CCAGAGTTTC GAATATTATT TGAAAAACGG AAATCTTTTT
901 ATTGCACAAT CTTGACGGT AGCATTGAAA GCGGATGGCG TAACGGCGGA
951 TATGCAGACC TATCATGCGC AACAGACGTG GTATTGGAT GCGGGGCGGA
1001 TATCCGCGA AGAGAAACAG GGAGACAGAC TGCTGATT TTCTTTGAAC
1051 TTGGAAGATT TGGAAAAAGA GGTGAGCCGT TATGCAGAGG CTGCGGCGAG
1101 ACGTTCGGGC GGCAGGCGCG GCCTTTCTCA CTGA

```

This corresponds to the amino acid sequence <SEQ ID 2458; ORF 728>:

```

g728.pep
1  MFKFKPVL L SFFALVFAFW LGTGIAYEIN PRWFLSDTAT EVPENPNFV
51  AKLARLFERNA DRVVIVKES MRTEESLAGA VDDGPLQSEK DYLA LAIRLS
101 RLKEKAKWFH VTEQEHGEEV WLDYYIGEGG LVAVSLSQRS PEA FVNAEYL
151 YRNDRPFSVN VYGGTAHGEN YETTGEYRVV WQPDGVSFDA AGRGKIGEDV
201 YEHCLGICYQM AQVYLAKYRD VANDEQKVWD FREESNRIAS DSRDYVFYQN
251 MRELMPRGMK ANSLVVG YDA DGLPQKVYWS FDNGKKRQSF EYYLKNGNLF
301 IAQSSSTVALK ADGVTADMOT YHAQQTWYLD GGRIIREEKQ GDRLPDFPLN
351 LEDLEKEVSR YAEAAAARRSG GRRGLSH*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2459>:

```

m728.seq
1  ATGTTTAAAA AATTCAAACC GGTACTGTTG TCATTTTTTG CACTTGTATT
51  TGCCTTTTGG CTGGGAACCG GTATTGCCTA TGAGATTAAT CCGCGTTGGT
101 TTTTGAGCGA TACGGCAACT GAAGTACCTA AAAATCCGAA TGCTTTTGTG
151 GCGAAACTTG CCCGCCTGTT CCGAAATGCC GACAGGGCGG TTGTCATCGT
201 GAAGGAATCG ATAAGGACGG AGGAAATCT TGCCGGAAC GTGGATGACG
251 GTCCGTTGCA GTCGGAGAAG GATTATCTCG CGCTCGCTAT CCGGCTCAGT
301 CGTTTGAAAG AAAAGGCGAA ATGGTTTCAC GTAACGGAGC AGGAACATGG
351 GAAAGAGGTT TGGCTGGATT ACCATATCGG CGAGGGCGGT TTGGTTGCGG
401 TTTTCGCTTC GCAACGCTCG CCGGAAGCAT TTGTTAATGC CGAATATCTG
451 TATCGGAACG ATCGTCCGTT TTCTGTAAAT GTGTACGGCG GAACGGTTCA

```

m728.per

1	MEFKKFKPVLL	SFFALVFVAFW	LGTGIAYEIN	PRWFLSDTAT	EVPKNPNAFV
51	AKLARLFRNA	DRAVYIVKES	IRTEENLACT	VDDGPLQSEK	OYLALAIRLS
101	RLKEKAKWFH	VTEQEHGKEV	WLDYHIGEGT	LVAVLSLSQR	PEAFVNAEYL
151	YRNDRPFVSN	VYGGTVHGEN	YETTGeyRVV	WQPDGSVFDA	AGRGKIGEDV
201	YEHCLGCYQM	AQVYLAKYRD	VANDEQKVWD	FRKESNRIAS	DSRNSVFYQN
251	MRELMPRGMK	ANSLVVGYDA	DGLPQKVYVS	FDNGKKRQSF	EYYLKNGNLF
301	IAQSSTVALK	ADGVTADMQT	YHAQQTWYLD	GGRIVREEKQ	GDRLPDPFLN
351	LENLEKEVRR	YAEAAARRSG	GRDDLSH*		

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 728 shows 96.3% identity over a 377 aa overlap with a predicted ORF (ORF728.a) from *N. gonorrhoeae*:

m728 / q728

	10	20	30	40	50	60
m728.pep	<u>MFKKFKPVLISFFALVFAFWLGTGIAYEINPRWFLSDTATEVPPKNPNAFVAKLARLFRNA</u>					
g728	<u>MFKKFKPVLISFFALVFAFWLGTGIAYEINPRWFLSDTATEVPPKNPNAFVAKLARLFRNA</u>					
	10	20	30	40	50	60
m728.pep	70	80	90	100	110	120
g728	70	80	90	100	110	120
	130	140	150	160	170	180
m728.pep	WLDYHIGEGGLVAVSLSQRSPEAFVNAEYLYRNDRPFSVNVIYGGTWHGENYETTGEYRVV					
g728	WLDYHIGEGGLVAVSLSQRSPEAFVNAEYLYRNDRPFSVNVIYGGTWHGENYETTGEYRVV					
	130	140	150	160	170	180
m728.pep	190	200	210	220	230	240
g728	190	200	210	220	230	240
	250	260	270	280	290	300
m728.pep	DSRNSVFYQNMRELMPRGMKANSVLVGYDADGLPQKVYWSFDNGKKRQSFYLLKNGNLF					
g728	DSRNSVFYQNMRELMPRGMKANSVLVGYDADGLPQKVYWSFDNGKKRQSFYLLKNGNLF					
	250	260	270	280	290	300
m728.pep	310	320	330	340	350	360
g728	IAQSSTVALKADGVTADMQTYHAQQTWYLDGGRIVREEKQGDRLPDFPLNLENLEKEVRR					

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g728 IAQSSTVALKADGVTADMQTYHAQQTWYLDGGRIIREEKQGDRLPDFPLNLEDLEKEVSR
 310 320 330 340 350 360

 370

m728.pep YAEAAARRSGGRRDLSHX
 |||||
 g728 YAEAAARRSGGRRGLSHX
 370

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2461>:

a728.seq

1	ATGTTTAAAA	AATTCAAACC	GCTACTGTTG	TCATTTTTTG	CACTTGTATT
51	TGCCTTTTGG	CTGGGAACGG	GTATTGCCTA	TGAGATTAAT	CCGCGTTGGT
101	TTTTGAGCGA	TACGGCAACT	GAAAAACCGA	ATGCTTTTGT	GGCGAAACTT
151	GCCCGCCTGT	TCCGAAATGC	CGACAGGGCG	GTTGTATCG	TGAAGGAATC
201	GATGAGGACG	GAGGAAAGTC	TTGCCGGAGC	TGTGGATGAC	GGTCCGTTGC
251	AGTCGGAGAA	GGATTATCTT	GCACTCGCTG	TCCGGCTCAG	TCGTTTGAAA
301	GAAAAGGCGA	AATGGTTTCA	CGTAACGGAG	CAGGAACATG	GGGAAGAGGT
351	TTGGCTGGAT	TACTATATCG	GCGAGGGCGG	TTTGGTTGCG	GTTTCGCTTT
401	CGCAACGCTC	GCCGGAAGCG	TTTGTTAATG	CCGAATATCT	GTATCGGAAC
451	GATCGTCCGT	TTTCTGTAAA	TGTGTACGGC	GGAACGGTTC	ACGGGGAAAA
501	TTATGAACAG	ACAGGAGAAT	ATCGGGTTGT	TTGGCAACCG	GACGGTTCGG
551	TATTTGATGC	GTCGGGGCGC	GGGAAATCG	GGGAAGATGT	TTATGAGCAT
601	TGCCTCGGGT	GTTATCAGAT	GGCCAGGTA	TATTTGGCGA	AATATCGGGA
651	TGTCGCGAAT	GATGAGCAGA	AGGTTTGGGA	CTTCCGCGAA	GAGAGTAACC
701	GGATTGCGTC	GGACTCGCGC	GATTCTGTGT	TTTATCAGAA	TATGCGGGAA
751	TTGATGCCCC	GAGGGATGAA	GGCAAACAGT	CTTGTGGTCG	GCTATGATGC
801	GGACGGTCTG	CCGCAGAAAG	TCTATTGGAG	TTTCGACAAT	GGGAAAAAAC
851	GCCAGAGTTT	CGAATATTAT	TTGAAAAACG	GAAATCTTTT	TATTGCACAA
901	TCTTCGACGG	TAGCATTGAA	AGCGGATGGC	GTAACGGCGG	ATATGCAGAC
951	CTATCATGCG	CAACAGACGT	GGTATTTAGA	TGGCGGGCGG	ATTGTCCCGG
1001	AAGAGAAACA	GGGGGACAGA	CTGCCTGATT	TTCTTTTGAA	CTTGGAAGAT
1051	TTGGAAAAAG	AGGTGAGCCG	TTATGCAGAG	GCTGCGGCGA	GACGTTCCGG
1101	CGGCAGGCGC	GACCTTTCTC	ACTGA		

This corresponds to the amino acid sequence <SEQ ID 2462; ORF 728.a>:

a728.pep

1	MFKKFKPVLL	SFFALVF	FWLGT	GIAYEIN	PRWFLSD	TATE---	NPNAFVAKL	ARLFRNA
51	ARLFRNADRA	VVIVKESMRT	EESLAGAVDD	GPLQSEKDYL	ALAVRLSRLK			
101	EKAKWFHVTE	QEHGEEVWLD	YYIGEGGLVA	VSLSQRSPEA	FVNAEYLYRN			
151	DRPFSVNVYG	GTVHGENYET	TGEYRVVWQP	DGSVFDASGR	GKIGEDVYEH			
201	CLGQYQMAQV	YLAKYRDVAN	DEQKVWDFRE	ESNRIASDSR	DSVFYQNMRE			
251	LMPRGMKANS	LVVGYDADGL	PQKVYWSFDN	GKKRQSF EY	LKNGNLFIAQ			
301	SSTVALKADG	VTADMQTYHA	QQTWYLDGGR	IVREEKQGDR	LPDFPLNLED			
351	LEKEVSRYAE	AAARRSGGRR	DLSH*					

a728 / m728 96.3% identity in 377 aa overlap

a728.pep	10	20	30	40	50	
	MFKKFKPVLLSFFALVF	FWLGTGIAYEIN	PRWFLSDTATE---	NPNAFVAKL	ARLFRNA	
m728	10	20	30	40	50	
	MFKKFKPVLLSFFALVF	FWLGTGIAYEIN	PRWFLSDTATEV	PKNPNAFVAKL	ARLFRNA	
a728.pep	60	70	80	90	100	110
	DRAVVIVKESMRT	EESLAGAVDD	GPLQSEKDYL	ALAVRLSRLK	EKAKWFHVTE	QEHGEEV
m728	60	70	80	90	100	110
	DRAVVIVKESIRTEEN	LAGTVDD	GPLQSEKDYL	ALAIRLSRLK	EKAKWFHVTE	QEHGKEV
a728.pep	120	130	140	150	160	170
	WLDYYIGEGGLVAV	VSLSQRSPEAF	VNAEYLYRNR	DRPFSVNVYGG	TVHGENYETT	TGEYRVV
m728	120	130	140	150	160	170
	WLDYHIGEGGLVAV	VSLSQRSPEAF	VNAEYLYRNR	DRPFSVNVYGG	TVHGENYETT	TGEYRVV
	130	140	150	160	170	180

1177

	180	190	200	210	220	230
a728.pep	WQPDGVSFVDASGRGKIGEDVYEHCLGCVYMAQVYLAKYRDVANDEQKVWDFREESNRIAS					
	: : : : : :					
m728	WQPDGVSFVDAAGRKGIGEDVYEHCLGCVYMAQVYLAKYRDVANDEQKVWDFRKESNRIAS					
	190	200	210	220	230	240
	240	250	260	270	280	290
a728.pep	DSRDSVFYQNMRELMPRGMKANSILVVGVDADGLPQKVYWSFDNGKKRQSFEEYLLKNGNLF					
	: : : : : :					
m728	DSRNSVFYQNMRELMPRGMKANSILVVGVDADGLPQKVYWSFDNGKKRQSFEEYLLKNGNLF					
	250	260	270	280	290	300
	300	310	320	330	340	350
a728.pep	IAQSSTVALKADGVTADMQTYHAQQTWYLDGGRIVREEKQGDRLPDFPLNLEDLEKEYSR					
	: : : : : :					
m728	IAQSSTVALKADGVTADMQTYHAQQTWYLDGGRIVREEKQGDRLPDFPLNLENLEKEYRR					
	310	320	330	340	350	360
	360	370				
a728.pep	YAEAAARRSGGRRDL SHX					
	: : : : :					
m728	YAEAAARRSGGRRDL SHX					
	370					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2463>:

g729.seq

```

1  ATGAATACTA CATTGAAAAC TACCTTGACC TCTGTTGCAG CAGCCTTTGC
51  ATTGTCTGCC TGCACCATGA TTCCTCAATA CGAGCAGCCC AAAGTCGAAG
101 TTGCGGAAAC CTTCCAAAAC GACACATCGG TTCTTTCCAT CCGCGCGGTT
151 GATTGGGTTT GGCATGACTA TTTTGCCGAC CCGCGCCTGC AAAAGCTGAT
201 CGACATCGCA CTCGAGCGCA ATACCACTTT GCGTACAGCC GTATTGAACA
251 GCGAAATCTA CCGCAAACAA TACATGATCG AGCGCAACAA CCTCTGCCC
301 ACGCTTGCCG CCAATGCGAA CGGCTCGCGC CAAGGCAGCT TGAGCGGCg
351 caaTTGTCAG AGCAGCTACA ATGTGCGACT GGGTGcGGca tCTTACGAAC
401 TCGATCTGTT CgGGCGCGTG CGCagcaacA GcgaagcAGC ACTGcaggGC
451 tATTTTGCCA GCGTTGCCAA CcgGATGCG GCACATTTGa ttCtGATTGC
501 CACCGTTGCC AAAGCCTATT TCAAcgaGcG TTATGCCGAA AAAGcgatgT
551 CTTGGCGCa gcGTGTCTTG AAAACGCGCG AGGAAACCTA CAAGCTGTCC
601 GAATTGCGGT ACAAGGCAGG CGTGATTTCG GCCGTGCGCC TCGCCAGCA
651 GGAAGCCTTG ATTGAATCTG CCAAAGCCGA TTATGCCCAT GCCGCGCScA
701 gcCGGAACA GCGCGCAAT GCCTTGCCAA CCTTGATTAA ccGTCCGATA
751 CCCGAagaCC TGCCCGCCGG TTTGCCGTTG GACAagcAGT TTTTGTGTA
801 AAAACTGCCT GCCGTTTGA GTTCCGAAGT ATTGCTCGAC CGTCCCGACA
851 TCCGCGCCGC CGAACACGCG CTCAAACAGG CAAACGCCAA TATCGGTGCG
901 gcgCGCGCCg ccTTTTTCCC GTCCATCCGC CTGACCGGAA GCGTCGGTAC
951 GGGTTCTGTC GAATTGGGCG GGCTGTTCAA AAGCGGCACG GCGGTTTGGG
1001 CGTTCGCTCC GTCTATTACC CTGCCGATT TTA CTG GGG AACGAACAAG
1051 GCGAACCTTG ATGTGGCAA ACTGCGCCAA CAGGCACAAA TTGTTGCCTA
1101 TGAATCCGCC GTCCAATCCG CCTTCAAGA CGTGGCAAAC GCATTGGCGG
1151 CGCGCGAGCA GCTGGATAAA GCCTATGACG CTTAAGCAA ACAAGCCGC
1201 GCCTCTAAAG AAGCGTTGCG CTTGGTCGGA CTGCGTTACA AACACGGCGT
1251 ATCCGCGCGC CTCGATTTCG TCGATGCGGA ACGCATCAGC TATTCGGCGG
1301 AAGTTCGCGC TTTGTGCGCA CAACTGACCC GCGCGAAAA CCTTGCCGAT
1351 TTGTACAAGG CGCTCgacGG CGGATTGAAA CGGATACCC AAACCGGCAA
1401 ATAA

```

This corresponds to the amino acid sequence <SEQ ID 2464; ORF 729>:

g729.pep

```

1  MNITLKTTLT SVAAAFALSA CTMIPQYEQP KVEVAETFQN DTSVSSIRAV
51  DLGWHDFYAD PRLQKLIDIA LERNLSLRTA VLNSEIYRKQ YMIERNLLP
101 TLAANANGSR QGSLSGGNVS SSYNVGLGAA SYELDLFGRV RSNSEAALQG
151 YFASVANRDA AHLILIATVA KAYFNERYAE KAMSLAQRVL KTREETYKLS

```


1179

	70	80	90	100	110	120
m729.pep	PRLOKLIDIALERNTSLRTAVLNSEIYRKQYMIERNLLPTLAANANDSRQGSLSGGNV					
g729	PRLOKLIDIALERNTSLRTAVLNSEIYRKQYMIERNLLPTLAANANGSRQGSLSGGNV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m729.pep	SSYKVGGLGAASYELDLFGRVRSSEALQGYFASTANRDAHLSLIATVAKAYFNERV					
g729	SSYNVGLGAASYELDLFGRVRSNSEALQGYFASVANRDAHLIILATVAKAYFNERV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m729.pep	EAMSLAQRLVLTREETYKLSELRYKAGVISAVALRQQEALIESAKADYAHAAARSREQ					
g729	KAMSLAQRLVLTREETYKLSELRYKAGVISAVALRQQEALIESAKADYAHAAARSREQ					
	190	200	210	220	230	240
	250	260	270	280	290	300
m729.pep	ALATLINRPIPEDLPAGLPLDKQFFVEKLPAGLSSEVLLDRPDIRAAEHALKQANAN					
g729	ALATLINRPIPEDLPAGLPLDKQFFVEKLPAGLSSEVLLDRPDIRAAEHALKQANAN					
	250	260	270	280	290	300
	310	320	330	340	350	360
m729.pep	ARAAFFPSIRLTGTGTGSAELGGLFKSGTGVWSFAPSITLPIFTWGTNKANLDVAKLR					
g729	ARAAFFPSIRLTGSVGTGSVELGGLFKSGTGVWAFAPSITLPIFTWGTNKANLDVAKLR					
	310	320	330	340	350	360
	370	380	390	400	410	420
m729.pep	QVQIVAYESAVQSAFQDVANALAAREQLDKAYDALSKQSRASKEALRLVGLRYKHGVS					
g729	QAQIVAYESAVQSAFQDVANALAAREQLDKAYDALSKQSRASKEALRLVGLRYKHGVS					
	370	380	390	400	410	420
	430	440	450	460		
m729.pep	LDLLDAERSSYAEGAALSAQLTRAENLADLYKALGGGLKRDQTQDKX					
g729	LDLLDAERISYSAEGAALSAQLTRAENLADLYKALDGGGLKRDQTQGX					
	430	440	450	460		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2467>:

a729.seq

```

1  ATGGATACTA CATTGAAAAC CACCTTGACT TCTGTTGCAG CAGCCTTCGC
51 ATTATCCGCC TGCACCATGA TTCCCAATA CGAGCAGCCC AAAGTCGAAG
101 TTGCCGAAAC GTTCAAAAAC GATACCGCCG ACAGCGGCAT CCGTGCGGTC
151 GATTTGGGTT GGCATGACTA TTTTGCCGAC CCGCGCCTGC AAAAGCTGAT
201 CGACATCGCA CTCGAGCGCA ATACCAGTTT GCGTACCGCC GTATTGAACA
251 GCGAAATCTA CCGCAAACAA TACATGATTG AGCGCAACAA CCTCTGCCCC
301 ACGCTTGCCG CCAATGCGAA CGACTCGCGC CAAGGCAGCT TGAGCGCGCG
351 CAATGTAAGC AGCAGCTACA AAGTCGGACT GGGTGCGGCA TCTTACGAAC
401 TCGATCTGTT CGGGCGTGTA CGCAGCAGCA GCGAGGCGGC ACTGCAAGGC
451 TATTTGCGCA GCACCGCCAA CCGCGATGCG GCACATTTGA GCCTGATTGC
501 CACCGTTGCC AAAGCCTATT TCAACGAACG TTATCCGAA GAAGCGATGT
551 CTTTGGGCGA ACGTGTTTGG AAAACGCGCG AGGAAACCTA CAAGCTGTCC
601 GAATTACGTT ACAAGGCAGG CGTGATTTC GCGTCGCCC TACGTCAGCA
651 GGAAGCCCTA ATCGAATCTG CCAAGCCGA TTATGCCCAT GCCGCGCGCA
701 GCCGCGAACA GCGCGCAAT GCCTTGGCAA CCCTGATTAA CCAACCGATA
751 CCCGACGACC TGCCCGCCGG TTTGCCGTTG GACAAGCAGT TTTTGTGTTGA
801 GAAGCTGCGG GCCGTTTGA GTTCCGAAGT ATTGCTCGAC CGTCCCGATA
851 TCCGTGCTGC CGAACACGCG CTCAAACAGG CAAACGCCAA TATCGGTGCG
901 GCACGCGCGC CCTTTTCCC ATCCATCCGC CTGACCGGAA GCGTCGATAC
951 GCATTCTGCC GAATTGGGCG GGCTGTTCAA AAGCGGCACC GGCCTTGGT
1001 TGTTGCGACC TTCCATTACC CTGCCGATT TTACCTGGGG TACGAACAAG

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1180

```
1051 GCGAACCTCG ATGTAGCCAA GCTGCGCCAA CAGGCACAAA TCGTTGCCTA
1101 TGAAGCCGCC GTCCAATCCG CATTTCAAGA CGTGGCAAAC GCATTGACCG
1151 CGCGCGAGCA GTTGGATAAA GCCTATGACG CTTTAAGCAA ACAAGCCGC
1201 GCCTCTAAAG AAGCGTTGCG TTTGGTCGGT CTGCGTTACA AACACGGCGT
1251 ATCCGGCGCG CTCGACTTGC TCGATGCGGA ACGCAGCAGC TATTCGGCGG
1301 AAGGTGCGGC TTTGTGCGCA CAACTGACCC GCGCCGAAAA CCTTGCCGAT
1351 TTGTACAAGG CACTCGGCGG CGGATTGAAA CGGGATACCC AAACCGACAA
1401 ATAA
```

This corresponds to the amino acid sequence <SEQ ID 2468; ORF 729.a>:

a729.pep

```
1 MDITLKTTLT SVAAAFALSA CTMIPOYEQP KVEVAETFKN DTADSGIRAV
51 DLGWHDFAD PRLQKLIDIA LERNTSLRTA VLNSEIYRKQ YMIERNNLLP
101 TLAANANDSR QGSLSGGNVS SSYKVLGAA SYELDLFGRV RSSSEALQG
151 YFASTANRDA AHLSLIATVA KAYFNERYAE EAMSLAQRVL KTREETYKLS
201 ELRYKAGVIS AVALRQOEAL IESAKADYAH AARSREQARN ALATLINQPI
251 PDDLPAGLPL DKQFFVEKLP AGLSSEVLLD RPDIRAAEHA LKQANANIGA
301 ARAAFFPSIR LTGSVDTHSA ELGGLFKSGT GVWLFAPSIT LPIFTWGTNK
351 ANLDVAKLRQ QAQIVAYEAA VQSAFQDVAN ALTAREQLDK AYDALSKQSR
401 ASKEALRLVG LRYKHGVSVA LDLLDAERSS YSAEGAALSA QLTRAENLAD
451 LYKALGGGLK RDTQTDK*
```

a729 / m729 98.1% identity in 467 aa overlap

	10	20	30	40	50	60
a729.pep	MDITLKTTLT SVAAAFALSA CTMIPOYEQP KVEVAETFKN DTADSGIRAV DLGWHDFAD					
m729	MDITLKTTLT SVAAAFALSA CTMIPOYEQP KVEVAETFKN DTADSGIRAV DLGWHDFAD					
	10	20	30	40	50	60
	70	80	90	100	110	120
a729.pep	PRLQKLIDIALERNTSLRTAVLNSEIYRKQYMIERNNLLPTLAANANDSRQGSLSGGNVS					
m729	PRLQKLIDIALERNTSLRTAVLNSEIYRKQYMIERNNLLPTLAANANDSRQGSLSGGNVS					
	70	80	90	100	110	120
	130	140	150	160	170	180
a729.pep	SSYKVLGAASYELDLFGRVRSSEALQGYFASTANRDA AHLSLIATVA KAYFNERYAE					
m729	SSYKVLGAASYELDLFGRVRSSEALQGYFASTANRDA AHLSLIATVA KAYFNERYAE					
	130	140	150	160	170	180
	190	200	210	220	230	240
a729.pep	EAMSLAQRVLK TREETYK LSELRYKAGVIS AVALRQOEAL IESAKADYAH AARSREQARN					
m729	EAMSLAQRVLK TREETYK LSELRYKAGVIS AVALRQOEAL IESAKADYAH AARSREQARN					
	190	200	210	220	230	240
	250	260	270	280	290	300
a729.pep	ALATLINQPI PDDLPAGLPLDKQFFVEKLPAGLSSEVLLDRPDIRAAEHALKQANANIGA					
m729	ALATLINQPI PEDLPAGLPLDKQFFVEKLPAGLSSEVLLDRPDIRAAEHALKQANANIGA					
	250	260	270	280	290	300
	310	320	330	340	350	360
a729.pep	ARAAFFPSIRLTGSVDTHSAELGGLFKSGTGVWLFAPSITLPIFTWGTNKANLDVAKLRQ					
m729	ARAAFFPSIRLTGTGTGSALGGLFKSGTGVWLFAPSITLPIFTWGTNKANLDVAKLRQ					
	310	320	330	340	350	360
	370	380	390	400	410	420
a729.pep	QAQIVAYEAAVQSAFQDVANALTAREQLDKAYDALSKQSRASKEALRLVGLRYKHGVSQA					
m729	QVQIVAYESAVQSAFQDVANALAREQLDKAYDALSKQSRASKEALRLVGLRYKHGVSQA					
	370	380	390	400	410	420

1181

	430	440	450	460
a729.pep	LDLLDAERSSSYAEGAALSAQLTRAENLADLYKALGGGLKRDQTQDKX			
m729	LDLLDAERSSSYAEGAALSAQLTRAENLADLYKALGGGLKRDQTQDKX			
	430	440	450	460

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2469>:

g730.seq

```

1   GTGAAACCGC TGCCGAGACT GACAAACCTC CTTGCCGCCT GCGCCGTAGC
51  GCGCGTCGCA CTCATACAGC CCGCCCTCGC GCGCGACTTG GCGCAAGACC
101 CGTTCATTAC CGATAACACC CAACGGCAGC ACTACGAACC CCGCGGCAAA
151 TACCACCTCT TCGGCGaCCC GCGCGGAGC GTTTCGACG GCACCGGCAA
201 AATCAACGTC ATCCAAGACT ATACCCACCA GATGGGCAAC CTGCTCATCC
251 AACAGCGCGC AATCCAAGGC AATCTGGT ACACCGTCCG CTTTCCGGA
301 CACGGACACG AAGAACACGC CCCCTTCGAC AACCACGCCG CCGACAGCGC
351 AAGCGAAGAA AAAGGCAACG TTGACGACGG CTTTACCGTG TACCGGCTCA
401 ACTGGGAAGG ACACGAACAT CATCCGCGCG ATGCCTACGA CGGCCGAAG
451 GCGCGCAATT ACCCCAAACC TACGGGCGCA CGAGACGAAT ACACCTATCA
501 CGTCAACGGC ACAGCCCGCA GTATCAAACT CAATCCGACC GACACCGCA
551 GCATCCGGCA ACGCATATTC GACAACTACA ACAACCTCGG CAGCAATTTC
601 TCCGACCGCG CCGATGAAGC CAACAGAAAA ATGTTGAGC ACAATGCCAA
651 GCTCGACCGC TGGGGCAACA GCATGGAGTT TGTCACCGC GTCGCCGCCG
701 GCGCGCTCAA CCCCTTTATC AGCGCGGCGG AAGCCTTGGG CATAGCGGAC
751 ATACTGTACG GAACCGGCTA TGCCATAGAC AAAGCCGCGA TGGCAACAT
801 CGCCCCCTTA CCCGCCGAGG GCAAATTCGC CGCCATCGGC GGCTTGGGCA
851 GCGCGGCGGG CTTTGAAAAA AATACGCGCG AAGCCGTTGA CCGGTGGATA
901 CAGGAAAACC CCAATGCCGC CGAAACCGTC GAAGCCCTGG TCAACGTCCT
951 GCCGTTTGCC AAAGTCAAAA ACCTGACAAA GCGGCAAAA CCGGGGAAGG
1001 CTGCGGTTAG TGGGGATTTT TCTAAATCCT ACACCTGCTC CTTCCACGGC
1051 AGCACCTTGG TCAAAACGGC AGACGGCTAC AAAGCCATTG CCCATATTCA
1101 AGCCGGAGAC CGGTCCTTT CCAAGGACGA GGCAAGCGGA GAAACGGGAT
1151 ACAACCCCGT TACCGCCGCA TACGGCAATC CGTATCAAGA AACCGTTTAC
1201 ATTGAAGTTT CAGACGGCAT CGGCAACAGC CAAACCTGTA TTTCCAACCG
1251 CATCCACCCG TTTTATTCGG ACGGCAAATG GATTAAGGCG GAAGATTTAA
1301 AAGCGGGAAG CCGGCTGTTA TCCGAAAGCG GCAAACCCA AACCGTCCGC
1351 AACATCGTTG TCAAACCAA ACCGCTCAA GCCTACAA TCAGCGTTGC
1401 CGATTGGCAT ACCTACTTCG TCAAGGGTAA TCAGGCGGAA ACGGAAGGGG
1451 TTTGGGTTCA TAAATGATTGT CCGCTAAAC CAAACCAAC CAATCATGCC
1501 CAACAAAGAA AAGAAGAAGC TAAAAACGAT TCTCATCGAA GTGTGGGAGA
1551 TTCCAATCGT GTCGTTCCGG AAGGAAAGCA ATATTTAGAT TCCGACACAG
1601 GAAACCATGT TTATGTAAAA GGAGATAAAG TGGTTATTCT AACTCCTGAT
1651 GGAAGACAGG TAACTCAATT TAAGAACTCG AAAGCCAATA CGTCAAAAAG
1701 GGTAAAAAAT GGGAAATGGA CACCAAAATA A

```

This corresponds to the amino acid sequence <SEQ ID 2470; ORF 730.ng>:

g730.pep

```

1   VKPLRLRLTNL LAACAVAAVA LIQPALAADL AODPFITDNT QRQHYEPGGK
51  YHLEGDPRGS VSDRTGKINV IQDYTHQMGH LLIQAAAIQG NLGYTVRFSG
101 HGHEEHAFPD NHAADSASEE KGNVDDGFTV YRLNWEGHEH HPADAYDGPK
151 GGNYPKPTGA RDEYTYHVNG TARSIKLNPT DTRSIRQRIE DNYNNLGSNF
201 SDRADANRK MFEHNAKLDR WGNMSEFVNG VAAGALNPFI SAGEALGIGD
251 ILYGTRYAID KAAMRNIAPI PAEGKFAAIG GLGSAAGFEK NTREAVDRWI
301 QENPNAETV EALVNVLPFA KVKNLTKAAK PGKAAVSGDF SKSYTCSFHG
351 STLVKTADGY KAIAHIQAGD RVLKDEASG ETGYPVTAR YGNPYQETVY
401 IEVSDGIGNS QTLISNRIEP FYSDGKWIKA EDLKAGSRLI SESGKTQTVR
451 NIVVKPKPLK AYNLTVADWH TYFVKGNQAE TEGVWVHND C PPKPKPTNHA
501 QQRKEEAKND SHRSVGDSNR VVREGKQYLD SDTGNHVYVK GDKVVILTFD
551 GROVTQFKNS KANTSKRVKN GKWTFK*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2471>:

m730.seq

```

1   GTGAAACCGC TGCCGAGACT GACAAACCTC CTTGCCGCCT GCGCCGTAGC
51  GCGCGCGCGA CTCATACAGC CCGCCCTCGC GCGCGACTTG GCGCAAGACC

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1182

```

101 CGTTCATTAC CGATAACGCC CAACGGCAGC ACTACGAACC CGGCGGCAAA
151 TACCACCTCT TCGGCGACCC GCGCGGACG GTTTCGACC GCACCGGCAA
201 AATCAACGTC ATCCAAGACT ATACCCACCA GATGGGCAAC CTGCTCATCC
251 AACAGGCAAA CATCAACGGC ACAATCGGCT ACCACACCCG CTTTCCGGA
301 CACGGACACG AAGAACACGC CCCCTTCGAC AACCACGCCG CCGACAGCGC
351 GAGCGAAGAA AAAGGCAACG TTGACGAAGG CTTTACCGTA TACCGGCTCA
401 ACTGGGAAGG ACACGAACAT CATCCCGCG ATGCCTACGA CGGCCGAAG
451 GCGGCAATT ACCCCAAACC TACGGGCGCA CGAGACGAAT ACACCTATCA
501 CGTCAACGGC ACAGCCGCA GTATCAAACT CAATCCGACC GACACCGCA
551 GCATCCGGCA ACGCATATCC GACAATTACA GCAACCTCGG CAGCAATTTC
601 TCCGACCGCG CCGATGAAGC CAACAGAAAA ATGTTGAGC ACAATGCCAA
651 GCTCGACCGC TGGGGCAACA GCATGGAGTT TATCAACGGC GTCCGCGCCG
701 GCGCGCTCAA CCCCTTTATC AGCGCGGCG AAGCCTTGGG CATAGGCGAC
751 ATACTGTACG GAACGCGCTA TGCCATAGAC AAAGCCGCAA TGCACAACAT
801 CGCCCCCTTG CCCGCCGAGG GCAAATTCGC CGTCATCGGC GGCTTGGGCA
851 GCGTGGCGGG CTTTGAAAAG AATACGCGC AAGCCGTGTA CCGGTGGATA
901 CAGGAAAAAT CCAATGCCGC CGAAACCGTC GAAGCCGTCT TCAACGTTGC
951 CGCAGCAGCC AAAGTCGCGA AGTTGGCAA GGCGGCAAAA CCAGGGAAGG
1001 CTGCGGTTAG CGGGGATTTT GCTGATTCTT ATAAAAAGAA ATTGGCTTTG
1051 TCTGATAGTG CGAGACAGTT ATATCAAAAT GCAAAGTATA GAGAAGCTCT
1101 AGATATACAT TATGAAGATT TAATTAGAAG AAAAAGTAT GGTTCATCAA
1151 AATTTATTAA CGCAGAGAA ATTGACGCTG TTACGAATGA TGCTTTAATA
1201 CAAGCCAAAA GAACAATTTC AGCAATAGAT AAACCTAAAA ATTTCTTAAA
1251 TCAAAAAAAT AGAAAGCAA TTAAGCAAC CATCGAAGCA GCAAACCAAC
1301 AGGGAACACG TGCAGAATT TGGTTTAAAT ACGGTGTCA TTCACAAGTT
1351 AAGTCATATA TTGAATCAA AGGCGGCATT GTTAAACAG GTTTAGGAGA
1401 TTA

```

This corresponds to the amino acid sequence <SEQ ID 2472; ORF 730>:

```

m730.pep
1  VKPLRRLTNL LAACAVAAAA LIQPALAADL AQDPFITDNA QRQHYEPGGK
51  YHLFGDPRGS VSDRTGKINV IQDYTHQMGN LLIQANING TIGYHTRFSG
101 HGHEEHAPFD NHAADSASEE KGNVDEGFTV YRLNWEGHEH HPADAYDGPK
151 GGNYPKPTGA RDEYTYHVNG TARSIKLNPT DTRSIRQRIS DNYSNLGSNF
201 SDRADENRKF MFEHNAKLDR WGSMEFING VAAGALNPFI SAGEALGIGD
251 ILYGTRYAID KAAMRNIAFL PAEGKFVIG GLGSVAGFEK NTREAVDRWI
301 QENPNAETV EAVFNVAAPA KVALAKAAK PGKAAVSGDF ADSYKKKLAL
351 SDSARQLYQN AKYREALDIH YEDLIRKTD GSSKFINGRE IDAVTNDALI
401 QAKRTISAID KPNFLNQKN RKQIKATIEA ANQQGKRAEF WFKYGVHSQV
451 KSYIESKGGI VKTGLGD*

```

g730 / m730 93.0% identity in 344 aa overlap

	10	20	30	40	50	60
g730.pep	VKPLRRLTNLLAACAVAAVALIQPALAADLAQDPFITDNTQRQHYEPGGKYHLFGDPRGS					
m730	VKPLRRLTNLLAACAVAAVALIQPALAADLAQDPFITDNAQRQHYEPGGKYHLFGDPRGS					
	10	20	30	40	50	60
g730.pep	VSDRTGKINV IQDYTHQMGNLLIQAAIQGNLGYTVRFSGHGHEEHAPFDNHAADSASEE					
m730	VSDRTGKINV IQDYTHQMGNLLIQANINGTIGYHTRFSGHGHEEHAPFDNHAADSASEE					
	70	80	90	100	110	120
g730.pep	KGNVDDGFTVYRLNWEGHEHHPADAYDGPKGGNYPKPTGARDEYTYHVNGTARSIKLNPT					
m730	KGNVDEGFTVYRLNWEGHEHHPADAYDGPKGGNYPKPTGARDEYTYHVNGTARSIKLNPT					
	130	140	150	160	170	180
g730.pep	DTRSIRQRIFDNYNNLGSNFSADRAENRKMFEHNAKLDRWGSMEFVNGVAAGALNPFI					
m730	DTRSIRQRISDNYSNLGSNFSADRAENRKMFEHNAKLDRWGSMEFINGVAAGALNPFI					
	190	200	210	220	230	240

1183

	250	260	270	280	290	300
g730.pep	SAGEALGIGDILYGTRYAIDKAAMRNIAPLPAEGKFAAIGGLGSAAGFEKNTREAVDRWI					
m730	SAGEALGIGDILYGTRYAIDKAAMRNIAPLPAEGKFAVIGGLGSAAGFEKNTREAVDRWI					
	250	260	270	280	290	300
	310	320	330	340	350	360
g730.pep	QENPNAAETVEALVNLPFAKVKNLTAAKPGKAAVSGDFSYSYCSFHGSTLVKTADGY					
m730	QENPNAAETVEAVFNVAARVAKLAKAAKPGKAAVSGDFADSYKKKLALSDSARQLYQN					
	310	320	330	340	350	360
	370	380	390	400	410	420
g730.pep	KALAHIQAGDRVLSKDEASGETGYKPVRTARYGNPYQETVYIEVSDGIGNSQTLISNRHP					
m730	AKYREALDIHYEDLIRRKTDGSSKFINGREIDAVTNDALIQAKRTISAIDKPKNFLNQKN					
	370	380	390	400	410	420

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2473>:

```

a730.seq
1  GTGAAACCGC  TGCGAAGACT  CATCAAGCTC  CTTGCCGCCT  GTGCCGTAGC
51  GCGCGCCGCA  CTCATACAGC  CCGCCCTCGC  GCGCGACTTG  GCGCAAGACC
101 CGTTCATTAC  CGATAACGCC  CAACGGCAGC  ACTACGAACC  CGGAGGCAAA
151 TACCACCTCT  TCGCGGACCC  GCGCGGCAGC  GTCTCCGACC  GCACCGGTCA
201 AATCAACGTC  ATCCAAGACT  ATACCCACCG  GATGGGCAAC  CTGCTCATCC
251 AGCAGGCAAA  CATCAACGGC  ACAATCGGCT  ACCACACCCG  CTTTTCCGGA
301 CACGGATACG  AAGAACACGC  CCCCTTCGAC  AACCACGCCG  CCGACAGCGC
351 GAGCGAAGAA  AAAGGCAACG  TTGACGAAGG  CTTTACCGTA  TACCGGCTCA
401 ACTGGGAAGG  ACACGAACAT  CATCCGCGCG  ATGCCTACGA  CGGCCCGAAG
451 GCGGGCAATT  ACCCCAAACC  TACGGGTGCA  CGCGACGAAT  ACACCTATCA
501 CGTCAACGGC  ACAGCACGCA  GCATCAAAC  CAATCCGACC  GACACCCGCA
551 GCATCCGGCA  ACGCATATCC  GACAATTACA  GCAACCTCGG  CAGCAATTTT
601 TCCGACCGCG  CCGATGAAGC  CAACAGAAAA  ATGTTTCGAGC  ACAATGCCAA
651 GCTCGACCGC  TGGGGCAACA  GCATGGAGTT  TATCAACGGC  GTCGCGCGCG
701 GCGCGCTCAA  CCCCTTTATC  AGCGCGGGCG  AAGCCTTGGG  CATAGGCGAC
751 ATACTGTACG  GAACGCGCTA  TGCCATAGAC  AAAGCCGCAA  TGCGCAACAT
801 CGCCCCCTTG  CCCGCCGAGG  GCAAATTCGC  CGTCATCGGC  GGCTTGGGCA
851 GCGTGGCGGG  CTTTGAAAAA  AATACGCGCG  AAGCCGTGTA  CCGGTGGATA
901 CAGGAAACC  CCAATGCCGC  CGAAACCGTC  GAAGCCCTGG  TCAACGTCCT
951 GCCGTTTGCC  AAAGTCAAAA  ACCTGACAAA  GCGGCAAAA  CCGGGGAAGG
1001 CTGCGGTTAG  CGGGGATTTT  TCTGCTGCAT  ACAATACAAG  AACAAC TAGA
1051 AAAGTTACTA  CAGAAACAGA  GGGGTTAAAT  AGAATCAGAC  AGAACCAGAA
1101 AAATAGTAAT  ATACATGAGA  AAAATTATGG  AAGAGATAAT  CCTAATCATA
1151 TTAATGTTTT  ATCTGGAAAT  TCTATACAAC  ATATACTGTA  TGGAGATGAA
1201 GCAGGAGGTG  GGCATCTTTT  TCCTGGCAAA  CCTGGTAAGA  CAACATTTCC
1251 CCAACATTGG  TCAGCCAGTA  AAATAACTCA  TGAAATTAGT  GATATCGTTA
1301 CATCCCCAAA  AACGCAATGG  TATGCACAGA  CTGGAACAGG  CGGCAATAT
1351 ATTGCTAAAG  GAAGACCAGC  TAGGTGGGTA  TCATATGAAA  CGAGAGATGG
1401 AATTCGTATC  AGAACAGTTT  ATGAACCTGC  AACAGGAAAA  GTGGTAACTG
1451 CATTCCCCGA  TAGAACCTCT  AATCCCAAAT  ATAACCCTGT  AAAATAAA

```

This corresponds to the amino acid sequence <SEQ ID 2474; ORF 730.a>:

```

a730.pep
1  VKPLRRLIKL  LAACAVAAAA  LIQPALAADL  AQDPFITDNA  QRQHYEPGGK
51  YHLFGDPRGS  VSDRTGQINV  IQDYTHRMGN  LLIQQANING  TIGYHTRFSG
101 HGYEEHAPFD  NHAADSASEE  KGNVDEGFTV  YRLNWEGHEH  HPADAYDGPK
151 GGNYPKPTGA  RDEYTYHVNG  TARSIKLNPT  DTRSIRQRIS  DNYSNLGSNF
201 SDRADEANRK  MFEHNAKLDR  WGNSEMFING  VAAGALNPFI  SAGEALGIGD
251 ILYGTRYAID  KAAMRNIAPL  PAEGKFAVIG  GLGSAAGFEK  NTREAVDRWI
301 QENPNAAETV  EALVNLPFA  KVKNLTKAAK  PGKAAVSGDF  SAAYNTRTTR
351 KVTTETEGLN  RIRNQKNSN  IHEKNYGRDN  PNHNVLSGN  SIQHILYGDE
401 AGGGHLFPGK  PGKTTFPOHW  SASKITHEIS  DIVTSPKTQW  YAQTGTGGKY
451 IAKGRPARWV  SYETRDGIRI  RTVYEPATGK  VVTAFPDRTS  NPKYNPVK*

```


1184

a730 / m730 88.6% identity in 376 aa overlap

	10	20	30	40	50	60
a730.pep	VKPLRRLIKLLAACAVAAAALIQPALAADLAQDPFITDNAQRQHYEPGGKYHLFGDPRGS					
		:				
m730	VKPLRRLTNLLAACAVAAAALIQPALAADLAQDPFITDNAQRQHYEPGGKYHLFGDPRGS					
	10	20	30	40	50	60
	70	80	90	100	110	120
a730.pep	VSDRTGQINVIQDYTHRMGNLLIQANINGTIGYHTRFSGHGYEEHAPFDNHAADSASEE					
		:				
m730	VSDRTGKINVIQDYTHQMGNLLIQANINGTIGYHTRFSGHGHEEHAPFDNHAADSASEE					
	70	80	90	100	110	120
	130	140	150	160	170	180
a730.pep	KGNVDEGFTVYRLNWEGHEHHPADAYDGPKGKNYPKPTGARDEYTYHVNGTARSIKLNPT					
m730	KGNVDEGFTVYRLNWEGHEHHPADAYDGPKGKNYPKPTGARDEYTYHVNGTARSIKLNPT					
	130	140	150	160	170	180
	190	200	210	220	230	240
a730.pep	DTRSIQRISDNYSNLGSNFSRDADEANRKMFEHNAKLDRWNSMEFINGVAAGALNPFI					
m730	DTRSIQRISDNYSNLGSNFSRDADEANRKMFEHNAKLDRWNSMEFINGVAAGALNPFI					
	190	200	210	220	230	240
	250	260	270	280	290	300
a730.pep	SAGEALGIGDILYGTRYAIDKAAMRNIAPLPAEGKFAVIGGLGSGVAGFEKNTREAVDRWI					
m730	SAGEALGIGDILYGTRYAIDKAAMRNIAPLPAEGKFAVIGGLGSGVAGFEKNTREAVDRWI					
	250	260	270	280	290	300
	310	320	330	340	350	360
a730.pep	QENPNAAETVEALVNVLPFAKVKNLTAAKPGKAAVSGDFSAAYNTRTTTRKVTETEGLN					
m730	QENPNAAETVEAVFNVAATAAKVAKLAKAAGKPGKAAVSGDFADSY-----KKKLALSDSAR					
	310	320	330	340	350	
	370	380	390	400	410	420
a730.pep	RIRQNQKNSNIHEKNYGRDNPNHINVLSGNSIQHILYGDEAGGHLFPKPGKTTFPQHW					
	::	:	:	:	:	:
m730	QLYONAKYREALDIHYEDLIRRKTDGSSKFINGREIDAVTNDALIQAKRTISAIKPKNF					
	360	370	380	390	400	410

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2475>:

```

g731.seq
1  gattttcgag cgttttcatG CGAGAACGGT TTGTCTGTGC GCGTCCGCAA
51  TTTGGACGGC GGCAAAATCG CGTTGCGGCT GGACGGCAGG CGTGCCGTCC
101 TCTCTTCCGA CGTTGCCGCA TCCGGCGAAC GCTATACCGC CGAACACGGT
151 TTGTTCCGAA ACGGAACCGA GTGGCACCAG AAAGGCGGCG AAGCCTTTT
201 CGGCTTTACC GATGCCTACG GCAATTCGGT CGAAACTTCC TGCCGCGCCC
251 GTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2476; ORF 731.ng>:

```

g731.pep
1  DFRAFSCENG LSVVRNLDG GKIALRLDGR RAVLSSDVAA SGERYTAEHG
51  LFGNGTEWHQ KGGEAFFGFT DAYGNSVETS CRAR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2477>:

```

m731.seq
1  ATGAATATCA GGTTTTTCGC GCTGACCGTA CCGGTTTTGT CTTTGGCSGC
51  CTGTGCCGTG CCGGAGGCGT ATGATGACGG CGGACGCGGG CATATGCCGC
101 CCGTTCAAAA CCAAGCCGGC ACGGACGATT TTCGGGCGTT TTCCTGCGAG
151 AACGGTTTGT CTGTGCGCGT CCGCCATTG GACAGCGGCA AAGTCGCGTT
201 GCGGCTGGAC GGCAGGCGTG CCGTCCTCTC TTCCGACGTT GCCGCATCCG

```

1185

```

251 GCGAACGCTA TACCGCCGAA CACGGTTTGT TCGGAAACGC AACCGAGTGG
301 CACCAGAAAG GCGGCGAAGC CTTTTTCGGC TTTACCGATG CCTACGGCAA
351 TTCGGTCGAA ACTTCCTGCC GCGCCCGTTA A

```

This corresponds to the amino acid sequence <SEQ ID 2478; ORF 731>:

```

m731.pep
  1 MNIRFFALTV PVLSLAACAV PEAYDDGGRG HMPPVQNQAG TDDFRAFSCE
 51 NGLSVRVRHL DSGKVALRLD GRRAVLSSDV AASGERYTAE HGLFGNATEW
101 HQKGGEAFFG FTDAYGNSVE TSCRAR*

```

g731/m731 95.2% identity in 84 aa overlap

```

                                10      20      30
g731.pep                      DFRFSCENGLSVRVRNLDGGKIALRLDGR
                                |||
m731      LSLAACAVPEAYDDGGRGHMPPVQNQAGTDDFRAFSCEGLSVRVRHLDSGKVALRLDGR
              20      30      40      50      60      70

                                40      50      60      70      80
g731.pep      RAVLSSDVAASGERYTAEHGLFGNGTEWHQKGGEAFFGFTDAYGNSVETSCRARX
              |||
m731      RAVLSSDVAASGERYTAEHGLFGNATEWHQKGGEAFFGFTDAYGNSVETSCRARX
              80      90      100     110     120

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2479>:

```

a731.seq
  1 ATGAATATCA GGTTTTTCGC GCTGACCGTA CCGGTTTGT CTTGGCGGC
 51 CTGTGCCGTG CCGGAGGCGT ATGATGACGG CGGACGAGGG CATATGCCGC
101 CCGTTCAAAA CCAAGCCGGC ACGGCAGATT TTCGGGCATT TTCCTGCGAG
151 AACGGTTTGT CTGTGCACGT CCGCCGTTG GACGGCGGCA GAATCGCGTT
201 GCGGTTGGAC GGCAGGCGTG CCGTCCTCTC TTCCGACGTT GCCGCATCCG
251 GCGAACGCTA TACCGCCGAA CACGGTTTGT TCGGAAACGG AACCGAGTGG
301 CATCAGAAAG GCGGCGAAGC CTTTTTCGGC TTTACCGATG CCTACGGCAA
351 TTCGGTCGAA ACCTCCTGCC GCGCCCGCTA A

```

This corresponds to the amino acid sequence <SEQ ID 2480; ORF 731.a>:

```

a731.pep
  1 MNIRFFALTV PVLSLAACAV PEAYDDGGRG HMPPVQNQAG TADFRAFSCE
 51 NGLSVHVRRL DGGRIALRLD GRRAVLSSDV AASGERYTAE HGLFGNGTEW
101 HQKGGEAFFG FTDAYGNSVE TSCRAR*

```

a731/m731 94.4% identity in 126 aa overlap

```

                                10      20      30      40      50      60
a731.pep      MNIRFFALTVPVLSLAACAVPEAYDDGGRGHMPPVQNQAGTADFRFSCENGLSVHVRRL
              |||
m731      MNIRFFALTVPVLSLAACAVPEAYDDGGRGHMPPVQNQAGTDDFRAFSCEGLSVRVRHL
              10      20      30      40      50      60

                                70      80      90      100     110     120
a731.pep      DGGRIALRLDGRRAVLSSDVAASGERYTAEHGLFGNGTEWHQKGGEAFFGFTDAYGNSVE
              |||
m731      DSGKVALRLDGRRAVLSSDVAASGERYTAEHGLFGNATEWHQKGGEAFFGFTDAYGNSVE
              70      80      90      100     110     120

a731.pep      TSCRARX
              |||
m731      TSCRARX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2481>:

```

g732.seq
  1 ATGTCGAAAC CTGTTTTTAA GAAAATCGCA CTTTATACTT TGGGTGCAAT
 51 CAGCGGCGTG GCCGTAAAGT TGGCGGTGCA GGGTTTGCC GCCGagaagg
101 ACGGgcgGGA TAACGAagtc CTGCCGTGTC AATCCATCCG TACGATGGCG

```

```

151 GAGGTTTACG GTCAGATTAA GGCAAACCTAC TATCATGACA AACCCGATGC
201 CGATTTGTTT GAAGGTGCGA TGAAGGGTAT GGTGGCCGGT TTGGATCCGC
251 ATTCGGAATA TATGGATAAA AAAGGTTATG CCGAGATAAA GGAGTCCACC
301 AGCGGCGAAT TTGGCGGCTT GGGGATGGAA ATCGGGCAGG AAGACGETTT
351 TGTCAAAGTG GTTTCGCCGA TTGAGGACAC GCCTGCCGAA CGGCGGAGG
401 TGAAAAGCGG CGATTTTCATT GTGAAAATCG ATAATGTTTC GACGCGCGGT
451 ATGACGGTGA GCGAAGCGGT GAAAAAATG CGGGGCAAGC CGGGTACGAA
501 GATTACTTTG ACGTTGTTCG GCAAAAATG CGACAAGCCG ATAGTCGTCA
551 ACCTGACCCG TGCCATTATT AAAGTGAAAA GCGTCCGCCA TCACCTGATC
601 GAACCCGATT ACGGCTATAT CCGCGTGTCT CAGTTCCAAG AGCGGACGGT
651 CGAAAGCGTC AATACCGCCG CAAAAGAGCT GGTAAAGGAA AATAAAGGAA
701 AACCGCTCAA GGGGCTGGTG TTGGATTGCG GCGACGACCC CGGCGGGCTT
751 TTGACCGGGC CGGTCGGCGT GTCGGCGGCG TTTCTGCCGT CTGAAGCGGT
801 CGTCGTCAGC ACCAAGGGAC GCGACGGCAA AGACGGCATG GTACTGAAAG
851 CCGTTCGCCA GGATTATGTG TACGGTATGG GCGCGACCC TTTGGCGGGT
901 ATTCTGCCC AGTTGAAAAC GATTCCGATG ACGtaATTGG TcaaTTCCGG
951 TTCggcttCG GCGTCGGAGA TTGtcgCCGG CGCATTGCAG GACCACAAAC
1001 GCGCGGTCAT CGTCGGTACG CAGAGCTTCG GTAAAGGTTT GGTTCAGACT
1051 TTGATTCCCT TGTCCAACGG CAGCGCGGTC AAGTTGACGA CCGCCCTGTA
1101 TTACACGCCG AACGACCGTT CCATTTCAGC ACAGGGGATT GTTCCCGATG
1151 TCgaaGTAAA AGATAAGGAA CGTACTTTTG AAAGCCGCGA GCGCGACCTG
1201 GTCGGACACA TCGGCAATCC CTTgggcGGC GAGGATGTGA ACAGTGAAAC
1251 CcttgcCGTA CCGCTTGAAG AAGATGCGGA TAAGCCCGCT GCAAAAGAAA
1301 AAGGTAAAAA GAAAAAGGAC GAGGATTTGT CTCAAGGCG GATTCCGAAC
1351 CCTGCGAAAG ACGATCAGTT GCGTAAGGCT TTGGATTGG TCAAGTCGCC
1401 CGAGCAGTGG CAGAAGTCTT TGGGGCTGGC GGCGAAAAA CCGGTTTCAA
1451 ATAAAGATAA AAAAGATAAG AAGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2482; ORF 732>:

g732.pep

```

1 MSKPVFVKIA LYTLGAISGV AVSLAVQGF AEKDRDNEV LPVQSIRTMA
51 EVYQGIKANY YHDKPDADLF EGAMKGMVAG LDPHSEYMDK KGYAEIKEST
101 SGEEFGLGME IGQEDGFVKV VSPIEDTPAE RAEVKSDFI VKIDNVSTRG
151 MTVSEAVKKM RGKPGTKITL TLRKNADKP IVVNLTRAI KVSVRHHLI
201 EPDYGYIRVS QFQERTVESV NTAAKELVKE NKGKPLKGLV LDLRDDPGGL
251 LTGAVGVSA FLPSEAVVVS TKGRDGDGDM VLKAVPEDYV YMGGDPLAG
301 IPAELKTIEM TVLVNSGSAS ASEIVAGALQ DHKRAVIVGT QSFKGSVQT
351 LIPLSNGSAV KLTALYYTP NDRSIQAQGI VPDVEVKDKE RTFESREADL
401 VGHIGNPLGG EDVNSETLAV PLEKDAKPA AKEKGKKKK EDLSSRRIPN
451 PAKDDQLRKA LDLVKSPEQW QKSLGLAAKK PVSNKDKKDK K*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2483>:

m732.seq

```

1 ATGTCGAAAC CTGTTTTTAA GAAAATCGCA CTTTATACTT TGGGTGCAAT
51 CAGCGGCGTG GCCGTGAGTC TGGCGGTGCA GGGTTTTGCC GCCGAGAAGG
101 ACA3GCGGGA TAACGAAGTC CTGCCGGTGC AATCCATCCG CACAATGGCG
151 GAG3TTTACG GTCAAATCAA GGCAAACCTAC TATCAGGACA AACCCGATGC
201 CGATTTGTTT GAAGGTGCGA TGAAGGGTAT GGTGGCCGGT TTGGATCCGC
251 ATTCGGAATA TATGGATAAA AAAGGTTATG CCGAGATAAA GGAGTCCACC
301 AGCGGCGAAT TTGGCGGCTT GGGGATGGAA ATCGGGCAGG AAGACGGATT
351 TGTCAAAGTG GTTTCGCCGA TTGAGGACAC GCCTGCCGAA CGGCGGGGGG
401 TGAAAAGCGG CGATTTTCATT GTGAAAATCG ATAATGTTTC GACACGCGGC
451 ATGACGGTCA GCGAAGCGGT GAAGAAAATG CGGGCAAGC CGGGTACGAA
501 GATTACTTTG ACGCTGTCTG GCAAAAATGCG CGACAAGCCG ATAGTCGTCA
551 ACCTGACCCG TGCCATTATT AAAGTGAAAA GCGTCCGCCA TCACCTGATC
601 GAACCCGATT ACGGCTATAT CCGCGTGTCT CAGTTCCAAG AGCGGACGGT
651 CGAAAGCGTC AATACCGCCG CAAAAGAGCT GGTAAAGGAA AATAAAGGAA
701 AACCGCTCAA GGGGCTGGTG TTGGATTGCG GCGACGACCC CGGCGGGCTT
751 TTGACTGGCG CGGTCGGCGT GTCGGCGGCA TTTCTGCCGT CTGAAGCAGT
801 CGTCGTCAGC ACCAAGGGAC GCGACGGCAA AGACCGCATG GTACTGAAAG
851 CATTCCTGAG AGATTATGTG TACGGGATGG GCGGCGATTG GTTGGCGGGC
901 ATTCTGCCC AGTTGAAAAC CATACCGATG ACGGTATTGG TCAATTCCGG
951 TTCGGCTTCC GCGTCGGAGA TTGTCGCAGG TGCATTGCAG GATCATAAAC
1001 GCGCGGTCAT CGTCGGTACG CAGAGCTTCG GCAAAGGTTT GGTTCAGACT
1051 TTGATTCCCT TGTCCAACGG CAGCGCGGTC AAGCTGACAA CGGCACTGTA

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1187

```

1101 TTATACGCCG AACGACCGTT CTATTCAGGC GCAGGGGATT GTTCCCGATG
1151 TCGAAGTAAA AGATAAGGAA CGCATTTTTG AAAGCCGCGA GCGCGATTTC
1201 GTCGGACACA TCGGCAATCC CTTGGGCGGC GAGGATGTGA ACGGTGAAAC
1251 CCTTGCCGTG CCGCTTGAAA AAGATGCGGA TAAGCCCGCT GTAAAAGAAA
1301 AAGGTAAAAA GAAAAAGGAC GAGGATTTGT CTCAAGGCG GATTCCTAAC
1351 CCTGCCAAG ACACCAGTT GCGGAAAGCT TTGGATTAG TCAAGTCGCC
1401 CGAGCAGTGG CAGAAGTCTT TGGGGCTGGC GCGGAAAAAG CCGGTTTCAA
1451 ATAAAGATAA GAAAGATAA AAGATAAGA AGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2484; ORF 732>:

m732.pep

```

1 MSKPVFKKIA LYTLGAISGV AVSLAVOGFA AEKDRRDNEV LPVQSIRTMA
51 EVYGOIKANY YQDKPDADLF EGAMKGMVAG LDPHSEYMDK KGYAEIKEST
101 SGEFGGLGME IGQEDGFVKV VSPIDTPAE RAGVKSDFI VKIDNVSTRG
151 MTVSEAVKMM RGKPGTKITL TLRKNADKP IVVNLTRALI KVKSVRHHLI
201 EPDYGIRVS QFQERTVESV NTAAKELYKE NKGKPLKGLV LDLRDDPGGL
251 LTGAVGVSAF FLPSEAVVVS TKGRDGKDRM VLKAIPEYV YGMGGDSLAG
301 IPAEKTIPTM TVLVNNGSAS ASEIVAGALQ DHKRAVIVGT QSFSGKSVQT
351 LIPLSNGSAV KLTALYYP NDRSIQAQGI VPDVEVKDKE RIFESREADL
401 VGHIGNPLGG EDVNGETLAV PLEKADAKPA VKEKGKKKKD EDLSSRRIPN
451 PAKDDQLRKA LDLVKSPEQW QKSLGLAAKK PVSNNKDKDK KDKK*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* menA with menB

ORF 732 shows 98.2% identity over a 491 aa overlap with a predicted ORF (ORF732.a) from *N. gonorrhoeae*:

m732/g732 98.2% identity in 491 aa overlap

	10	20	30	40	50	60
m732.pep	MSKPVFKKIALYTLGAISGVAVSLAVOGFAAEKDRRDNEVLPVQSIRTMAEVYGOIKANY					
g732	MSKPVFKKIALYTLGAISGVAVSLAVOGFAAEKDRRDNEVLPVQSIRTMAEVYGOIKANY					
	10	20	30	40	50	60
m732.pep	YQDKPDADLFEGAMKGMVAGLDPHSEYMDKKGYAEIKESTSGEFGGLGMEIGQEDGFVKV					
g732	YHDKPDADLFEGAMKGMVAGLDPHSEYMDKKGYAEIKESTSGEFGGLGMEIGQEDGFVKV					
	70	80	90	100	110	120
m732.pep	YQDKPDADLFEGAMKGMVAGLDPHSEYMDKKGYAEIKESTSGEFGGLGMEIGQEDGFVKV					
g732	YHDKPDADLFEGAMKGMVAGLDPHSEYMDKKGYAEIKESTSGEFGGLGMEIGQEDGFVKV					
	70	80	90	100	110	120
m732.pep	VSPIDTPAERAGVKSDFIVKIDNVSTRGMTVSEAVKMMRGKFGTKITLTLRKNADKP					
g732	VSPIDTPAERAEVKSDFIVKIDNVSTRGMTVSEAVKMMRGKFGTKITLTLRKNADKP					
	130	140	150	160	170	180
m732.pep	VSPIDTPAERAGVKSDFIVKIDNVSTRGMTVSEAVKMMRGKFGTKITLTLRKNADKP					
g732	VSPIDTPAERAEVKSDFIVKIDNVSTRGMTVSEAVKMMRGKFGTKITLTLRKNADKP					
	130	140	150	160	170	180
m732.pep	IVVNLTRAIKVKSVRHHLIEPDYGYIRVSQFQERTVESVNTAAKELVKENKGLKGLV					
g732	IVVNLTRAIKVKSVRHHLIEPDYGYIRVSQFQERTVESVNTAAKELVKENKGLKGLV					
	190	200	210	220	230	240
m732.pep	IVVNLTRAIKVKSVRHHLIEPDYGYIRVSQFQERTVESVNTAAKELVKENKGLKGLV					
g732	IVVNLTRAIKVKSVRHHLIEPDYGYIRVSQFQERTVESVNTAAKELVKENKGLKGLV					
	190	200	210	220	230	240
m732.pep	LDLRDDPGGLLTGAVGVSAFLPSEAVVSTKGRDGKDRMVLKAIPEYVYGMGGDSLAG					
g732	LDLRDDPGGLLTGAVGVSAFLPSEAVVSTKGRDGKDRMVLKAIPEYVYGMGGDSLAG					
	250	260	270	280	290	300
m732.pep	LDLRDDPGGLLTGAVGVSAFLPSEAVVSTKGRDGKDRMVLKAIPEYVYGMGGDSLAG					
g732	LDLRDDPGGLLTGAVGVSAFLPSEAVVSTKGRDGKDRMVLKAIPEYVYGMGGDSLAG					
	250	260	270	280	290	300
m732.pep	IPAEKTIPTMTVLVNNGSASASEIVAGALQDHKRAVIVGTQSFSGKSVQTLIPLSNGSAV					
g732	IPAEKTIPTMTVLVNNGSASASEIVAGALQDHKRAVIVGTQSFSGKSVQTLIPLSNGSAV					
	310	320	330	340	350	360
m732.pep	IPAEKTIPTMTVLVNNGSASASEIVAGALQDHKRAVIVGTQSFSGKSVQTLIPLSNGSAV					
g732	IPAEKTIPTMTVLVNNGSASASEIVAGALQDHKRAVIVGTQSFSGKSVQTLIPLSNGSAV					
	310	320	330	340	350	360

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```

          370      380      390      400      410      420
m732.pep  KLTITALYYPNDRSIQAQGIVPDVEVKDKERIFESREADLVGHIGNPLGGEDVNGETLAV
          |||||
g732       KLTITALYYPNDRSIQAQGIVPDVEVKDKERTFESREADLVGHIGNPLGGEDVNSETLAV
          370      380      390      400      410      420

          430      440      450      460      470      480
m732.pep  PLEKDADKPAVKEKGKKKKDEDLSSRRIPNPAKDDQLRKALDLVKSPEQWQKSLGLAAKK
          |||||
g732       PLEKDADKPAAKEKGKKKKDEDLSSRRIPNPAKDDQLRKALDLVKSPEQWQKSLGLAAKK
          430      440      450      460      470      480

          490
m732.pep  PVSNNKDKKDKKDKKX
          |||||
g732       PVSNNKDKKDKKX
          490

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2485>:

```

a732.seq
1  ATGTCGAAAC CTGTTTTTAA GAAAATCGCA CTTTATACTT TGGGTGCAAT
51  CAGCGGCGTG GCCGTCAGTC TGGCGGTGCA GGGTTTTGCC GCCGAGAAGG
101 ACAGGCGGGA TAACGAAGTC CTGCCGTGTC AATCCATCCG CACAATGGCG
151 GAGGTTTACG GTCAAATCAA GGCAACTAC TATCAGGACA AACCCGATGC
201 CGATTTGTTT GAAGGTGCGA TGAAGGTAT GGTGGCCGCT TTGGATCCGC
251 ATTCCGAATA TATGGATAAA AAAGGTTATG CCGAGATAAA GGAGTCCACC
301 AGCGGCGAAT TTGGCGGCTT GGGATGGAA ATCGGGCAGG AAGACGGATT
351 TGTCAAAGTG GTTTCGCGA TTGAGGACAC GCCTGCGGAA CGGGCGGGGG
401 TGAAAAGCGG CGATTTCATT GTGAAAATCG ATAATGTTTC GACACGCGGC
451 ATGACGCTCA GCGAAGCGGT GAAGAAAATG CGGGGCAAGC CGGGTACGAA
501 GATTACTTTG ACGCTGTGCG GCAAAAATGC CGACAAGCCG ATAGTCGTCA
551 ACCTGACCCG TGCCATTATT AAAGTGAAAA GCGTCCGCCA TCACCTGATC
601 GAACCCGATT ACGGCTATAT CCGCGTGTCT CAGTTCCAAG AGCGGACGGT
651 CGAAAGCGTC AATACCGCCG CAAAAGAGCT GGTAAGGAA AATAAGGAA
701 AACCGCTCAA GGGGCTGGTG TTGGATTGCG GCGACGACCC CGGCGGGCTT
751 TTGACTGGCG CGGTCCGCGT GTCGGCGGCA TTTCTGCCGT CTGAAGCAGT
801 CGTCGTCAGC ACCAAGGGAC GCGACGGCAA AGACCGCATG GACTGAAAG
851 CCGTTCCTGA AGATTATGTG TACGGGATGG GCGGCGATTC GTTGGCGGGC
901 ATTCCTGCCG AGTTGAAAAC CATACCGATG ACGGTATTGG TCAATTCCGG
951 TTCGGCTTCC GCGTCGAGAG TTGTCGAGG TGCATTGCAG GATCATAAAC
1001 GCGCGGTCAT CGTCGGTACG CAGAGCTTCG GCAAAGGTTT GGTTCAGACT
1051 TTGATTCCCT TGTCCAACGG CAGCGCGGTC AAGCTGACAA CGGCACTGTA
1101 TTATACGCCG AACGACCGTT CTATTCAGGC GCAGGGGATT GTTCCCGATG
1151 TCGAAGTAAA AGATAAGGAA CGCATTTTTG AAAGCCGCGA GCGGATTGTT
1201 GTCGGACACA TCGGCAATCC TTTGGGCGGC GAGGATGTGA ACAGTGAAAC
1251 CTTTGCCGTG CCGCTTGAAA AAGATGCGGA TAAGCCCGCT GTAAAAGAAA
1301 AAGGTAAAAA GAAAAAGGAC GAGGATTGTG CTTCAAGGCG GATTCCCAAC
1351 CTGCCCCAAG ACGACCAAGT GCGGAAAGCT TTGGATTAGT TCAAGTCGCC
1401 CAGACAGTGG CAGAAGTCTT TGGGGCTGGC GGCGAAAAAG CCGGTTTCAA
1451 ATAAAGATAA GAAAGATAAA AAAGATAAGA AGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2486; ORF 732.a>:

```

a732.pep
1  MSKPVFVKIA LYTLGAISGV AVSLAVQGFA AEKDRRDNEV LPVQSIRTMA
51  EVYGOIKANY YQDKPDADLF ECAMKGMVAG LDPHSEYMDK KGYAEIKEST
101 SGEFGGLGME IGQEDGFVKV VSPIDTPAE RAGVKSDFI VKIDNVSTRG
151 MTVSEAVKMK RGKPGTKITL TFSRNADKP IVVNLTRAI KVKSVRHHLI
201 EPDYGIVRSV QFQERTVESV NTAAKELVKE NKGKPLKGLV LDLRDPGGL
251 LTGAVGVSAF FLPSEAVVVS TKGRDGKDRM VLKAVPEDYV YMGGDSLAG
301 IPAELKTIPM TVLVNNGSAS ASEIVAGALQ DHKRAVIVGT QSFKGKSVQT
351 LIPLNSGSAV KLTITALYYP NDRSIQAQGI VPDVEVKDKE RIFESREADL
401 VGHIGNPLGG EDVNSETLAV PLEKDADKPA VKEKGKKKKD EDLSSRRIPN
451 PAKDDQLRKA LDLVKSPEQW QKSLGLAAKK PVSNNKDKKDK KDKK*

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1189

a732/m732 99.6% identity in 494 aa overlap

a732.pep	MSKPVFKKIALYTLGAISGVAVSLAVQGFAAEKDRRDNEVLPVQSIRTMAEVYGOIKANY
m732	MSKPVFKKIALYTLGAISGVAVSLAVQGFAAEKDRRDNEVLPVQSIRTMAEVYGOIKANY
a732.pep	YQDKPDADLFEGAMKGMVAGLDPHSEYMDKKGYAEIKESTSGEFGGLGMEIGQEDGFVKV
m732	YQDKPDADLFEGAMKGMVAGLDPHSEYMDKKGYAEIKESTSGEFGGLGMEIGQEDGFVKV
a732.pep	VSPIEDTPAERAGVKSGDFIVKIDNVSTRGMTVSEAVKKMRGKPGTKITLTLSRKNADKP
m732	VSPIEDTPAERAGVKSGDFIVKIDNVSTRGMTVSEAVKKMRGKPGTKITLTLSRKNADKP
a732.pep	IVVNLTRAIKVKSVRHHLIEPDYGYIRVSQFQERTVESVNTAAKELVKENKGKPLKGLV
m732	IVVNLTRAIKVKSVRHHLIEPDYGYIRVSQFQERTVESVNTAAKELVKENKGKPLKGLV
a732.pep	LDLRDDPGLLTGAVGVSA AFLPSEAVVSTKGRDGKDRMVLKAVPEDYVYGMGGDSL
m732	LDLRDDPGLLTGAVGVSA AFLPSEAVVSTKGRDGKDRMVLKAI PEDYVYGMGGDSL
a732.pep	IPAEKLTIPMTVLVNSGSASASEIVAGALQDHKRAVIVGTQSFGKGSVQTLIPLSNGSAV
m732	IPAEKLTIPMTVLVNSGSASASEIVAGALQDHKRAVIVGTQSFGKGSVQTLIPLSNGSAV
a732.pep	KLTTALYYTPNDRSIQAQGIVPDVEVKDKERIFESREADLVGHIGNPLGGEDVNSETLAV
m732	KLTTALYYTPNDRSIQAQGIVPDVEVKDKERIFESREADLVGHIGNPLGGEDVNSETLAV
a732.pep	PLEKDADKPAVKEKGKKKKDEDLSSRRIPNPAKDDQLRKALDLVKSPEQWQKSLGLAAKK
m732	PLEKDADKPAVKEKGKKKKDEDLSSRRIPNPAKDDQLRKALDLVKSPEQWQKSLGLAAKK
a732.pep	PVSNKDKKDKKDKKX
m732	PVSNKDKKDKKDKKX

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2487>:

g733.seq

```

1  ATGATGAATC CGAAAACCTT GGGCCGTTTG TCGCTGTGTG CGGCGGTCTT
51 GGCTCTGACC GCCTGCGCCG GCGGCGGGCA TAAAAACCTG TATTATTACG
101 GCGGTTATCC CGATACCGTC TATGAAGGTT TGA AAAACG cGACACTTCG
151 TTGGGCAAGC AGACCGAAAA GATGGA AAAA TACTTTGCGG AAGCCGCCAA
201 CAAAAAATG AATGCCGCCG CGGGTGCGCA CGCCCATTTG GGA CTGCTGC

```

1190

251 TTTCCCGTTC GGGAGACAAA GAGGGCGCGT TCCGCCAATT TGAAGAAGAG
 301 AAAAGGCTGT TTCCCGAATC GGGCGTATTT ATGGACTTCC TGATGAAAAC
 351 CGGtaaAGGA GGCAAGCGAT GA

This corresponds to the amino acid sequence <SEQ ID 2488; ORF 733>:

g733.pep

1 MMNPKTLGRL SLCAAVLALT ACAGGGHKNL YYYGGYPDTV YEGLKNDDTS
 51 LGKQTEKMEK YFAEAANKKM NAAPGAHAHL GLLLSRSGDK EGAFRQFEEE
 101 KRLFPESGVF MDFLMKTGKG GKR*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2489>:

m733.seq

1 ATGATGAATC CGAAAACCTT GAGCCGTTTG TCGCTGTGTG CGGCGGTCTT
 51 GGCTCTGACC GCCTGCGGCG GCAACGGGCA AAAATCCCTG TATTATTACG
 101 GCGGCTATCC CGATACCGTC TATGAAGGTT TGAAAAACGA CGACACTTCG
 151 TTGGGCAAGC AGACCGAAAA GATGGAAAAA TACTTTGTGG AAGCCGGCAA
 201 CAAAAAATG AATGCCGCC CGGTGCGCA CGCCCATCTG GGAAGCTGTC
 251 TTTCCCGTTC GGGAGACAAA GAGGGCGCGT TCCGCCAGTT TGAAGAAGAG
 301 AAAAGGCTGT TTCCCGAATC GGCGTATTT ATGGACTTCC TGATGAAAAC
 351 CGGTAAAGGA GGCAAGCGAT GA

This corresponds to the amino acid sequence <SEQ ID 2490; ORF 733>:

m733.pep

1 MMNPKTL SRL SLCAAVLALT ACGGNGQKSL YYYGGYPDTV YEGLKNDDTS
 51 LGKQTEKMEK YFVEAGNKKM NAAPGAHAHL GLLLSRSGDK EGAFRQFEEE
 101 KRLFPESGVF MDFLMKTGKG GKR*

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 733 shows 94.3% identity over a 123 aa overlap with a predicted ORF (ORF733.a) from *N. gonorrhoeae*:

m733/g733

	10	20	30	40	50	60
m733.pep	MMNPKTL	SRLSLCAAVLALTACGGNGQKSL	YYYGGYPDTV	YEGLKNDDTS	LGKQTEKMEK	
g733	MMNPKTL	LGRLSLCAAVLALTACAGGGHKNL	YYYGGYPDTV	YEGLKNDDTS	LGKQTEKMEK	
	10	20	30	40	50	60
	70	80	90	100	110	120
m733.pep	YFVEAGNKKMNAAPGAHAHL	GLLLSRSGDKEGA	FRQFEEKRLFPESGVFMDFLMKTGKG			
g733	YFAEAANKKMNAAPGAHAHL	GLLLSRSGDKEGA	FRQFEEKRLFPESGVFMDFLMKTGKG			
	70	80	90	100	110	120
m733.pep	GKRX					
g733	GKRX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2491>:

a733.seq

1 ATGATGAATC CGAAAACCTT GAGCCGTTTG TCGCTGTGTG CGGCGGTCTT
 51 GGCTCTGACC GCCTGCGGCG GCAACGGGCA AAAATCCCTG TATTATTACG
 101 GCGGCTATCC CGATACCGTC TATGAAGGTT TGAAAAACGA CGACACTTCG
 151 TTGGGCAAGC AGACCGAAAA GATGGAAAAA TACTTTGTGG AAGCCGGCAA
 201 CAAAAAATG AATGCCGCC CGGTGCGCA CGCCCATCTG GGAAGCTGTC
 251 TTTCCCGTTC GGGAGACAAA GAGGGCGCGT TCCGCCAGTT TGAAGAAGAG
 301 AAAAGGCTGT TTCCCGAATC GGGCGTATTT ATGGACTTCC TGATGAAAAC
 351 CGGTAAAGGA GGCAAGCGAT GA

This corresponds to the amino acid sequence <SEQ ID 2492; ORF 733.a>:

a733.pep

1191

```

1  MMNPKTLSRL SLCAAVLALT ACGGNGQKSL YYYGGYPDTV YEGLNDDTS
51 LGKQTEKMEK YFVEAGNKKM NAAPGAHAHL GLLLSRSGDK EGAFRQFEE
101 KRLFPESGVF MDFLMKTGKG GKR*

```

a733/m733 100.0% identity in 123 aa overlap

```

              10      20      30      40      50      60
a733.pep      MMNPKTLSRLSLCAAVLALTACGGNGQKSLYYYGGYPDTVYEGLNDDTSLGKQTEKMEK
              |||||
m733          MMNPKTLSRLSLCAAVLALTACGGNGQKSLYYYGGYPDTVYEGLNDDTSLGKQTEKMEK
              10      20      30      40      50      60

              70      80      90      100     110     120
a733.pep      YFVEAGNKKMNAAPGAHAHLGLLLSRSGDKEGAFRQFEEKRLFPESGVFMDFLMKTGKG
              |||||
m733          YFVEAGNKKMNAAPGAHAHLGLLLSRSGDKEGAFRQFEEKRLFPESGVFMDFLMKTGKG
              70      80      90      100     110     120

a733.pep      GKRX
              |||
m733          GKRX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2493>:

```

g734.seq
1  ATGATGAAAA AGATACTGGC AGTATCGGCA CTATGCCTGA TGA CTGCGGC
51  GGCACAGGCT GCCGATACTT ACGGCTATCT CGCCGTTTGG CAGAATCCGC
101 AGGATGCAAA CGATGTTTGT CAGGTTAAAA CCACAAAAGA AGATTCGGCG
151 AAAAGCGAAG CGTTTGGCGA GTTGGAAGCC TTTTGCAAAG GTCAGGACAC
201 GCTTGCGGGC ATTGCCGAAG ACGAGCCGAC CGGATGCCGG TCGGTCGTGT
251 CGCTGAACAA TACCTGTGTC TCGCTGGCAT ACCCGAAAGC CTTGGGCGCG
301 ATGCGCGTTG AAAACGCCCT CGTGATTACT TCTCCGCGTT TTACGAGCGT
351 TCATCAGGTC GCACTCAACC AGTGCAATAA AAAATACGGC GCACAGGGAC
401 AATGCGGCTT GGAACAGTGT TATTGCACGT CATCTTCTTA TTACGGCGGG
451 GCTGTTTCGT CCTTAATCCA ACACCTGAAA TAA

```

This corresponds to the amino acid sequence <SEQ ID 2494; ORF 734.ng>:

```

g734.pep
1  MMKKILAVSA LCLMTAAQA ADTYGYLAVW QNPQDANDVL QVKTTKEDSA
51  KSEAFAELEA FCKGQDTLAG IAEDEPTGCR SVVSLNNTCV SLAYPKALGA
101 MRVENAVVIT SPRFTSVHGV ALNQCIKKYG AQGQCGLQTV YCTSSSYGG
151 AVRSLIQHLK *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2495>:

```

m734.seq (partial)
1  TCGGGCATTG CTGAAGACGA GCCGACCGGA TGCCGGTCGG TCGTGTGCGT
51  GAACAATACC TGTGTCGCGC TGGCATACCC GAAAGCCTTG GGCGCGCTGC
101 GTGTCGACAA CGCCGTCGTG ATTACTTCTC CGCGTTTAC GAGCGTTCAT
151 CAGGTCGCAC TCAACCACTG CATCAAAAAA TACGGCGTAC AGGGACAATG
201 CGGCTTGGAA ACAGTGTATT GCACATCTTC TTCTTATTAC GGCGGAACTG
251 TGCGCTCTTT GATTCAAAAT CTCAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2496; ORF 734>:

```

m734.pep (partial)
1  SGIAEDEPTG CRSVSVLNNT CVALAYPKAL GALRVONAVV ITS PRFTSVH
51  QVALNQCIKK YGVQGQGLE TVYCTSSSY GGTVRSLIQN LK*

```

m734/g734 92.4% identity in 92 aa overlap

```

              10      20      30
m734.pep      SGIAEDEPTGCRSVSVLNNTCVALAYPKAL
              :|||
g734          VLQVKTTKEDSAKSEAFAELEAFCKGQDTLAGIAEDEPTGCRSVSVLNNTCVSLAYPKAL

```


40 50 60 70 80 90
 40 50 60 70 80 90
 m734.pep GALRVDNAVVITS~~PRFTSVHC~~VALNQCICKYGVQGCGLET~~VYCTSSSY~~GGTVRSLIQN
 ||::||:|||||~~|||||~~|||||~~|||||~~:|||||~~|||||~~|||||~~|||||~~:|||||~~|||||~~
 g'734 GAMRVENAVVITS~~PRFTSVHC~~VALNQCICKYGAQGCGLT~~VYCTSSSY~~GGAVRSLIQH
 100 110 120 130 140 150

 m734.pep LKX
 |||
 g734 LKX
 160

```
a734.seq
1  ATGATGAAAA AGATACTGGC CGTATCGGCA CTATGCCTGA TGA CTGCGGC
51  GGCACGGGCT GCCGATACTT ACGGCTATCT CGCGGTTTGG CAGAATCCGC
101 AGAATGCAAA CGATGTTTTG CAGGTATAAA CCACAAAAGA AGATTCTGACG
151 AAAAGCGAAG CGTTTGCCGA GTTGGAAAGT TCTTGCAAAAG GTCAGGACAC
201 GCTTGCGGGC ATTGCCGAAG ACGAGCCGAC CTGATGCCGG TCGGTCTGTG
251 CGCTGAACAA TACCTGTGTC GCGCTGGCAT ACCCGAAAGC CTTGGGCGCG
301 ATGCGCGTTG AAAACGCCGT TGTGATTACT TCCTCGCGTT TTACGAGCGT
351 TTATCAGGTC GCATCAACC AGTGCACTCA AAAATACG3C GCACAGGGAC
401 AATGCGGCTT GAAACACAGT TATTGCACGT CTTCTTCTTA TTACGGGGGA
451 ACTGTGCGCT CTTTGATTCA AATTCTCAA TAA
```

a734.pep

1	<u>MMKKILAVSA</u>	<u>LCLMTAAARA</u>	ADTYGYLAVW	QNPQNANDVL	QVKTTKEDST
51	KSEAFAELEA	FCKGQDTLAG	IAEDEPTGCR	SVVSLNNTCV	ALAYPKALGA
101	MVRNAVVT	SPRFTSVYQV	ALNQCIKKYG	AQGQCGLETV	YCTSSSYGG
151	TVRSLIQNLK	*			

	10	20	30	40	50	60
a734.pep	MMKKILAVSALCLMTAAARAADTYGYLAVWQNPQNANDVLQVKTTKEDSTKSEAFAELEA					
g734	MMKKILAVSALCLMTAAQAADTYGYLAVWQNPQDANDVLQVKTTKEDSAKSEAFAELEA					
	10	20	30	40	50	60
	70	80	90	100	110	120
a734.pep	FCKGQDTLAGIAEDEPTGCRSVVSLNNTCVALAYPKALGAMRVENAVVITSPRFTSVYQV					
g734	FCKGQDTLAGIAEDEPTGCRSVVSLNNTCVSLAYPKALGAMRVENAVVITSPRFTSVHQV					
	70	80	90	100	110	120
	130	140	150	160		
a734.pep	ALNQCIKKYGAQGCGLETVYCTSSSYGGTVRSLIQNLKX					
g734	ALNQCIKKYGAQGCGLETVYCTSSSYGGAVRSLIQHLKX					
	130	140	150	160		

```
m735.seq
1 ATGAATCTCG TGAAACTGCT GGCGAATAAC TGGAACCGA TGCCATTAT
51 CGCGCTTGTC GGCACGGGCT TGGCTGTGTC GCACCATCAA GGCTACAAGT
101 CGGCATTTCG GAAGCAGCAG CGCGTCATGC ACAAGATTGA GCGCAGCAAG
151 GCGCAAGCCC TGCTGTTGTC GGCTCAAAAC TATGCGCGCG AACTGGAACT
201 GGCACGCGCG GAAGCTAAAA AATATTAGCT CAAGCGCGAC GCTGTCGGCA
251 TGGCTTTGGC GAAAAAACAG CCGGAAGTCA GCCCTCTGAA AACGAAAAAT
301 AAAAAGGAAA TCGAAAAATGT CCTTACTCAA ACCGTAAAA ATGCAAGCGG
```

1193

351 CGGTTGCATT GACGGCTTTG GCTCTCACGG CCTGCAGCTC TACAACCGCG
401 CCCTCGGCTA CGGAAATTAA

This corresponds to the amino acid sequence <SEQ ID 2500; ORF 735>:

m735.pep
1 MNLVKLLANN WQPIAIIALV GTGLAVSHHQ GYKSAFAKQO AVIDKMERDK
51 AQALLLSAQN YARELELARA EAKKYEYKAH AVGMALAKKQ AEVSRLKTEN
101 KKEIENVLTQ DRKNASGGCI DFGSHGLQL YNRALGYGN*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2501>:

a735.seq
1 ATGAATCTCG TGAAGCTGCT GGCGAATAAC TGGCAACCGA TTGCCATCAT
51 CGCGCTTGTC GGCACGGGTT TGCGGTGTC GCACCATCAA GGCTACAAGT
101 CGGCTTTTGC GAAGCAGCAG GCGGTCATTG AGAAAATGAA GCGCGACAAG
151 GCGCAAGCCC TGCTGTTGTC GGCTCAAAAC TACGCCCGCG AACTGGAACA
201 GGCGCGTGCG GAAGCTAAAA AATATGAAGT CAAGGCGCAC GCCGTCGGCA
251 TGGCTTTGGC GAAAAACAG GCGGAAGTCA GCCGTCTGAA AACGGAAT
301 AAAAAGGAAA TCGAAATGT CCTTACTCAA GACCGTAAAA ATGCAGGCGG
351 CGGTTGTATT GACGGCTTTG GCCATCACGG CTTGCAGCTC TACAAGCGCG
401 CCCTCGGCTA CGGAAATTAA

This corresponds to the amino acid sequence <SEQ ID 2502; ORF 735.a>:

a735.pep
1 MNLVKLLANN WQPIAIIALV GTGLAVSHHQ GYKSAFAKQO AVIEKMKRDK
51 AQALLLSAQN YARELEQARA EAKKYEYKAH AVGMALAKKQ AEVSRLKTEN
101 KKEIENVLTQ DRKNAGGGCI DFGHHGLQL YKRALGYGN*

a735/m735 95.7% identity in 139 aa overlap

	10	20	30	40	50	60
a735.pep	MNLVKLLANNWQPIAIIALVGTGLAVSHHQGYKSAFAKQOAVIEKMKRDKAQALLLSAQN					
m735	MNLVKLLANNWQPIAIIALVGTGLAVSHHQGYKSAFAKQOAVIDKMERDKAQALLLSAQN					
	10	20	30	40	50	60
	70	80	90	100	110	120
a735.pep	YARELEQARAEAKKYEYKAHAVGMALAKKQAEVSRLKTENKKEIENVLTQDRKNAGGGCI					
m735	YARELELARA EAKKYEYKAHAVGMALAKKQAEVSRLKTENKKEIENVLTQDRKNASGGCI					
	70	80	90	100	110	120
	130	140				
a735.pep	DGFGHHGLQLYKRALGYGNX					
m735	DGFGSHGLQLYNRALGYGNX					
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2503>:

g736.seq
1 ATGAATTTTA TCCGTTCCGT CGGGGCGAAA ACCCTCGGCC TTATTCAATC
51 CTTCCGCACT ATCAGCTGT TTCTGCTGAA CATTTTGCG AAATCCGGCA
101 CGGCTTTTCG CCGTCCGCGC CTGAGCGTGC GCCAAGTGTA TTTTGCCGGC
151 GTGCTGTCGG TGCTGATTGT TGCCGTTTCG GGGCTGTTG TCGGTATGGT
201 TTTGGGTTTG CAGGGCTATA CGCAGTTGTC GAAATTCAAA TCCGCCGATA
251 TTTTGGGCTA TATGGTCGCG GCTTCTCTGT TCGCGAACT GGGTCCCGTG
301 TTGGCGGCGA TTCTGTTTGC CAGCAGCGCG GCGGTTGCGA TGACCAGCGA
351 AATCGGTTTG ATGAAAACGA CCGACAGCT CGAAGCGATG AACGTGATGG
401 CGGTCAACCC CGTCGCCCCG GTGGTTGCCC CGCGTTTTCG GCGGGGCGTG
451 TTTTCTATGC CGCTTTTGGC TTCGATTTTC AACGTCGCGG GCATTTTCGG
501 CGCGTATTTG GTCGGCGTGA GCTGGCTGGG TTTGGACAGC GGTATTTTCT
551 GGCCGCAGAT GCAGACAAC ATTACGATAC ATTACGATGT AATCAACGGT

1194

601 TTGATCAAAAT CCGCCGCGTT CGGCGTGCGG GTAACGCTGA TIGCCGTGCA
 651 TCAGGCTTC CACTGCATCC CGACTTCGGA AGGCATTTTG CCGCCAGCA
 701 CGCGCACGGT GGTTCGTCC GCCCTGACGA TTTTGCGGT CGATTTTATA
 751 TTGACCGCGT GGATGTTTAC AGATTGA

This corresponds to the amino acid sequence <SEQ ID 2504; ORF 736>:

g736.pep

1 MNFIRSVGAK TLGLIQSEGS ITLFLLNILA KSGTAFARPR LSVRQVYFAG
 51 VLSVLIVAVS GLFVGMVLGL QGYTQLSKFK SADILGYMVA ASLLRELGPV
 101 LAAILFASSA GGAMTSEIGL MKTTGQLEAM NVMVNPVAR VVAPRFWAGV
 151 FSMPLLASIF NVAGIFGAYL VGVSWLGLDS GIFWPQMNN ITIHYDVIING
 201 LIKSAAFGVA VTLIAVHQGF HCIPTSEGIL RASTRTVVSS ALTILAVDFI
 251 LTAWMFTD*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2505>:

m736.seq

1 ATGAATTTTA TCCGTTCGGT CGGGGCGAAA ACCCTCGGCC TTATTCAATC
 51 CTTCGGCAGT ATCACGCTGT TTCTGCTGAA CATTGTGGCG AAATCCGGCA
 101 CGGCTTTTCG CCGTCCGCGC CTGAGCGTGC GCCAAGTGTA TTTTGCCGGC
 151 GTGCTGTCGG TGCTGATTGT TGCCGTTTCG GGGCTGTTCC TCGGTATGGT
 201 TTTGGGTTTG CAGGCTATA CGCAGTTGTC GAAATTCAA TCCGCCGATA
 251 TTTTGGGCTA TATGGTCGCG GCTTCTCTGT TGCGCGAACT GGGTCCCGTG
 301 TTGGCGGCGA TTCTGTTTGC CAGCAGCGCG GCGGTGCGA TGACCAGCGA
 351 AATCGGTTTG ATGAAAACGA CCGACAGCT CGAAGCGATG AACGTGATGG
 401 CGGTCAACCC CGTCGCCCGC GTGGTTGCC CGCGTTTTG GCGGGCGTG
 451 TTTTCTATGC CGCTTTTGGC TTCGATTTT AACGTCGCG GCATTTTCGG
 501 CGCGTATTTG GTCGCGGTGA GCTGGCTGGG TTTGACAGC GGIATTTTCT
 551 GGCCGAGAT GCAGAACAA ATTACGATAC ATTACGATGT AATCAACGGT
 601 TTGATCAAAAT CCGCCGCGTT CGGCGTGCG GTAACGCTGA TTGCCGTGCA
 651 TCAGGCTTC CACTGCATCC CGACTTCGGA AGGCATTTTG CCGCCAGCA
 701 CGCGCACGGT GGTTCGTCC GCCCTGACGA TTTTGCGGT CGATTTTATA
 751 TTGACCGCGT GGATGTTTAC AGATTGA

This corresponds to the amino acid sequence <SEQ ID 2506; ORF 736>:

m736.pep

1 MNFIRSVGAK TLGLIQSLGS ITLFLLNILA KSGTAFVRPR LSVRQVYFAG
 51 VLSVLIVAVS GLFVGMVLGL QGYTQLSKFK SADILGYMVA ASLLRELGPV
 101 LAAILFASSA GGAMTSEIGL MKTTEQLEAM NVMVNPVAR VVAPRFWAGV
 151 FSMPLLASIF NVAGIFGAYL VGVTWLGLDS GIFWSQMNN ITIHYDVIING
 201 LIKSAAFGVA VTLIAVHQGF HCVPTSEGIL RASTRTVVSS ALTILAVDFI
 251 LTAWMFTD*

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 736 shows 97.7% identity over a 258 aa overlap with a predicted ORF (ORF736.ng) from *N. gonorrhoeae*:

m736/g736

	10	20	30	40	50	60
m736.pep	MNFIRSVGAKTLGLIQSLGSITLFLNLA KSGTAFVRPRLSVRQVYFAGVLSVLIVAVS					
g736	MNFIRSVGAKTLGLIQSEGSITLFLNLA KSGTAFARPRLSVRQVYFAGVLSVLIVAVS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m736.pep	GLFVGMVLGLQGYTQLSKFKSADILGYMVAASLLRELGPVLAAILFASSAGGAMTSEIGL					
g736	GLFVGMVLGLQGYTQLSKFKSADILGYMVAASLLRELGPVLAAILFASSAGGAMTSEIGL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m736.pep	MKTTEQLEAMNVMVNPVARVVAPRFWAGVFSMPLLASIFNVAGIFGAYLVGVSWLGLDS					
g736	MKTTGQLEAMNVMVNPVARVVAPRFWAGVFSMPLLASIFNVAGIFGAYLVGVSWLGLDS					

1195

	130	140	150	160	170	180
	190	200	210	220	230	240
m736.pep	GIFWSQMNNITIHVDVINGLIKSAAFGVAVTLIAVHQGFHCVPTSEGILRASTRTVVSS					
g736	GIFWPQMNNITIHVDVINGLIKSAAFGVAVTLIAVHQGFHCVPTSEGILRASTRTVVSS					
	190 200 210 220 230 240					
	250	259				
m736.pep	ALTILAVDFILTAWMFTDX					
g736	ALTILAVDFILTAWMFTDX					
	250					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2507>:

```

a736.seq
1  ATGAATTTTA TCCGTTCCGT CGGGGCGAAA ACCCTCGGCC TTATTCAATC
51  TCPCGGCAGT ATCAGCGCTGT TTCTGCTGAA TATCTGGCG AAATCCGGTA
101 CGGCTTTCGT CCGTCCGCGC CTGAGCGTGC GCCAAGTGTA TTTTGCCGGC
151 GTGCTGTCGG TGTGATTGT TCCCGTTTCA GGGCTGTTG TCGGCATGGT
201 CTTGGGTTTG CAGGGCTATA CGCAGTTGTC GAAATTCAA TC CGCCGATA
251 TTTTGGGCTA TATGGTCGCG GCTTCGCTGT TCGCGAACT GGGTCCGGTG
301 TTGGCGGCGA TTCTGTTTGC CAGCAGCGCG GCGGGTGCGA TGACCAGCGA
351 AATCGGTTTG ATGAAAACGA CCGAACAGCT CGAAGCGATG AACGTGATGG
401 CGGTAAACCC CGTCGCCCGA GTGGTTGCGC CGCGCTTTTG GCGGGCGTG
451 TTTTCCATGC CGCTTTTGGC TTCGATTTC AACGTGGCGG GTATTTTCGG
501 CGCGTATTG GTCGGTGTAA CCTGGCTGGG CTTGGACAGC GGTATTTTCT
551 GGTGCGAAAT GCAGAACAA ATCAGGATAC ATTACGATG AATCAACGGT
601 CTGATCAAA CCGCCCGGT CGGCGTGGCG GTAACGCTGA TTGCCGTGCA
651 TCAGGGCTTC CACTGCGTCC CGACCTCGGA AGGCATTTG CGGCCAGCA
701 CGCGCACGGT GGTTCGTCC GCCCTGACGA TTTGGCGGT CGATTTTATA
751 TTGACCGCGT GGATGTTTAC AGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 2508; ORF 736.a>:

```

a736.pep
1  MNFIRSVGAK TLGLIQSLGS ITLFLNILA KSGTAFVRPR LSVRQVYFAG
51  VLSVLIVAVS GLFVGMVLGL QGYTQLSKFK SADILGYMVA ASLLRELGPV
101 LAAILPASSA GGAMTSEIGL MKTTEQLEAM NMAVNPVAR VVAPRFWAGV
151 FSPMLLASIF NVAGIFGAYL VGVTLGLDS GIFWSQMNN ITIHVDVING
201 LIKSAAFGVA VTLIAVHQGF HCVPTSEGIL RASTRTVVSS ALTILAVDFI
251 LTAWMFTD*

```

a736/m736 100.0% identity in 258 aa overlap

	10	20	30	40	50	60
a736.pep	MNFIRSVGAKTLGLIQSLGSITLFLNILAKSGTAFVRPRLSVRQVYFAGVLSVLIVAVS					
m736	MNFIRSVGAKTLGLIQSLGSITLFLNILAKSGTAFVRPRLSVRQVYFAGVLSVLIVAVS					
	10	20	30	40	50	60
	70	80	90	100	110	120
a736.pep	GLFVGMVLGLQGYTQLSKFKSADILGYMVAASLLRELGPVLAAILFASSAGGAMTSEIGL					
m736	GLFVGMVLGLQGYTQLSKFKSADILGYMVAASLLRELGPVLAAILFASSAGGAMTSEIGL					
	70	80	90	100	110	120
	130	140	150	160	170	180
a736.pep	MKTTEQLEAMNMAVNPVARVVAPRFWAGVFSMPMLLASIFNVAGIFGAYLVGVTLGLDS					
m736	MKTTEQLEAMNMAVNPVARVVAPRFWAGVFSMPMLLASIFNVAGIFGAYLVGVTLGLDS					
	130	140	150	160	170	180
	190	200	210	220	230	240
a736.pep	GIFWSQMNNITIHVDVINGLIKSAAFGVAVTLIAVHQGFHCVPTSEGILRASTRTVVSS					

1196

```

m736      GIFWSQMNNITIHVDVINGLIKSAAFGVAVTLIAVHQGFHCVPTSEGILRASTRTVVSS
           190      200      210      220      230      240

           250      259
a736.pep   ALTILAVDFILTAWMFTDX
           |||||
m736      ALTILAVDFILTAWMFTDX
           250

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2509>:

g737.seq

```

1  atgaACATCA AACACCTTCT CTTGACCGCC GCCGCAACCG CACTGTTGGG
51 CATTTCCGCC CCCGCACTCG CCCACCACGA CGGACACGGC GATGACGACC
101 ACGGACACGC CGCACACCAA CACGGCAAAC AAGACAAAT CATCAGCCGC
151 GCCCAAGCCG AAAAAGCGGC TTGGCGCGT GTCGGCGGCA AAATCACCGA
201 CATCGATCTC GAACACGACG ACGGCCGTCC GCACTATGAT GTCGAAATCG
251 TCAAAAACGG ACAGGAATAC AAAGTCGTTG TCGATGCCCC TACCGGCCGC
301 GTGATTTCTT CCCGCCGCGA CGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2510; ORF 737>:

g737.pep

```

1  MNIKHLLLTA AATALLGISA PALAHDGHHG DDDHGHAHQ HGKQDKIISR
51 AQAEKAARAR VGGKITDIDL EHDGRPHYD VEIVKNGQY KVVVDARTGR
101 VISSRRDD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2511>:

m737.seq.

```

1  ATGAACATCA AACACCTTCT CTTGACCTCC GCCGCAACCG CACTGCTGAG
51 CATTTCCGCC CCCGCGCTCG CCCACCACGA CGGACACGGC GATGACGACC
101 ACGGACACGC CGCACACCAA CACAACAAAC AAGACAAAT CATCAGCCGC
151 GCCCAAGCCG AAAAAGCAGC GTTGGCGCGT GTCGGCGGCA AAATCACCGA
201 CATCGATCTC GAACACGACA ACGGCCGTCC GCACTATGAT GTCGAAATCG
251 TCAAAAACGG ACAGGAATAC AAAGTCGTTG TCGATGCCCC TACCGGCCGC
301 GTGATTTCTT CCCGCCGCGA CGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2512; ORF 737>:

m737.pep

```

1  MNIKHLLLTS AATALLSISA PALAHDGHHG DDDHGHAHQ HNKQDKIISR
51 AQAEKAALAR VGGKITDIDL EHDNGRPHYD VEIVKNGQY KVVVDARTGR
101 VISSRRDD*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* menA with menB

ORF 737 shows 95.4% identity over a 108 aa overlap with a predicted ORF (ORF737.a) from *N. gonorrhoeae*:

m737/g737

```

           10      20      30      40      50      60
m737.pep   MNIKHLLLTS AATALLSISA PALAHDGHHG DDDHGHAHQ HNKQDKIISR AQAEKAALAR
           |||||:|||||:|||||:|||||:|||||:|||||
g737       MNIKHLLLTA AATALLGISA PALAHDGHHG DDDHGHAHQ HGKQDKIISR AQAEKAARAR
           10      20      30      40      50      60

           70      80      90      100     109
m737.pep   VGGKITDIDLEHDNGRPHYDVEIVKNGQYKVVVDARTGRVISSRRDDX
           |||||:|||||:|||||:|||||:|||||:|||||
g737       VGGKITDIDLEHDDGRPHYDVEIVKNGQYKVVVDARTGRVISSRRDDX
           70      80      90      100

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2513>:

1197

a737.seq

```

1  ATGAACTTCA AACGCCTTCT CTTGACCGCC GCCGCAACCG CACTGATGGG
51  CATTTCCGCC CCCGCACTCG CCCACCACGA CGGACACGGC GATGACGACC
101 ACGGACACGC CGCACACCAA CACAGCAAAC AAGACAAAT CATCAGCCGC
151 GCCCAAGCCG AAAAAGCAGC GTTGGCGCGT GTCGGCGGCA AAATCACCGA
201 CATCGATCTC GAACACGACA ACGGCCGTCC GCACTATGAT GTCGAAATCG
251 TCAAAAACGG ACAGGAATAC AAAGTCGTTG TCGATGCCCG TACCGGCCCG
301 GTGATTTCCT CCCGCCGCGA CGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2514; ORF 737.a>:

a737.pep

```

1  MNFKRLLLLTA AATALMGISA PALAHHDHGHG DDDHGHAHQ HSKQDKIISR
51  AQAEEKAALAR VGGKITDIDL EHDNGRPHYD VEIVKNGQEY KVVVDARTGR
101 VISSRRDD*

```

a737/m737 94.4% identity in 108 aa overlap

	10	20	30	40	50	60
a737.pep	MNFKRLLLLTA	AATALMGISA	PALAHHDHGHG	DDDHGHAHQ	HSKQDKIISR	AQAEEKAALAR
	: :	:	:	:	:	:
m737	MNIKHLTLLTA	SAATALLSIS	PALAHHDHGHG	DDDHGHAHQ	QHNKQDKIISR	AQAEEKAALAR
	10	20	30	40	50	60

	70	80	90	100	109
a737.pep	VGGKITDIDLE	HDNGRPHYD	VEIVKNGQEY	KVVVDARTGR	VISSRRDDX
	:	:	:	:	:
m737	VGGKITDIDLE	HDNGRPHYD	VEIVKNGQEY	KVVVDARTGR	VISSRRDDX
	70	80	90	100	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2515>:

g738.seq

```

1  ATGTCCGCTG AAACGACCGT ATCCGGCGCG CGCCCCGCGG CCAAACGCGC
51  GATTACATC CTGCCCTGCT TCCTTTGGAT AGGCATCATC CCCTTTACCT
101 TCGCACTCAG GCTGAAACCG TCGCCCGACT TTTACCACGA TGCCGCGCGC
151 GCGGCGCGCC TGATTGTCTT GTTGTTCCTC ACGGCAGGAA AAAAGCTGTT
201 TGATGTCAAA ATCCCCGCCA TCAGCTTCCT CCTGTTTGCA ATGGCGGCAT
251 TTTGGTGCTC TCAGGCACGC CTGATGAACC TGATTTATCC CGGAATGAAC
301 GACATCGCCT CTTGGGTTTT CATCTTGCTC GCCGTACGCG CGTGGGCTTG
351 CAAGAGTTTG GTCGCACACT ACGGACAAGA ACGCATcgtT ACCCTGTTTG
401 CCTGGTCGCT GCTTATCGGC TCCCTGCTTC AATCCTGCAT CGTcgtCATC
451 CAGTTTGCCG GCTGGGAAAA CACCCCTCTG CTTCAAAACA TCATCGTTCA
501 CAGAGGGCAA GCGTAATCG GACACATCGG GCAGCGCAAC AACCTCGGAC
551 ACTACCTCAT GTGGGCGATA CTGGCTCCG CCTACCTCAA CGGACAACGA
601 AAAATCCCGC CAGCCCTCGG CGCAATCTGC CTGATTATGC AGACCGCGT
651 TTTAGGTTTG GTCAATTCGC GCACCATCTT GACCTACATA GCCGCCATCG
701 CCCTCATCCT TCCCTTCTGG TATTTCCGTT CGGACAAATC CAACAGACGG
751 ACGATGCTCG GCATAGCCCG AGCCGTATTC CTTACCGCGC TGTTCCAATT
801 TTCCATGAAC GCCATTCTGG AAACCTTTAC AGGCATCCGC TACGAACTG
851 CCGTCGAACG CGTCGCCAAC GGCGGTTTCA CAGACTTGCC GCGCCAAAGC
901 GAATGGAATA AAGCCCTTGC CGCCTTCCAG TCCGCCCGGA TATTCGGGCA
951 CGGCTGGAAC AGTTTGGCCC AACAAACCTT CCTGATCAAT GCCGAACAGC
1001 ACACCATACA CGACAACTTC CTCAGCACCT TGTTCACCCA TCCCAACAA
1051 ATCATCTCTC AACTCCTTGC AGAAATGGGG ATCAGCGGCA CGCTTCTGGT
1101 TGCGGCAACC CTGCTGACGG GCATTGCCGG GCTGCTGAAA CGCTCCCTGA
1151 CCCCCGCATC ACTTTTCCTG CTGTGCGCGC TTGCCGTCAG TATGTGCCAC
1201 AGTATGCTCG AATATCCTTT GTGGTATGTC TATTTCTCTA TCCCTTCCGG
1251 ACTGATGCTC TTTCTGTCCC CCGCAGAGGC TTCAGACGGC ATCGCCTTCA
1301 AAAAAGCCGC CAATCTCGGC ATACTGACCG CCTCCGCGGC CATATTCGCA
1351 GGATTGTGTC ACTTGGACTG GACATACACC CGGCTGGTTA ACTCCTTTTC
1401 CCCCAGCGCT GACGACAGTG CCAAAACCTT CAACCGGAAA ATCAACGAAC
1451 TCGCTATAT TTCCGCAAAC AGCCCGATGC TGTCTTTTTA TGCCGACTTC
1501 TCCCTCGTAA ACTTCGCCCT GCCGGAATAC CCCGAAACCC AGACTTGGGC
1551 GGAAGAAGCA ACCCTCAAAG CACTAAATA CCGCCCTTAC TCCGCCACCT

```

```

1601 ACCGCATCGC CCTCTACTTG ATGCGGCAAG GCAAAGTTGC AGAAGCAAAA
1651 CAATGGATGC GGGCAACACA GTCCTATTAC CCCTACCTGA TGCCCCGATA
1701 CGCCGACGAA ATCCGCAAAC TGCCCGTATG GGCACCGCTG CTGCCCGAAC
1751 TGCTCAAAGA CTGCAAAGCC TTCGCCGCCG CTCCCGGCCA TCCGGAACA
1801 AAACCTGCA AATGA

```

This corresponds to the amino acid sequence <SEQ ID 2516; ORF 738>:

g738.pep

```

1  MSAETTVSGA RPAAKLPYYI LPCFLWIGII PFTFALRLKP SPDFYHDAAA
51  AAGLIVLLFL TAGKKLFDVK IPAISFLLFA MAAFWWLOAR LMNLIYPGMN
101 DIASWFVILL AVSAWACKSL VAHYGQERIV TLFWSLLIG SLLQSCIVVI
151 QFAGWENTPL LQNIIVHRGQ GVIGHIGQRN NLGHYLMWGI LASAYLNGQR
201 KIPAAALGAIC LIMQTAVLGL VNSRTILTYI AAIALILPFW YFRSDKSNRR
251 TMLGIAAAVF LTALFQFSMN AILEFTTGIR YETAVERVAN GGFTDLPRQS
301 EWNKALAAFO SAPIFGHGW N SFAQQTFLIN AEQHTIHDNF LSLFTHSHN
351 IILQLLAEMG ISGTLVAAT LLTGIAGLLK RSLTPASLFL LCALAVSMCH
401 SMLEYPLWYV YFLIPFGLML FLSPAASDG IAFKKAANLG ILTASAAIFA
451 GLHLHDWYTY RLVSNSFSPA DDSAKTLNRK INELRYISAN SPMLSFYADF
501 SLVNFALPEY PETQTWAEAA TLKALKYRPY SATYRIALYL MRQKVAEAK
551 QWMRATQSYV PYLMPRYADE IRKLPVWAPL LPELLKDCKA FAAAPGHPET
601 KPCK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2517>:

m738.seq

```

1  ATGCCCGCTG AAACGACCGT ATCCGGCGCG CACCCCGCCG CCAAACCTGCC
51  GATTTACATC CTGCCCTGCT TCCTTTGGAT AGGCATCGTC CCCTTTACCT
101 TCGCGCTCAA ACTGAAACCG TCGCCCGACT TTACCACGA TGCCGCGGCC
151 GCAGCCGGCC TGATTGTCTT GTTGTCTCTC ACGGCAGGAA AAAAAGTGT
201 TGATGTCAAA ATCCCGGCCA TCAGCTTCCT TCTGTTTGCA ATGGCGGCGT
251 TTTGGTATCT TCAGGCACGC CTGATGAACC TGATTTACCC CGGTATGAAC
301 GACATCGTCT CTTGGATTIT CATCTTGCTC GCCGTACGC CGTGGGCTG
351 CCGGAGCTTG GTCGCACACT TCGGACAAGA ACGCATCGTG ACCCTGTTTG
401 CCTGTCGCTG GCTTATCGGC TCCCTGCTTC AATCCTGCAT CGTCGTCATC
451 CAGTTTGCCG GCTGGGAAGA CACCCCTCTG TTTCAAACA TCATCGTTTA
501 CAGCGGGCAA GGCCTAATCG GACACATCGG GCAGCGCAAC AACCTCGGAC
551 ATACCTCAT GTGGGGCATA CTCGCCGCGC CCTACCTCAA CGGACAACGA
601 AAAATCCCGC CCGCCCTCGG CGTAATCTGC CTGATTATGC AGACCGCCGT
651 TTTAGGTTTG GTCAACTCGC GCACCATCTT GACCTACATA GCCGCCATCG
701 CCCTCATCCT TCCCTTCTGG TATTTCGGT CGGACAAATC CAACAGGCGG
751 ACGATGCTCG GCATAGCCGC AGCCGTATTC CTACCGCGC TGTTCGAAT
801 TTCCATGCA ACCATTCTGG AAACCTTTAC TGGCATCCGC TACGAAACTG
851 CCGTCGAACG CGTCGCCAAC GCGGTTTCA CAGACTTGCC GCGCCAAATC
901 GAATGGAATA AAGCCCTTGC CGCCTCCAG TCCGCCCGCA TATTCGGGCA
951 CGGCTGGAAC AGTTTGGCCC AACAAACCTT CCTCATCAAT GCCGAACAGC
1001 ACAACATATA CGACAACCTC CTCAGCAACT TGTTCACCCA TTCCACAAC
1051 ATCGTCTCTC AACTCCTTGC AGAGATGGGA ATCAGCGGCA CGCTTCTGGT
1101 TGCCGCAACC CTGTGACGG GCATTGCCGG GCTGCTTAAA CGCCCCCTGA
1151 CCCCCGCATC GCTTTTCTTA ATCTGCACGC TTGCCGTGAG TATGTGCCAC
1201 AGTATGCTCG AATATCCTTT GTGGTATGTC TATTTCTCA TCCCTTTCTG
1251 ACTGATGCTC TTCCTGTCCC CCGCAGAGGC TTCAGACGGC ATCGCCTTCA
1301 AAAAAGCCGC CAATCTCGGC ATACTGACCG CCTCCGCCGC CATATTGCGA
1351 GGATTGCTGC ACTTGGACTG GACATACACC CGGCTGGTTA ACGCCTTTTC
1401 CCCGCGCACT GACGACAGT CCAAAACCTT CAACCGGAAA ATCAACGAGT
1451 TGCGCTATAT TTCCGCAAAC AGTCCGATGC TGTCTTTTA TGCCGACTTC
1501 TCCCTCGTAA ACTTCGCCCT GCCGGAATAC CCCGAAACCC AGACTTGGGC
1551 GGAAGAAGCA ACCCTCAAAT CACTAAAATA CCGCCCCAC TCCGCCACCT
1601 ACCGCATCGC CCTTACCTG ATGCGGCAAG GCAAAGTTGC AGAAGCAAAA
1651 CAATGGATGC GGGCGACACA GTCCTATTAC CCGTACCTGA TGCCCCGATA
1701 CGCCGACGAA ATCCGCAAAC TGCCCGTATG GCGCGCGCTG CTACCCGAAC
1751 TGCTCAAAGA CTGCAAAGCC TTCGCCCGCG CGCCCGGTCA TCCGGAAGCA
1801 AAACCTGCA AATGA

```

This corresponds to the amino acid sequence <SEQ ID 2518; ORF 738>:

m738.pep

```

1  MPAETTVSGA HPAAKLPYYI LPCFLWIGIV PFTFALKLKP SPDFYHDAAA

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1199

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51  AAGLIVLLFL TAGKKLFDVK IP AISFLLEFA MAAFWYLQAR LMNLIYPGMN
101 DIVSWIFILL AVSAWACRSL VAHFGQERIV TFAWSLLIG SLQSCIVVI
151 QFAGWEDTFL FQNIIVYSGQ GVIGHIGQRN NLGHYLMWGI LAAAYLNGQR
201 KIPAAALGVIC LIMQTAVLGL VNSRTILTYI AAIALILPEW YFRSDKSNRR
251 TMLGIAAAVF LTALFQFSMN TILETFTGIR YETAVERVAN GGFTDLPRQI
301 EWNKALAAFQ SAPIFGHWNSFAQQTFLIN AEQHNIDNL LSNLFTHSHN
351 IVLQLLAEMG ISGTLVAAT LLTGIAGLLK RPLTPASLEL ICTLAVSMCH
401 SMLEYPLWYV YFLIPFGLML FLSPAESDGI IAFKKAANLG ILTASAAIFA
451 GLLHLDWYTY RLVNAFSPAT DDSAKTLNRK INELRYISAN SPMLSFYADF
501 SLVNFALPEY PETQWAEAA TLKSLKYRPH SATYRIALYL MRQKVAEAK
551 QWMRATQSY PYLMPRYADE IRKLPVWAPL LPELLKDCKA FAAAPGHPEA
601 KPCK*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 738 shows 95.0% identity over a 604 aa overlap with a predicted ORF (ORF738.a) from *N. gonorrhoeae*:

m738/g738

m738.pep	10	20	30	40	50	60
	MPAETTVSGAHPAAKLPIYILPCFLWIGIVPFTFALKLKPSPDFYHDAAGLIVLLFL					
g738	MSAETTVSGARPAAKLPIYILPCFLWIGIIPFTFALRLKPSPDFYHDAAGLIVLLFL					
	10	20	30	40	50	60
m738.pep	70	80	90	100	110	120
	TAGKKLFDVKIP AISFLLFAMAFAFWYLQARLMNLIYPGMNDIVSWIFILLAVSAWACRSL					
g738	TAGKKLFDVKIP AISFLLFAMAFAFWYLQARLMNLIYPGMNDIASVWFILLAVSAWACKSL					
	70	80	90	100	110	120
m738.pep	130	140	150	160	170	180
	VAHFGQERIVTFLAWSLLIGSLQSCIVVIQFAGWEDTFLFQNIIVYSGQGVIGHIGQRN					
g738	VAHYGQERIVTFLAWSLLIGSLQSCIVVIQFAGWENTPLLQNIIVHRGQGVIGHIGQRN					
	130	140	150	160	170	180
m738.pep	190	200	210	220	230	240
	NLGHYLMWGI LAAAYLNGQRKIPAAALGVICLIMQTAVLGLVNSRTILTYIAAIALILPEW					
g738	NLGHYLMWGI LASAYLNGQRKIPAAALGAICLIMQTAVLGLVNSRTILTYIAAIALILPEW					
	190	200	210	220	230	240
m738.pep	250	260	270	280	290	300
	YFRSDKSNRR TMLGIAAAVF LTALFQFSMN TILETFTGIR YETAVERVANGGFTDLPRQI					
g738	YFRSDKSNRR TMLGIAAAVF LTALFQFSMN AILETFTGIR YETAVERVANGGFTDLPRQS					
	250	260	270	280	290	300
m738.pep	310	320	330	340	350	360
	EWNKALAAFQ SAPIFGHWNSFAQQTFLINAEQHNIDNLLSNLFTHSHNIVLQLLAEMG					
g738	EWNKALAAFQ SAPIFGHWNSFAQQTFLINAEQHTIHDNLFSTLFTHSHNIIQLLAEMG					
	310	320	330	340	350	360
m738.pep	370	380	390	400	410	420
	ISGTLVAATLLTGIAGLLKRPLTPASLFLICTLAVSMCHSMLEYPLWYVYFLIPFGLML					
g738	ISGTLVAATLLTGIAGLLKRSLTPASLFLCALAVSMCHSMLEYPLWYVYFLIPFGLML					
	370	380	390	400	410	420
m738.pep	430	440	450	460	470	480
	FLSPAESDGI IAFKKAANLG ILTASAAIFAGLLHLDWYTYRLVNAFSPATDDSAKTLNRK					
g738	FLSPAESDGI IAFKKAANLG ILTASAAIFAGLLHLDWYTYRLVNSFSPAADDSAKTLNRK					

1200

	430	440	450	460	470	480
	490	500	510	520	530	540
m738 . pep	INELRYISANSPMLSFYADFSLVNFALPEYPETQTWAEATLKSLKYRPHSATYRIALYL					
g738	INELRYISANSPMLSFYADFSLVNFALPEYPETQTWAEATLKALKYRPYSATYRIALYL					
	490	500	510	520	530	540
	550	560	570	580	590	600
m738 . pep	MRQ GKVAEAKQWMRATQSYYPYLMRYADEIRKLPVWAPLLPELLKDCKAFAAAPGHPEA					
g738	MRQ GKVAEAKQWMRATQSYYPYLMRYADEIRKLPVWAPLLPELLKDCKAFAAAPGHPEA					
	550	560	570	580	590	600
m738 . pep	KPCCKX					
g738	KPCCKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2519>:

```

a738 . seq
1  ATGCCCGCTG AAACGACCGT ATCCGGCGCG CACCCCGCGG CCAAACCTGCC
51  GATTTACATC CTGCCCTGCT TCCTTTGGAT AGGCATCGTC CCCTTTACCT
101 TTGCGCTCAG GCTGCAACCG TCGCCCGACT TTTACCACGA TGCCGCCGCG
151 GCAGCCGCCG TGATTGTCTT GTTGTTCTCT ACGGCAGGAA AAAAGCTGTT
201 TGATGTCAAA ATCCACCTA TCAGCTTCCT TCTGTTTGCA ATGGCGGCGT
251 TTTGGTATCT TCAGGCACGC CTGATGAACC TGATTTACCC CGGTATGAAC
301 GACATCGTCT CTTGGATTTT CATCTTACTC GCCGTCAGCG CGTGGGCCTG
351 CCGGAGCTTG GTCGCACACT ACGGACAAGA ACGCATCGTT ACCCTGTTTG
401 CCTGTCGCT GCTTATCGGC TCCCTGCTTC AATCCTGCAT CGTCGTCATC
451 CAGTTTGCCG GCTGGGAAGA CACCCTCTG TTTCAAAACA TCATTGTTTA
501 CAGCGGGCAA GCGTAATCG GACACATCG ACAGCGCAAC AACCTCGGAC
551 ACTACCTCAT GTGGGCATA CTCGCCGCG CCTACCTCAA CGGACAACGA
601 AAAATCCCGC CCGCCTTGGG TGCAATCTGC CTGATTATGC AGACGCGCGT
651 TTTAGGTTTG GTCAATTGCG GCACCATCTT GACCTACATA GCCGCCATCG
701 CCCTCATCCT TCCCTTCTGG TATTTCGGT CGGACAAATC CAACAGGCGG
751 ACGATACTCG GCATAGCCGC AGCCGTATTC CTTACCGCGC TGTTCCAATT
801 TTCCATGAAC ACCATTCTGG AAACCTTTAC CGGCATCCGC TACGAAACCG
851 CCGTCGAACG CGTCGCCAAC GCGGTTTCA CAGACCTGCC GCGCAAAATC
901 GAATGGCGCA AAGCCTCGC GCCTTCCAG TCCGCCCGA TATTCGGGCA
951 CGGCTGGAAC AGTTTGTCCC AACAAACCTT CCTCATCAAT GCCGAACAGC
1001 ACAACATACA CGACAACCTC CTCAGCAACT TGTTCACCCA TTCCACAAC
1051 ATCGTTCTCC AACTCCTTGC AGAGATGGGG ATCAGCGGCA CGCTTCTGGT
1101 TGCGCAACACC CTGCTGACGG GCATTGCCGG GCTGCTGAAA CGCCCCCTGA
1151 CCCCCGCATC GCTTTTCTTG ATCTGCACAC TTGCCGTCAG TATGTGCCAC
1201 AGTATGCTCG AATATCCTTT GTGGTATGTC TATTTCCTCA TCCCCTTCGG
1251 ACTGATGCTC TTTCTGTCCC CCGCAGAGGC TTCAGACGCG ATCGCCTTCA
1301 AAAAAGCCGC CAATCTCGGC ATACTAACCG CCTCCGCCGC CATATTGCGA
1351 GGATTGCTGC ACTTGGAAGT GACATACACC CGGATGGTTA ACGCCTTTTC
1401 CCCC GCCACT GACGACAGT CAAAACCTT CAACCGGAAA ATCAACGAGT
1451 TGCGCTATAT TTCCGCAAAC AGTCCGATGC TGTCTTTTTA TGCCGACTTC
1501 TCCCTCGTAA ACTTCGCCCT GCCGGAATAC CCGGAAACCC AGACTTGGGC
1551 GGAAGAAGCA ACCCTCAAAT CACTAAATA CCGCCCCAC TCCGCCACCT
1601 ACCGCATCGC CCTCTACCTG ATGCGGCAAG GCAAAGTTGC AGAAGCAAAA
1651 CAATGGATGC GGGCGACACA GTCTATTAC CCCTACCTGA TGCCCCGATA
1701 CGCCGACGAA ATCCGCAAAC TSCCGTATG GCGCGCGCTG CTACCCGAAC
1751 TGCTCAAAGA CTGCAAAGCC TTGCGCGCGG CGCCCGGTCA TCCGGAAGCA
1801 AAACCTGCA AATGA

```

This corresponds to the amino acid sequence <SEQ ID 2520; ORF 738.a>:

```

a738 . pep
1  MPAETTVSGA HPAAKLPYIY LPCFLWIGIV PFTFALRLQP SPDFYHDAEA
51  AAGLIVLLFL TAGKKLFDVK IPPISFLLEA MAEFWYLOAR IMNLIYFGMN
101 DIVSWIFILL AVSAWACRSL VAHYQERIV TFAWSLLIG SLQSCIVVI
151 QFAGWEDTPL FQNIIVYSQ GVIGHIGQRN NLGHYLMWGI LAAAYLNGQR

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1201

201 KIPPALGAIC LIMQTAVLGL VNSRTILTYI AAIALILPFW YFRSDKSNRR
251 TILGIAAAVF LTALFQFSMN TILEFTGIR YETAVERVAN GGFTDLPRQI
301 EWRKALAAFO SAPIFGHWN SFAQQTFLIN AEQHNHNDL LSNLFTHSHN
351 IVLQLLAEMG ISGTLLVAAT LLTGIAGLLK RPLTPASLFL ICTLAVSMCH
401 SMLEYPLWYV YFLIPFGLML FLSPAASDG IAFKKAANLG ILTASAAIFA
451 GLLHLDWYTY RMVNAFSPAT DDSAKTLNRK INELRYISAN SPMLSFYADF
501 SLVNFALPEY PETQTWAEAA TLKSLKYRPH SATYRIALYL MRQGVAEAK
551 QWMRATQSY PYLMPRYADE IRKLPVWAPL LPELLKDCKA FAAAEGHPEA
601 KPCK*

a738/m738 98.3% identity in 604 aa overlap

a738.pep	10	20	30	40	50	60
m738	10	20	30	40	50	60
a738.pep	70	80	90	100	110	120
m738	70	80	90	100	110	120
a738.pep	130	140	150	160	170	180
m738	130	140	150	160	170	180
a738.pep	190	200	210	220	230	240
m738	190	200	210	220	230	240
a738.pep	250	260	270	280	290	300
m738	250	260	270	280	290	300
a738.pep	310	320	330	340	350	360
m738	310	320	330	340	350	360
a738.pep	370	380	390	400	410	420
m738	370	380	390	400	410	420
a738.pep	430	440	450	460	470	480
m738	430	440	450	460	470	480
a738.pep	490	500	510	520	530	540
m738	490	500	510	520	530	540

1202

	550	560	570	580	590	600
a738 . pep	MRQGGKVAFAKQWMRATQSYYPYLMFPRYADEIRKLPVWAPLLPELLKDCKAFAAAPGHPEA					
m738	MRQGGKVAFAKQWMRATQSYYPYLMFPRYADEIRKLPVWAPLLPELLKDCKAFAAAPGHPEA					
	550	560	570	580	590	600
a738 . pep	KPCKX					
m738	KPCKX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2521>:

g739 . seq

```

1  ATGGCAAAAA AACCGAACAA ACCCTTCAGG CTGACCCCCA AACTCCTGAT
51  ACGCGCCGTA TTGCTCATCT GTATCACC GC CATCGGCGCA TTGGCAGTAG
101 GCATCGTCAG CACATTCAAC CCGAACGGCG AAAAAACCTT CCAAACCGAA
151 CCGCAACACA CCGACAGCCC CCGCGAAACC GAATTCTGGC TGCCAAACGG
201 CGCCGTCGGA CAAGATGCCG CCCAACCCGA ACACCACCAC GCCGCCTCAT
251 CCGAACCCGC ACAGCCGGAC GGCACAGAAG AAAGCGGCAG CGGACTGCCG
301 TCCCTTGCCG CACCAAGAA AAACCGGGTc AAACCGGCC CTTCGGATGC
351 GGCCCGGGCA GCCGATTCGT TAACCGGCAC CGGAACACAA GCTGAAAACA
401 CACTCAAAGA AACCCCGTA CTGCCACAA ACGCCCCCA TCCCGAACCC
451 CGAAAAGAAA CACCCGAAA ACAGGCGCAG CCCAAAGAAA CACCCAAAGA
501 AAAAGAAACG CCCAAAGAAA ACCATACCAA ACCGACACC CCGAAAACA
551 CGCCGGCCAA ACCCCATAAA GAGATTCTCG ACAACCTCTT TTGA

```

This corresponds to the amino acid sequence <SEQ ID 2522; ORF 739>:

g739 . pep

```

1  MAKKPNKPFER LTPKLLIRAV LLICITAIGA LAVGIVSTFN PNGDKTLQTE
51  PQHTDSPRET EFWLPNGAVG QDAAQPEHHH AASSEPAQPD GTEESGSGLP
101 SPAAPKKNRV KERPSDAARA ADSLTGTGTQ AENTLKETPV LPTNAPHPEP
151 RKETPEKQAO PKETPKKET PKENHTKPD T PKNTPAKPHK EILDNLF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2523>:

m739 . seq

```

1  ATGGCAAAAA AACCGAACAA ACCCTTCAGG CTGACCCCCA AACTCCTGAT
51  ACGCGCCGTA TTGCTCATCT GTATCGCCGC CATCGGCGCA TTGGCAATAG
101 GCATCGTCAG CACATTCAAC CCGAACGGCG AAAAAACCTT TCAAGCCGAA
151 CCGCAACACA CCGACAGCCC CCGCGAAACC GAATTCTGGC TGCCAAACGG
201 CGTAGTCGGA CAAGATGCCG CCCAACCCGA ACACCACCAC GCCGCCTCAT
251 CCGAACCCGC ACAGCCGGAC GGCACAGACG AAAGCGGCAG CGGACTGCCG
301 TCCCTTGCCG CACCAAGAA AAACCGGGTC AAACCGCAAC CTGCCGACAC
351 AGCTCAAACC GACAGGCAGC CGGACGACGC CGGAACACAA GCTGAAAACA
401 CACTCAAAGA AACCCCGTA CTGCCACAA ACGTCCCCCG TCCCGAACCC
451 CGAAAAGAAA CACCCGAAA ACAGGCGCAG CCCAAAGAAA CGCCCAAAGA
501 AAACCATACC AAACCGGACA CCGCGAAAA CACGCCGCC AAACCCATA
551 AAGAAATTCT CGACAACTC TTC

```

This corresponds to the amino acid sequence <SEQ ID 2524; ORF 739>:

m739 . pep

```

1  MAKKPNKPFER LTPKLLIRAV LLICIAAIGA LAIGIVSTFN PNGDKTLQAE
51  PQHTDSPRET EFWLPNGVVG QDAAQPEHHH AASSEPAQPD GTDESGSGLP
101 SPAAPKKNRV KPQPADTAQT DRPDAGTQ AENTLKETPV LPTNVPRPEP
151 RKETPEKQAO PKETPKENHT KPDTPKNTTP KPHKEILDKL F

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 739 shows 86.3% identity over a 197 aa overlap with a predicted ORF (ORF739.a) from *N. gonorrhoeae*:

m739/g739

1203

	10	20	30	40	50	60
m739.pep	MAKKPNKPFRLTPKLLIRAVLLICITAAIGALAIGIVSTFNPNGDKTLQAEPOHTDSPRET					
	: : : : : :					
g739	MAKKPNKPFRLTPKLLIRAVLLICITAIGALAVGIVSTFNPNGDKTLQTEPOHTDSPRET					
	10	20	30	40	50	60
	70	80	90	100	110	120
m739.pep	EFWLPGVVGQDAAQPEHHHAASSEPAQPDGTDESGSGLPSAAPKKNRVKQPADTAQT					
	: : : : : :					
g739	EFWLPGVVGQDAAQPEHHHAASSEPAQPDGTEESGSGLPSAAPKKNRVKPRPSDAARA					
	70	80	90	100	110	120
	130	140	150	160	170	
m739.pep	DRQPDAGTQAENTLKETPVLPTNVPRPEPRKETPEKQAQPKETPKE-----NHTKPD					
	: : : : : : :					
g739	ADSLTGTGTQAENTLKETPVLPTNAPHPEPRKETPEKQAQPKETPKEKETPENHTKPD					
	130	140	150	160	170	180
	180	190				
m739.pep	PKNTPPKPKHEILDKLF					
	: :					
g739	PKNTPAKPKHEILDNLFX					
	190					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2525>:

```

a739.seq
1  ATGGCAAAAA AACCGAACAA ACCCTTCAGG CTGACCCCCA AACTCCTGAT
51  ACGCGCCGTA TTGCTCATCT GTATCACCGC CATCGGCGCA TTGGCAATAG
101 GCATCGTCAG CACATTCAAC CCGAACGGCG ACAAACCTT CCAAACCGAA
151 CCGCAACACA CCGACAGCCC CCGCGAAACC GAATTCTGGC TGCCAAACGG
201 CGTAGTCGGA CAAGATGCCG CCCAACCCGA ACACCACCAC GCCTCCTCAT
251 CCGCACCCGC ACAGCCGGAC GGCACAGACG AAAGCGGCAG CGGACTGCCG
301 TCCCCTGCCG CACCAAGAA AAACCGGGTC AAACCGCAAC CTGCCGACAC
351 AGCTCAAACC GACAGGCAGC CGGACGACGC CGGAGCACA SGTGAAACAA
401 CACTCAAAGA AACCCCGTA CTGCCACAA ACGTCCCCCG TCCCGAACCC
451 CGAAAAGAAA CACCCGAAAA ACAGGCACAG CCAAAGAAA CACCAAGAA
501 AAAAGAAACG CCAAAGAAA ACCATACCAA ACCGGACACC CCGAAAAACA
551 CGCCGCCTAA ACCCATAAA GAAATTCTCG ACAACCTCTT CTGA

```

This corresponds to the amino acid sequence <SEQ ID 2526; ORF 739.a>:

```

a739.pep
1  MAKKPNKPFRLTPKLLIRAVLLICITAIGA LAIGIVSTFNPNGDKTLQTE
51  POHTDSPRET EFWLPGVVGQDAAQPEHHH ASSSAPAQPD GTDESGSLP
101 SPAAPKKNRV KQPADTAQT DRQPDAGAQ AENTLKETPV LPTNVPRPEP
151 RKETPEKQAQ PKETPKEKET PENHTKPD PKNTPPKPKH EILDNLFX*

```

a739/m739 93.9% identity in 197 aa overlap

	10	20	30	40	50	60
a739.pep	MAKKPNKPFRLTPKLLIRAVLLICITAIGALAIGIVSTFNPNGDKTLQTEPOHTDSPRET					
	: : : : : :					
m739	MAKKPNKPFRLTPKLLIRAVLLICITAAIGALAIGIVSTFNPNGDKTLQAEPOHTDSPRET					
	10	20	30	40	50	60
	70	80	90	100	110	120
a739.pep	EFWLPGVVGQDAAQPEHHHASSSAPAQPDGTDESGSGLPSAAPKKNRVKQPADTAQT					
	: : : : : :					
m739	EFWLPGVVGQDAAQPEHHHAASSEPAQPDGTDESGSGLPSAAPKKNRVKQPADTAQT					
	70	80	90	100	110	120
	130	140	150	160	170	180
a739.pep	DRQPDAGAQAEENTLKETPVLPTNVPRPEPRKETPEKQAQPKETPKEKETPENHTKPD					
	: : : : : :					
m739	DRQPDAGTQAENTLKETPVLPTNVPRPEPRKETPEKQAQPKETPK-----ENHTKPD					
	130	140	150	160	170	

1204

```

                190
a739.pep      PKNTPPKPKHKEILDNLFX
                |||||
m739          PKNTPPKPKHKEILDKLF
                180    190

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2527>:

```

g740.seq
1  ATGTCCCGAA ACCTGCTTGT CCGCTGGCTC GCCGTCTGCC TCATCCCCTT
51 GgcgACGCTT GCCGTTTTCG CCGCCAATcc gcCCGAAGAC AAACCCAGC
101 ATCTGATCAA CGGCATCATC CTTGCCTGCG AAGCGACGTT TTTGTTTAAa
151 ttcgtgctCT TTGAAACCAT CAAGCATCAT CTTAaacaag gGTTTGATTT
201 GAAACgtcaa ACCATGTTTC TGTATTATCC GATTGTTTGG CTGGTTGTGT
251 ATTGTGCCA CTATTTCGGC GCGTTTtag

```

This corresponds to the amino acid sequence <SEQ ID 2528; ORF 740.ng>:

```

g740.pep
1  MSRNLLVRWL AVCLIPLATL AVFAANPPED KPQHLINGII LACEATFLFK
51 FVLFETIKHH LKQGFDLKRQ TMLFPIPIVL LVVYLFHYFG AF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2529>:

```

m740.seq
1  ATGTCCCGAA ACCTGCTTGT CCGCTGGCTT GCCGTCTGCC TCATCCCCTT
51 GCGGACGCTT GCCGTTTTCG CCGCCAATCC GCCCGAAGAC AAACCCAGC
101 ATCTGATCAA CGGCATCATC CTTGCCTGCG AAGCGACGTT TTTGTTTAAA
151 TTCGTCCTTT TCGACACCAT CAAGCATCAT TTGAAACAAG AGTTTGATTT
201 GAAACGTCAA ACTATGTTGC TGTATTATCC GATTATTTTG CTGATTGTGT
251 ATTTGTTCCA CTATTTTGGC GCGTTTtag

```

This corresponds to the amino acid sequence <SEQ ID 2530; ORF 740>:

```

m740.pep
1  MSRNLLVRWL AVCLIPLATL AVFAANPPED KLOHLINGII LACEATFLFK
51 FVLFDTIKHH LKQEFDLKRQ TMLFPIPIIL LIVYLFHYFG AF*

```

m740/g740 93.5% identity in 92 aa overlap

```

                10      20      30      40      50      60
m740.pep      MSRNLLVRWLAVCLIPLATLAVFAANPPEDKLOHLINGIILACEATFLFKFVLFDTIKHH
                |||||
g740           MSRNLLVRWLAVCLIPLATLAVFAANPPEDKPQHLINGIILACEATFLFKFVLFETIKHH
                10      20      30      40      50      60

                70      80      90
m740.pep      LKQEFDLKRQTMLLFPIIILLIVYLFHYFGAFX
                |||
g740           LKQGFDLKRQTMFLFPIIVLLVVYLFHYFGAFX
                70      80      90

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2531>:

```

a740.seq
1  ATGTCCCGAA ACCTGCTTGT CCGCTGGCTT GTCGTCTGCC TGATACCCTT
51 GCGGACGCTT GCCGTTTTCG CCGCCAATCC GCCCGAAGAC AAACCCAGC
101 ATCTGATTAA CGGCATCATC CTTGCCTGCG AAGCGACGTT TTTGTTCAAA
151 TTCGTCCTTT TCGACACCAT CAAGCATCAT TTGAAACAAG AGTTTGATTT
201 GAAACGTCAA ACTATGTTGC TGTATTATCC GATTATTTTG CTGATTGTGT
251 ATTTGTTCCA CTATTTTGGC GCGTTTtag

```

This corresponds to the amino acid sequence <SEQ ID 2532; ORF 740.a>:

```

a740.pep
1  MSRNLLVRWL VVCLIPLATL AVFAANPPED KPQHLINGII LACEATFLFK
51 FVLFDTIKHH LKQEFDLKRQ TMLFPIPIIL LIVYLFHYFG AF*

```

a740/m740 97.8% identity in 92 aa overlap

```

                10      20      30      40      50      60

```

1205

```

a740.pep  MSRNLLVRWLVVCLIPLATLAVFAANPPEDKPOHLINGIILACEATFLFKFVLFDTIKHH
          |||||
m740      MSRNLLVRWLVVCLIPLATLAVFAANPPEDKPOHLINGIILACEATFLFKFVLFDTIKHH
          10      20      30      40      50      60

          70      80      90
a740.pep  LKQEFDLKRQTMLLFIPILLIVLYLFHYFGAFX
          |||||
m740      LKQEFDLKRQTMLLFIPILLIVLYLFHYFGAFX
          70      80      90

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2533>:

```

g741.seq
1  GTGAACCGAA CTACCTTCTG CTGCCTTTCT TTGACCGCCG GCCCTGATTG
51  TGACCGCCTG CAGCAGCGGA GGGCGGAGG CGGTGGTGTG GCCGCCGACA
101 TCGGCACGGG GCTTGCCGAT GCATTAACCG CGCCGCTCGA CCATAAAGAC
151 AAAGGTTTGA AATCCCTAAC ATTGGAAGCC TCCATTCCCC AAAACGGAAC
201 ACTGACCCTG TCGGCACAAG GTGCGGAAAA AACTTTCAAA GCCGGCGGCA
251 AAGACAACAG CCTCAACACG GGCAAACTGA AGAACGACAA AATCAGCCGC
301 TTCGACTTCG TGCAAAAAAT CGAAGTGGAC GGACAAACCA TCACACTGGC
351 AAGCGGCGAA TTTCAAATAT ACAAACAGGA TCACTCCGcc gtcgtTgcCC
401 TaccgATTGA AAAAATCAAC AACCCCGACA AAATCGACAG CCGATAAAC
451 CAACGCTCCF TCCTTGTCAG CGATTGGGCG GGAGAACATA CCGCCTTCAA
501 CCAACTGCCT GACGGCAAAG CCGAGTATCA CGGCAAAGCA TTCAGCTCCG
551 ACGATGCCGA CGGAAACTG ACCTATACCA TAGATTTGCG CGCAAACAG
601 GGACACGGCA AAATCGAACA CCTGAAACA CCGAGCAGA ATGTTGAGCT
651 TGCTCCGCC GAACTCAAAG CAGATGAAAA ATCACACGCC GTCATTTTGG
701 GCGACACGGC CTACGGCGGC GAAGAGAAAG GCACTTACCG CCTCGCCCTT
751 TTCGGCGACC GCGCCCAAGA AATCGCTGGC TCGGCAACCG TGAAGATAGG
801 GGAAAAGGTT CACGAAATCG GCATCGCCGA CAAACAGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2534; ORF 741.ng>:

```

g741.pep
1  VNRTTFCCLS LTAGPDSRL QRRGGGGGV AADIGTGLAD ALTAPLDHKD
51  KGLKSLTLEA SIPONGTLTL SAQGAEKTFK AGGKDNSLNT GKLNKDKISR
101 FDFVQKIEVD GQTITLASGE FQYKQDHSV VVALRIEKIN NPDKIDSLIN
151 QRSFLVSDLG GEHTAFNQLP DGKAEYHGKA FSSDDADGKL TYTIDFAAKQ
201 GHGKIEHLKT PEQNVELASA ELKADEKSHA VILGDTRYGG EEKGTYRLAL
251 FGDRAQEIAG SATVKIGKEV HEIGIADKQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2535>:

```

m741.seq
1  GTGAATCGAA CTGCCTTCTG CTGCCTTTCT CTGACCACTG CCTGATTCT
51  GACCGCCTGC AGCAGCGGAG GGGGTGGTGT CGCCGCCGAC ATCGGTGCGG
101 GGCTTGCCGA TGCACTAACC GCACCGCTCG ACCATAAGA CAAAGGTTTG
151 CAGTCTTTGA CGCTGGATCA GTCCGTCAGG AAAAACGAGA AACTGAAGCT
201 GCGGCACAAA GGTGCGGAAA AACTTATGG AAACGGTGAC AGCCTCAATA
251 CGGGCAAATT GAAGAAGGAC AAGGTACAGC GTTTCGACTT TATCCGCCAA
301 ATCGAAGTGG ACGGGCAGCT CATTACCTTG GAGAGTGGAG AGTTCCAAGT
351 ATACAAACAA AGCCATTCCG CCTTAACGCG CTTTCAGACC GAGCAAATAC
401 AAGATTCCGA GCATTCCGGG AAGATGGTTG CGAAACGCCA GTTCAGAATC
451 GCGACATAG CGGGCGAACA TACATCTTTT GACAAGCTTC CCGAAGGCGG
501 CAGGGCGACA TATCGCGGGA CGGCGTTCGG TTCAGACGAT GCCGGCGGAA
551 AACTGACCTA CACCATAGAT TCGCCGCCA AGCAGGGAAA CGGCAAAATC
601 GAACATTTGA AATCGCCAGA ACTCAATGTC GACCTGGCCG CCGCCGATAT
651 CAAGCCGGAT GGAAGACGCC ATGCCGTCAT CAGCGGTTCC GTCCTTTACA
701 ACCAAGCCGA GAAAGGCAGT TACTCCCTCG GTATCTTTGG CGGAAAAGCC
751 CAGGAAGTTG CCGGCAGCGC GGAAGTGAAA ACCGTAAACG GCATACGCCA
801 TATCGGCCCTT GCCGCCAAGC AATAA

```

This corresponds to the amino acid sequence <SEQ ID 2536; ORF 741>:

```

m741.pep
1  VNRTAFCCLS LTTALILTAC SSGGGGVAAD IGAGLADALT APLDHDKDKL
51  QSLTLDQSVR KNEKLKLAAG GAEKTYGNGD SLNTGKLKND KVSRLFDFIRQ
101 IEVDGQLITL ESGEFQVYKQ SHSALTAFQT EQIQDSEHSG KMVAKRQFRI

```

1206

151 GDIAGEHTSF DKLPEGGRAT YRGTAFGSDD AGGKLTYYTID FAAKQNGKI
 201 EHLKSPELNV DLAAADIKPD GKRHAVISGS VLYNQAEGKS YSLGIFGGKA
 251 QEVAGSAEVK TVNGIRHIGL AAKQ*

m741/g741 61.4% identity in 280 aa overlap

	10	20	30	40	50
m741.pep	VNRTAFCCLSLTT---	ALILTACSSGGGGV	AADIGAGLADALT	APLDHKDKGLQ	SLTLTDQ
g741	: :	:	: :	:	:
	10	20	30	40	50
	60	70	80	90	100
m741.pep	SVRKNEKLKLAQA	EKTY---	GN GDSLNTGK	LKNDKVS	RFD FIRQIEVD
g741	SIPQNGTLT	LSAQA	EKTFKAGG	KDNLNTGK	LKNDKISR
	70	80	90	100	110
	120	130	140	150	160
m741.pep	FQVYKQSHS	ALTAFQTE	QIQDSEHSG	KMVAKRQ	FRIGDIA
g741	FQIYKQDHS	AVVALRIE	KINNFPD	KIDSLIN	QRSFLV
	130	140	150	160	170
	180	190	200	210	220
m741.pep	AFGSDDAGG	KLTYYTID	FAAKQNGK	IEHLKSP	ELNVDLAA
g741	AFSSDDADG	KLTYYTID	FAAKQGHG	KIEHLKT	PEQNVEL
	180	190	200	210	220
	240	250	260	270	
m741.pep	QAEKGSYS	SLGIFGGK	AEVAGSAE	VKT VNGI	RHIGLAAKQX
g741	GEEKGT	YRLALFGD	RAQEIAGS	ATVKIGE	KVHEIGIADKQX
	240	250	260	270	280

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2537>:

a741.seq
 1 GTGAACCGAA CTGCCTTCTG CTGCCTTTCT TTGACCGCCG CCCTGATTCT
 51 GACCGCCTGC AGCAGCGGAG GCGGCGGTGT CGCGCGCGAC ATCGGCGCGG
 101 TGCTTGCCGA TGCACCTAAC GCACCGCTCG ACCATAAAGA CAAAAGTTTG
 151 CAGTCTTTGA CGCTGGATCA GTCCGTCAGG AAAAACGAGA AACTGAAGCT
 201 GGCGGCACAA GGTGCGGAAA AAACCTATGG AAACGCGGAC AGCCTCAATA
 251 CGGGCAAATT GAAGAACGAC AAGGTCAGCC GCTTCGACTT TATCCGTCAA
 301 ATCGAAGTGG ACGGGCAGCT CATTACCTTG GAGAGCGGAG AGTTCCAAGT
 351 GTACAAACAA AGCCATTCCG CCTTAACCGC CCTTCAGACC GAGCAAGTAC
 401 AAGATTGCGA GCATTTCAGG AAGATGTTG CGAAACGCCA GTTCAGAATC
 451 GGCGATATAG CGGGTGAACA TACATCTTTT GACAAGCTTC CCGAAGGCGG
 501 CAGGGCGACA TATCGCGGGA CGGCATTTCG TTCAGACGAT GCCAGTGGAA
 551 AACTGACCTA CACCATAGAT TTCGCGGCCA AGCAGGGACA CGGCAAAATC
 601 GAACATTGTA AATCGCCAGA ACTCAATGTT GACCTGGCCG CCTCCGATAT
 651 CAAGCCGGAT AAAAACGCC ATGCCGTCAT CAGCGGTTCC GTCCTTTACA
 701 ACCAAGCCGA GAAAGGCAGT TACTCTCTAG GCATCTTTGG CGGGCAAGCC
 751 CAGGAAGTTG CCGGCAGCGC AGAAGTGGAA ACCGCAAACG GCATACGCCA
 801 TATCGGTCTT GCCGCCAAGC AGTAA

This corresponds to the amino acid sequence <SEQ ID 2538; ORF 741.a>:

a741.pep
 1 VNRTAFCCLS LTAALILTAC SSGGGVVAAD IGAVLADALT APLDHKDKSL
 51 QSLTLQSVR KNEKLKLAQA EAKTYGN GDSLNTGK LKNDKVS RFD FIRQ
 101 IEVDGQLITL ESGEFQVYKQ SHSALTALQ EQVQDSEHSG KMAKRQFRI
 151 GDIAGEHTSF DKLPEGGRAT YRGTAFGSDD ASGKLTYYTID FAAKQGHGKI
 201 EHLKSPELNV DLAAADIKPD KKRHAVISGS VLYNQAEGKS YSLGIFGGQA
 251 QEVAGSAEVE TANGIRHIGL AAKQ*

a741/m741 95.6% identity in 274 aa overlap

1207

	10	20	30	40	50	60
a741.pep	VNRTAFCCISLTAALILTACSSGGGGVAADIGAVLADALTAPLDHDKSLQSLTLDQSVR					
m741	VNRTAFCCLSLTALILTACSSGGGGVAADIGAGLADALTAFLDHDKDKGLQSLTLDQSVR					
	10	20	30	40	50	60
	70	80	90	100	110	120
a741.pep	KNEKLKLAQAQAEKTYGNGDSLNTGKLNKDKVSRFDIFIRQIEVDGQLITLESGEFQVYKQ					
m741	KNEKLKLAQAQAEKTYGNGDSLNTGKLNKDKVSRFDIFIRQIEVDGQLITLESGEFQVYKQ					
	70	80	90	100	110	120
	130	140	150	160	170	180
a741.pep	SHSALTALQTEQVQDSEHSGKMWAKRQFRIGDIAGEHTSFDKLPEGGRATYRGTAFGSD					
m741	SHSALTAFQTEQIQDSEHSGKMWAKRQFRIGDIAGEHTSFDKLPEGGRATYRGTAFGSD					
	130	140	150	160	170	180
	190	200	210	220	230	240
a741.pep	ASGKLTYYTIDFAAQOGHGKIEHLKSPENVDLAASDIKPKKRHAVISGSVLYNQAEKGS					
m741	AGGKLTYYTIDFAAQOGNGKIEHLKSPENVDLAADIKPDGKRHAVISGSVLYNQAEKGS					
	190	200	210	220	230	240
	250	260	270			
a741.pep	YSLGIFGGQAQEVAGSAFVETANGIRHIGLAQX					
m741	YSLGIFGGKAQEVAGSAEVKTVNGIRHIGLAQX					
	250	260	270			

g742.seq not found yet

g742.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2539>:

```

m742.seq
1  ATGGTTACG GCATTGCCGA AGCCGATGCG GGCACAGCA GTGTGCTTAC
51  TTTGGCGGC ATGTATCAGA AGAGTAGGGA GGTTCCTGAT TTTCGGGCA
101 TTATTTTGCC CTGTGAAAAT CAGAAAACG CCCGTTTCTG TTCAACGCCT
151 GCCTGCAACC GGCCTTTGCA ACTGCCGCGC AACACTTATT TGGGGGAGGA
201 TTGGTCGCGG TTAAGTGCCG ACAAATACAA CCTTTCTCA GGATTCAAAC
251 ATGTGTTTGA CAACGGTTGG CAGCTCAATG CCGAAGTGTC TTATACCAAG
301 AATGAATCCG ATGCGAAGGT GGGCGAGTTT TTTCTGAAA ACGAATATGC
351 GCGGGGTTG TCGGGTGAGG ATGCGGTAGG CTTTTGACT GAAAAAACG
401 AAGTCATCCC GTTCGAGCCG AAAGATAAGG CATGGAGAA ACTGAAAGCA
451 TATCGTGATG AAACCGCCAA GGAATACCGG GAGCGCAAAG ACGATTTTGT
501 TAAAAACCGT TTCGATAATA CTGCTTTTGA ACAGTATCGC AGCCGCCGTG
551 CCGCAGAACG CAAAGCCGGT TTTGACAAGT GTATGAGTGA CCCTTTCGG
601 CTGGACTTTA TCTGTCAAGG TTCTGGGGG GATCCGGGCG TTGATGCCGA
651 CAAGGCGGAA TTTGTCGATA AAGCCCTTGC GAAGGAGGCG ATCTTTAATA
701 ATGCGGCACA ACGTTTTCCT AACAGCCTGT ATGACTCTTC CTTAATCCG
751 AAGGCTACCG CCAACCGACG ATACAGTTAT ATGCCGTTGC GGCATACCAA
801 AGACGACCGC CAATGGGGAA TTAACTTGA CCTGACCGGC ACATATGGGC
851 TGTTCCGGCG GGAGCATGAT TTCTTTGTCG GCTATGCCTA CGGTGATGAA
901 AAGATACGTT CGGAATATCT AGAAATCTAC GAACGCCGCT ACAGAGTACG
951 TCCGAATACG GGGGCAACGC ACGCGGTGTA TCGGGGAAGT TGTACGAGG
1001 AGCCGGACCG CGATTGTGCG TCTCCTTTGG TCAGGGGGCA TAAAGAACCC
1051 GATTGGCAGG CGTACGATGA AAAAGGCAAC CGTACCGTTT ATGCCGAAGA
1101 ATGCAGGAAC GCCAAGAAAA TAAAAACCGA GCCCAAGCTC GATGCCGAAG
1151 GCAAGCAGGT GTATTACTAT GACGAATACA GCGCAGCGG GACACCGTA
1201 TATGTCGATG TATATGAGCT GSACGAAAAA GGCAACAAGA TTCAGGAGAC
1251 CAATCCCGAC GGCACGCCTG CTTTACCGG TTTTCCGGT ACGGTGCCGG
1301 TTTGAAAAAC CGTCAAAGTG GCAGACGACC ATGTTCTCTG GCTGTATAAC
1351 TACGCCAAAT ACCTCAACAC CAACAAAACC CATTCGCTGA CTGCCAGCAC
1401 GCGTTTCAAC GTAACCGGCC GACTGCACCT TTTGGGCGG CTGCACTACA

```



```

1451 CGCGCTATGA GACTTCGCAA ACCAAAGATA TGCCTGTCCG CTATGGGCAG
1501 CCGGCAAGCG ATTTTCAGAC GGCATCGAGC ATTAGGGCGG ATCAGGACCA
1551 TTACACGGCC AAGATGCAAG GTCATAAATT GACGCCCTAT GCAGGCATTA
1601 CCTATGACTT GACACGCAA CAGAGTATTT ACGGAAGTTA TACCAAAATC
1651 TTCAAACAGC AGGATAATGT CGATGTCAGT GCCAAAACCG TTTTACCGCC
1701 TTTGGTCGGC ACAAACTATG AGGTAGGCTG GAAAGGCGCG TTCTTGCAAG
1751 GACGGCTGAA TGCTTCGTTC GCATTGTTTT ACCTCGAACA GAAAAACCGC
1801 ACGGTCGTCG ATTTCCGGCTA TGTTCCCGGA GCAGGCGGCA AGCAGGGGTC
1851 GTTCCAAACC GTTGCCAAAC CGATAGGCAA AGTGGTCAGC AGGGGTGCGG
1901 AATTTCGAGT GTCCGGTGAG TTGAACGAAG ATTGGAAAGT CTTTGCGGGT
1951 TACACCTACA ACAAGAGCCG CTACAAAAC GCCGCCGAAG TCAACGCCGA
2001 ACGCCTTGCC AAAAATTCCA GTGCAGACCC GTACAACTTC AGCAATTTCA
2051 CACCCGTGCA CATATTCCGT TCGGAACGA GCTTCCATAT ACCGAATACG
2101 GGGCTGACCG TCGGCGGCGG CGTGTCGCA CAAAGCGGCA CAAGCAGTCT
2151 GTATAACATC AGGCAGGGCG GCTACGGGCT GATAGACGGT TTCGTCCGTT
2201 ACGAATTGGG CAAACACGCC AAATTGAGCC TCATCGGTAC GAACCTIAAAC
2251 GGACGCACCT ATTTTGAGAA CAACTACAAC CGTACGCGCG GCGCAAAACA
2301 CTTCTACGGA GAGCCGCGCA CTGTCAGCAT GAAACTGGAT TGGCAGTTTT
2351 AA

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This corresponds to the amino acid sequence <SEQ ID 2540; ORF 742>:

```

m742.pep
1  M V Y G I A E A D A G D S S V L T L G G M Y Q K S R E V P D F S G I I L P C E N O K T A P F S S T P
51  A C N R P L Q L P R N T Y L G E D W S R L S A D K Y N L F S G F K H V F D N G W Q L N A E V S Y T K
101 N E S D A K V G Q F F L K N E Y A A G L S G E D A V G F L T E K N E V I P F E P K D K A L E K L K A
151 Y R D E T A K E Y R E R K D D F V K N R F D N T A F E Q Y R S R R A A E R K A G F D K C M S D P F A
201 L D F I C Q G S W G D P G V D A D K A E F V D K A L A K E G I F N N A A Q R F P N S L Y D S S F N R
251 K A T A N R R Y S Y M P L R H T K D D R Q W G I K L D L T G T Y G L F G R E H D F F V G Y A Y G D E
301 K I R S E Y L E I Y E R R Y R V R P N T G A T H G V Y A G S C Q E E P D G D L S P L V R G H K E P
351 D W Q A Y D E K G N R T V Y A E E C R N A K K I K T E P K L D A E G K Q V Y Y Y D E Y S G S R T P V
401 Y V D V Y E L D E K G N K I Q E T N P D G T P A F T G F S G T V P V W K T V K V A D D H V P A L Y N
451 Y A K Y L N T N K T H S L T A S T R F N V T G R L H L L G G L H Y T R Y E T S Q T K D M P V R Y G Q
501 P A S D F Q T A S S I R A D Q D H Y T A K M Q G H K L T P Y A G I T Y D L T P Q Q S I Y G S Y T K I
551 F K Q Q D N V D V S A K T V L P P L V G T N Y E V G W K G A F L Q G R L N A S F A L F Y L E Q K N R
601 T V V D F G Y V P G A G G K Q G S F Q T V A K P I G K V V S R G A E F E L S G E L N E D W K V F A G
651 Y T Y N K S R Y K N A A E V N A E R L A K N S S A D P Y N F S N F T P V H I F R F G T S F H I P N T
701 G L T V G G G V S A Q S G T S S L Y N I R Q G G Y G L I D G F V R Y E L G K H A K L S L I G T N L N
751 G R T Y F E N N Y N R T R G A N N F Y G E P R T V S M K L D W Q F *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2541>:

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a742.seq
1  A T G G T T T A C G G C A T T G C C G A A G C C G A T G C G G G C G A C A G C A G T G T G C T T A C
51  T T T G G G C G G C A T G T A T C A G A A G A T A G G A G G T T C C T G A T T T T C G G G C A
101 T T A T T T T G T C T G T G A A A A T C A G A A A A C T G C C C G T T C A G T T C A A C G C C T
151 C C C T G C A A C C G G C C T T T G C A A C T G C C G C G C A A C A C T A T T T G G G G G A G G A
201 T T G G T C G C G G T T G A G T G C T G A C A A A T A C A A C C T T T T C T C A G G T T C A A A C
251 A T G T G T T T G A C A C G G T T G G C A G C T C A A T G C C G A A G T G T C T T A T A C C A A G
301 A A T G A A T C C G A T G C G A A G G T G G G C A G T T T T T C T G A A A A A C G A A C A T G C
351 G C G G G T T T G T C A G A T G A G A T G C G G T A G G C T T T T T G A C C G A A A A A A C G
401 A A G T C A T C C C G T T C G A G C C G A A A G A T A A G G C A T T G G A G A A A C T G A A A G C A
451 T A T C G T G A C G A A A C C G C C A A G G A T A C C G T G A G C G C A A A G A C G A T T T T G T
501 T A A A A A C C G T T T C G A T A A T A C T G C T T T C G A G C A G T A C C G C A G C C G C T G
551 C C G C A G A A C G C A A A G C C G G T T T T G A C G A G T G A T G A G T G C C C T T T T G C G
601 C T G G A C T T T A T C T G T C A A G G T T C T T G G G G G G A T C C G G G T G T T G A T G C C G A
651 C A A G T C G G A A T T T G T C G A T A A G C C C T T G C G A A G G A A S G C A T C T T T A A T A
701 A T G C G G C A C A A C G T T T T C C A A A C A G C C T G T A T G A C T C T T C C T T A A T C G G
751 A A G G T A C C G C C A A C C G A C G A T A C A G T T A T A T G C C G T T G C G G C A T A C C A A
801 A G A C G A C C G C C A A T G G G G A A T T A A A C T T G A C C T G A C C G C G C A C A T A T G G G C
851 T G T T C G G G C G G A G C A T G A T T T C T T T G T C G G C T A T G C C T A C G G C A T G A A
901 A A G A T A C G T T C C G A A T A C T G G A A T C T A C G A A C G C C G C A C A G A G T A C G
951 T C C G A A T A C A G G G C A A C G C A C G C G T G T A T G C G G G A A G T T G T C A G G G G G
1001 A G C C G A C G G T G A T T T G T C T T C C T T T G G T C A G G G G G C A T A A A G A A C C C
1051 G A T T G G C A G G C G T A C G A T G A A A A G G C A A C C G T A C C G T T T A T G C C G A A G A
1101 A T G C A G G A A T G C C A A G A A A T A A A A C C G A G C C A A G C T C G A T G C C G A A G
1151 G C A A G C A G G T G A T T A C T A T G A C G A A T A C A C G G C A G C C G G A C G C C A G T A

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1209

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1201 TATGTCGATG TATATGAACT GGATGAAAAA GGCAATAAGA TTCAGGAGAC
1251 CAATCCCGAC GGCACGCCTG CCTTTACCGG TTTTTCGGGT ACGGTGCCGG
1301 TTTGGAAAAC CGTCAAAGTG GCCGACGACC ATGTTCTCTG GCTGTATAAC
1351 TACGCCAAAT ACCTCAACAC CAACAAAACC CATTGCGTGA CTGCCGGCAC
1401 ACGTTTCAAC GTAACCGGCC GACTGCATCT TTTGGGCGGG CTGCACTACA
1451 CGCGCTATGA AACCTCGCAA ACCAAAGATA TGCCTGTCCG CTATGGGCAG
1501 CCGGCAAGCG ATTTTCAGAC GGCATCGAGC ATTAAGGCGG ATCAGGACCA
1551 TTATACGGCC AAGATGCAAG GTCATAAATT GACGCCCTAT GCAGGCATTA
1601 CCTATGATTT GACACCGCAA CAGAGTATTT ACGGAAGTTA TACCAAAATC
1651 TTCAAACAGC AGGATAATGT CGATGTCAGT GCCAAAACCG TTTTACCGCC
1701 TTTGGTCGGC ACAAACATATG AGGTAGGCTG GAAAGGCGCG TTCTTGCAAG
1751 GACGGCTGAA TGCTTCGTTC GCATTGTTTT ACCTCGAACA GAAAAACCGC
1801 ACGGTCGTCG ATTTTGGCTA TGTTCCCGGA GCAGGCGGCA AGCAGGGGTC
1851 GTTCCAAACC GTTGCCAAAC CGATAGGCAA AGTGGTCAGC AGGGGTGCGG
1901 AATTGAGATT GTCGGGTGAG TTGAACGAAG ATTGGAAGT CTTTGCGGGT
1951 TACACCTACA ACAAGAGCCG CTACAAAAC GCCGCGAAG TCAACGCCGA
2001 ACGCCTCGCC AAAAACACAG GCGCAGACCC GTACAACTTC AGCAATTTCA
2051 CACCCGTGCA CATATTCCGT TTCGGAACGA GCTTCCATAT ACCGAATACG
2101 GGGCTGACCG TCGGCGGCGG CGTGTCCGCA CAAAGCGGCA CAAGCAGTCT
2151 GTATAACATC AGGCAGGCGG GCTACGGGCT GATAGACGGT TCGTCCGTT
2201 ACGAATTGGG CAAACACGCT AAATTGAGCC TCATCGGTAC GAACTTAAAC
2251 GGACGCACTT ATTTTGAGAA CAACTACAAC CGTACGCGCG GCGCAAACAA
2301 CTTCTATGGA GAGCCGCGCA CTGTCAGCAT GAAACTGGAT TGGCAGTTTT
2351 AA

```

This corresponds to the amino acid sequence <SEQ ID 2542; ORF 742.a>:

a742.pep

```

1  MVYGIAEADA GDSSVLTGG MYQKSREVPD FSGIILSCEN QKTAPFSSTP
51  ACNRPLQLPR NTYLGEDWSR LSADKYNLFS GFKHVFNDGW QLNAEVSYTK
101 NESDAKVGQF FLKNEHAAGL SDEDAVGFLT EKNEVIPFEP KDKALEKLKA
151 YRDETAKEYR ERKDDFVKNR FDNTAFEQYR SRRAAERKAG FDECM SAPFA
201 LDFICQGSWG DPGVDADKSE FVDKALAKEG IFNNAQRFP NSLYDSSFN
251 KATANRRYSY MPLRHTKDDR QWGIKLDLTG TYGLFGREHD FFVGYAYGDE
301 KIRSEYLEIY ERRHRVRPNT GATHGVYAGS CQGE PDGDL S PLVRGHKEP
351 DWQAYDEKGN RTVYAEECRN AKKIKTEPKL DAEGKQVYYY DEYSGSRTPV
401 YVDVYELDEK GNKIQETNPD GTPAFTGFSG TVPVWKT VKV ADDHVPALYN
451 YAKYLNTNKT HSLTAGTREN VTGRLHLLGG LHYTRYETSQ TKDMPVRYGQ
501 PASDFQTASS IKADQDHYTA KMQGHKLTPY AGITYDLTPQ QSIYGSYTKI
551 FKQQDNVDVS AKTVLPPLVG TNYEVGWKGA FLQGRNLNASF ALFYLEQKNR
601 TVVDFGYVPG AGGKQGSFQT VAKPIGKVVS RGAEFELSGE LNEWDKVFAG
651 YTYNKSRYKN AAEVNAERLA KNTGADPYNF SNETPVHIFR FGTSFHIPNT
701 GLTVGGGVSA QSGTSSLYNI RQGGYGLIDG FVRYELGKHA KLSLIGTNLN
751 GRTYFENNYN RTRGANNFYG EPRTVSMKLD WQF*

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a742/m742 98.5% identity in 783 aa overlap

	10	20	30	40	50	60
a742.pep	MVYGIAEADAGDSSVLTGGMYQKSREVPDFSGIILSCENQKTAPFSSTPACNRPLQLPR					
m742	MVYGIAEADAGDSSVLTGGMYQKSREVPDFSGIILPCENQKTAPFSSTPACNRPLQLPR					
	10	20	30	40	50	60
a742.pep	NTYLGEDWSRLSADKYNLFSGFKHVFNDGWQLNAEVSYTKNESDAKVGQFFLKNEHAAGL					
m742	NTYLGEDWSRLSADKYNLFSGFKHVFNDGWQLNAEVSYTKNESDAKVGQFFLKNEYAAGL					
	70	80	90	100	110	120
a742.pep	SDEDAVGFLTEKNEVIPFEPKDKALEKLKAYRDETAKEYRERKDDFVKNRFDNTAFEQYR					
m742	SGEDAVGFLTEKNEVIPFEPKDKALEKLKAYRDETAKEYRERKDDFVKNRFDNTAFEQYR					
	130	140	150	160	170	180
a742.pep	SRRAAERKAGFDECM SAPFALDFICQGSWGDPGVDADKSEFVDKALAKEGIFNNAQRFP					
m742	SRRAAERKAGFDECM SAPFALDFICQGSWGDPGVDADKSEFVDKALAKEGIFNNAQRFP					
	190	200	210	220	230	240
a742.pep	SRRAAERKAGFDECM SAPFALDFICQGSWGDPGVDADKSEFVDKALAKEGIFNNAQRFP					
m742	SRRAAERKAGFDECM SAPFALDFICQGSWGDPGVDADKSEFVDKALAKEGIFNNAQRFP					

1210

m742
 190 200 210 220 230 240
 SRRAAERKAGFDKCMSDPFALDFICQGSWGDGVDACKAEFVDKALAKEGIFNNAQRF

a742.pep NSLYDSSFNRKATANRRYSYMLRHTKDDROWGIKLDLTGTYGLEFGREHDFVGYAYGDE

m742 NSLYDSSFNRKATANRRYSYMP^{LR}HTKDD^{RQ}WGIKLDLTGT^YGLFGR^{EH}DF^{FF}VG^YAYGDE

a742.pep · KIRSEYLEIYERRHRVRPNTGATHGVYAGSCOGEPDGLSSPLVRGHKEPDWOAYDEKGN

m742 KIRSEYLEIYERRYVRNPNTGATHGVYAGSCQEEDGDLSSPLVRGHKEPDWQAYDEKGN
310 320 330 340 350 360

a742.pep RTVYAEECRNAAKKIKTEPKLDAEGKQVYYYDEYSGSRTPVYVDVYELDEKGNKIOETNPD

m742 RTVYAECECRNAKKIKTEPKLDAEGKQVYYYDEYSGSRTPVYVDVYELEDEKGNKIQETNPD

430 440 450 460 470 480
a742.pep GTPAFTGFSGTVPVVKTKVKVADHDHVPALYNYAKYLN~~TK~~THSLTAGTRENVTGRHLHGG

m742 GTPAFTGPGSTVPVVKTVKVVADHDHPALYNYAKYLNTNKTHTSLTASTRENVVTGRLLHLLGG

430 440 450 460 470 480

a742.pep LHYTRYETSQTKDMPVRYGCPASDFOTASSIKADODHYTAKMOGHKLTPYAGITYDLTPQ

m742 LHYTRYETSQTKDMPVRYGCPASDFQTASSIRADQDHYAKMQGHKLTPTYAGITYDLTPQ
 490 500 510 520 530 540

550 560 570 580 590 600
a742.pep OSIYGSYTKIFKQODNVDSAKTVLPPLVGTNYEVGWKGAFLOGRLNASFALEYLEOKNR

m742 QSIYGSYTKIFKQQDNVDVSAKTVLPLVGNTNYEVGWKGAFLLQGRNLNASFALFYLBQKNR
 550 560 570 580 590 600

TVVDFGYVPGAGGKQGSFOTVAKPIGKVVSARGAEFELSGELNEDWKVFAGYTYNKSRYKN

m742 TVVDFGYYPGAGGKQGSFOTVAKPIGKVVSRGAEFELSGELNEDWKVVFAGYTYNKSRYKN
610 620 630 640 650 660

670 680 690 700 710 720
a742.pep. AAEEVNAERLAKNTGAOPYNFSNETPVHIERFGTSPHIPNTGLTVGGGVSAQSGTSSLYNI

m742 AAEVNAERLAKNSSADPYNFSNFTPVHIFRFGTSEHIPNTGLTVGGGVSAQSGTSSLYNI
670 680 690 700 710 720

730 740 750 760 770 780
a742.pep ROGGYGLIDGFEVRYELGKHAKLSLIGTNLNGRTYFENNYNRRTRGANNEYGEPRVTYSMKLD

m742 RQGGYGLIDGFVRYELGKHAKLSLIGTNLNGRTYFENNYNRRTRGANNFYGEPRTVSMKLD
730 740 750 760 770 780

a742.pep WQFX

1111

m742 WQEX

a742/ p25184

sp|P25184|PUPA PSEPU

FERRIC-PSEUDOBACTIN

358

RECEPTOR

PRECURSOR

>qi|94923|pir||S15169

1211

ferric-pseudobactin receptor precursor - *Pseudomonas putida* >gi145723 (X56605)
pseudobactin uptake protein [*Pseudomonas putida*] Length = 819

Score = 152 bits (381), Expect = 6e-36

Identities = 110/356 (30%), Positives = 170/356 (46%), Gaps = 55/356 (15%)

Query: 436 KTVKVADUHV-PALYNYAKYLNTNKTSLTAGTRFNVNTRLHLLGGLHYTRYETSQTKDM 494
+T K DD + P + +Y +N+ +RFN+T LHL+ G + Y
Sbjct: 511 QTPKPGDDEIIPGI-----QYNISNRQSGYFVASRFNLTDLHLILGARASNYRFDYAL-- 564

Query: 495 PVRYGQPASDFQTASSIKADQDHYTAKMQGHKLTPYAGITYDLTPQQSIYGSYTKIFKQQ 554
R G + ++ ++ +TPYAGI YDLT +QS+Y SYT IFK Q
Sbjct: 565 -WRIGNEPAPYKM-----VERGVVTPYAGIVYDLTNEQSVYASYTDIFKPQ 609

Query: 555 DNVDVSAKTVLPPLVGTNYEVGWKGAFLOGRNLNASFALFYLEQKNRTVVDFGYVPGAGGK 614
+NVD++ K L P VG NYE+GWKG FL+GRLNA+ AL+ +++ N VP +GG
Sbjct: 610 NNVDTIGKP-LDPEVGKNYELGWKGEFLEGRLNANIALYMKRDNLAESTNEVVPDSSGGL 668

Query: 615 QGSFQTVAKPIGKVVSARGAEFELSGELNEDWKVFAGYTYNKSRYKNAEVAERLAKNTG 674
S + + ++G + ELSGE+ W VF GY++ ++
Sbjct: 669 IAS-----RAVDGAETKGVDELSEVLPGWNVFTGYSHTRTE-----D 707

Query: 675 ADPYNFSNFTPVHIFRFGTSFHIPN--TGLTVGGGVSAQSGTS---SLYN--IRQGGYGL 727
AD + P+ FRF ++ +P LT+GGGV+ S ++ + YN + Q Y +
Sbjct: 708 ADGKRLTPQLPMDTFRFWNTYRLPGEWEKLTGGGVNWNNSKSTLNFARYNSHVTQDDYFV 767

Query: 728 IDGFVRYELGKHAKLSLIGTNLNGRTYFENNYNRTRGANNFYGEPRTVSMKLDWQF 783
RY + + +L N+ + Y Y G+ YG PR ++ L + F
Sbjct: 768 TSLMARYRINESLAATLNVNNIFDKKY----YAGMAGSYGHYGAPRNATVTLYDF 819

g743.seq not found yet

g743.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2543>:

m743.seq

```

1 ATGAATCAAA ATCATTTTTC ACTTAAAT CTGACCGTTA TGCTGTTATC
51 GGCTTACGGT GGTTCCTTTG CAGACGGTGT TGTGCCTGTT TCAGACGGCA
101 ATACCGTCAG TCTGGATACG GTCAATGTAC GCGGCTCTCA TGCTTGTGTT
151 GGCAAGACCG AAAAGACCCG TTCTTATACG ATAGATCGGA TGTCACCCGC
201 CACAGGTATG AGGATTGCGG GCAAGGATAC GCCGCAGTCG GTCAGCGTCA
251 TCACGCGCAG CCGCCTTGAC GATAAGGCGG TGCATACGCT TGAAGAGGCA
301 ATGAAAAACA CGACGGGTGT CAACGTTGTG CGCGATTGAG GCTTGCAGAC
351 GCGGTTTTTG TCACGCGGTT TCTATATTGA TCAGATTGGT GAAGACGGTA
401 TGACCGTCAA TGTTGCAGGC CGTTCGGGAT ATACGGCGAA AATCGACGTG
451 TCTCCGAGTA CCGATTGGC GGTATTGAC CATATTGAAG TTGTACGGGG
501 TGCAACGGGG TTGACCCAAT CCAATTCAGA GCCGGGAGGA ACCGTCAATT
551 TGATCCGTAA GTGA

```

This corresponds to the amino acid sequence <SEQ ID 2544; ORF 743>:

m743.pep

```

1 MNQNHFSLKI LTVMLLSAYG GSFADGVVPV SDGNTVSLDT VNVRGSHALL
51 GKTEKTRSYT IDRMSTATGM RIAGKDTPOS VSVITRSLD DKAVHTLEEA
101 MKNVTTGVNVV RDSGLQTRFL SRGEYIDQIG EDGMTVNVAG RSGYTAKIDV
151 SPSTDLAVYD HIEVVRGATG LTQSNSEPGG TVNLIRK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2545>:

a743.seq

```

1 ATGAATCAAA ATCATTTTTC ACTTAAAT CTGACCGTTA TGCTGTTATC
51 GGCTTACGGT GGTTCCTTTG CAGACGGTGT TGTGCCTGTT TCAGACGGCA
101 ATACCGTCAG TTTGGATACG GTCAATGTAC GCGGCTCTCA TGCTCTGTGCG
151 GGCAAGACCG AGAAGACCCG TTCTTATACG ATAGATCGGA TGTCACCCGC
201 CACAGGTATG AGGATTGCGG GCAAGGATAC GCCGCAGTCG GTCAGCGTCA
251 TCACGCGCAG CCGCCTTGAC GATAAGGCGG TGCATACGCT TGAAGAGGCA
301 ATGAAAAACA CGACGGGTGT CAACGTTGTG CGCGATTGAG GCTTGCAGAC

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1212

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351 GCGGTTTTTG TCACGCGGTT TCTATATTGA TCAGATTGGT GAAGACGGTA
401 TTACCGTCAA TGTTGCAGGC CGTTCGGGAT ATACGGCGAA AATCGACGTG
451 TCTCCGAGTA CCGATTGGC GGGTTATGAC CATATTGAAG TTGTACGGGG
501 TGCAACGGGG TTGACCCAAT CCAATTCAGA GCCGGGTGGA ACCGTCAATT
551 TGATCCGTAA GCGA

```

This corresponds to the amino acid sequence <SEQ ID 2546; ORF 743.a>:

a743.pep

```

1  MNQNHFSLKI LTVMLLSAYG GSFADGVVPV SDGNTVSLDT VNVRGSHALS
51  GKTEKTRSYT IDRSTATGM RIAGKDTPOS VSVITRSLD DKAVHTLEEA
101 MKNTTGVNVV RDSGLQTRFL SRGFYIDQIG EDGITVNVAG RSGYTAKIDV
151 SPSTD LAVYD HIEVVRGATG LTQSNSEPGG TVNLIRKR

```

a743/m743 98.9% identity in 187 aa overlap

	10	20	30	40	50	60
a743.pep	MNQNHFSLKI	LTVMLLSAYG	GSFADGVVPV	SDGNTVSLDT	VNVRGSHALS	SGKTEKTRSYT
m743	MNQNHFSLKI	LTVMLLSAYG	GSFADGVVPV	SDGNTVSLDT	VNVRGSHALS	LGKTEKTRSYT
	10	20	30	40	50	60
	70	80	90	100	110	120
a743.pep	IDRSTATGM	RIAGKDTPOS	VSVITRSLD	DKAVHTLEEA	MKNNTGVNVV	RDSGLQTRFL
m743	IDRSTATGM	RIAGKDTPOS	VSVITRSLD	DKAVHTLEEA	MKNNTGVNVV	RDSGLQTRFL
	70	80	90	100	110	120
	130	140	150	160	170	180
a743.pep	SRGFYIDQIG	EDGITVNVAG	RSGYTAKIDV	SPSTD LAVYD	HIEVVRGATG	LTQSNSEPGG
m743	SRGFYIDQIG	EDGMTVNVAG	RSGYTAKIDV	SPSTD LAVYD	HIEVVRGATG	LTQSNSEPGG
	130	140	150	160	170	180
a743.pep	TVNLIRKR					
m743	TVNLIRKX					

g744.seq not found yet

g744.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2547>:

m744.seq

```

1  ATGAAACCGT TAAAAACATT AGAATTTGGA TTTGTGGATG CTGCAAACTA
51  CAGAAGAAGA GAAAATAAAG ATTTATTTAA CCGAATATTT GTAAAAGGAG
101 AATATTTGGA TGAATTATGT GAACCAATA TTTGTTTTTT AATCGGAGAA
151 AAGGGAACAG GAAAGACAGC ATATGCTGTT TATTTAACTA ATAACTTCTA
201 TAAAAACATA CATGCCACTA CTAAGTTTGT TCGTGAAACC GATTATTCAA
251 AATTTATTCA GCTAAAGAAA GCAAGACACT TAACTGTTTC AGATTTTACA
301 AGTATTTGGA AAGTCATTTT ATATCTCTTG ATATCAAATC AAATCAAATG
351 TAAAGAAAAC GGAATATTAT CTTCATATAT TAATAAATTT AAAGCCTTAG
401 ATGAGGCTAT AAATGAATAT TATTATGGCG CTTTGATCCG GAAATTGTA
451 CAAGCAATAA CTTTAATAGA AAATCAAAA GAAGCTGCGG AAATGATTTT
501 TGGAAAATTT GTTAAACTAG GTGAAGAGGA ATCCCAACAA ATAACTTTTA
551 CAGAAAGTAA ATTCCAAGCA AATTTAGGTT TTATTGAAAG AAAATTTAAA
601 GATGCTTTAT CTCAGTTAAA GCTAAAAGAT AATCATATTT TGTTTATTGA
651 TGGGATAGAT ATTAGACCAT CACAGATTCC ATTTGATGAA TATCATGAGT
701 GTGTAAAAGG TCTTGCTAAC GCCATATGGA TGTAAATAA TGATATCTTC
751 CCTTCCATTA AAGATAGTAA GGGAAAGGATG AGAGTGTGTG TATTGATTAG
801 ACCTGATATC TTTGATTGAT TAGGTTTACA AAATCAAAAT ACCAAACTTC
851 AAGATAATTC AGTATTTTGA GACTGGAGGA CGGATTATAA ATCTTATAGA
901 AGTTCAAAGA TTTTGGCGT TTTTGATCAT CTTTGTAGAA CCCAGCAAGA
951 AAAACAAGAT AGTTTAGAAA AAGGCAACTC ATGGGATTAT TATTTCCAT
1001 GGAATGCTCC TAATTTACAT GATGAGTATA AAAATTTAAC TTCATTTATT
1051 AGCTTCTTAA GAAAATCGTA TTATCGACCT CGCGATATTC TTCAGATGCT
1101 TACTTTGCTA CAAAAAATA AGAAAAGTAA GGAAGATTAT GTCGTAGCAG
1151 AAGATTTTGA TAATACTTCT TTTCAAAGAG AATACTCGAT ATATTACTT
1201 GGTGAAATCA AAGATCATCT TTTGTTTTAT TATAGTCAAA GTGATTATCA
1251 AAATTTCTCG AAATTTTTTG AATTTTAAA CGGAAAGAT AGATTTAAAT

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1213

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1301 ATAGTGATTT TTTAAAAGCA TTTGAACGTT TGA AAAAGCA CTTACAAACA
1351 ACATCAGTGG AAATACCTAA ATTTATGAGT ACTGCTAATG AGTTTTTGCA
1401 ATTTTTATTT GACTTGAATG TTATTGCTTA TTTAGATAAC CCAGAAGATG
1451 AAACGAAACC ATATATCCAT TGGTGCTTA AAGATAGAAA TTATGCAAAAT
1501 ATTTCTCCTA AAATAAAAAC TGA AACTGAA TATTTAATAT TTTCAGGATT
1551 ATCAAAAGCC CTTGATGTTG GTACTCCATT TAAGACAAA CAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2548; ORF 744>:

m744.pep

```

1 MKPLKTLFEG FVDAANYRRR ENKDLFNRIF VKGEYLDEL C EPNISFLIGE
51 KGTGKTAYAV YLTNNFYKNI HATTKFVRET DYSKFIQLKK ARHLTVSDFT
101 SIWKVILYLL ISNQIKCKEN GILSSIENKF KALDEAINEY YYGAFDPEIV
151 QAITLIENSK EAAEMIFGKF VKLGEESQO ITFTESKFQA NLGFIERKFK
201 DALSQLKLKD NHILFIDGID IRPSQIPFDE YHECVKGLAN AIWMLNNDIF
251 PSIKDSKGRM RVLLIRPDI FDSLGLQONN TKLQDNSVFL DWRTDYKSYR
301 SSKIFGVFDH LLRTQEQKD SLEKNSWDY YFPWNAPNLH DEYKNLTSFI
351 SFLRKSYYRP RDILQMLTLL QKNKSKEDY VVAEDFDNTS FQREYSIYLL
401 GEIKDHLLEY YSQSDYQNFL KFFEFLNGKD RFKYSDELKA FERLKKHLQT
451 TSVEIPKFMS TANEFLQFLF DLNVIAYLDN PEDETKPYIH WCFKDRNYAN
501 ISPKIKTETE YLIFSGLSKA LDVGTPEKKN Q*

```

g745.seq not found yet

g745.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2549>:

m745.seq

```

1 ATGTTTGGC AACTGACCGT TGTTTCAGTA ACCGCCGTCA TTGCACTGGG
51 GACAATATTC ATCAATAAGA AAAC TTCAA GCAAAAGGCG ACATTAGATG
101 TTATTTGAA TGATTACCAA GATGCACAAT TTGTAGAAGC CGACAATCAT
151 ATTTCCGCTT ATATTCGCGG CACGGCAGTT GACGACAACA ACGCGCGGAT
201 CGACCTGTAT GAAATTTATC AAAATAAGGG CGGACAATGG GAAAAAGAGA
251 GAGGGCATT ACTTACCGTA ATCAATCGGC ACGAGTTTGA TGCGTGCGCA
301 ATCAACTCGG GAGTATTGGA TGAGGATTGG TTTAAACGGC TGCATTGCAC
351 CAACTTCATA AAATTGTGGA ATGCAGTTTC GCCTCTTGT ATGAAAATAC
401 GCGAAGAAGA ACGCAAAGAC ACAATATTTA GAGAGTTGGA AATTTTGGTT
451 GCATTATGGA AAGCAAACCC CCTAAAGGCA TCTGATTTGT GA

```

This corresponds to the amino acid sequence <SEQ ID 2550; ORF 745>:

m745.pep

```

1 MFWQLTVVSV TAVIALGTIF INKKTSKOKA TLDVILNDYQ DAQFVEADNH
51 ISPIYRGTA DDNNARIDLY EIYQNKGGOW EKERGHLLTV INRHEFYACA
101 INSGVLDEL FKR LHCTNFI KLWNAVSPV MKIREEERKD TIFRELEILV
151 ALWKANPLKA SDL*

```

a745.seq not found yet

a745.pep not found yet

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2551>:

g746.seq

```

1 ATGTCCGAAA ACAACAAAA CGAAGTCCTG ACCGGTTACG AACAGCTGAA
51 ACGGCGCAAC CGCCGCCGCC TCGTAACGGC AAGCTCCCTG GTTGCCGCCT
101 CCTGCATCCT GCTGGCAGCC GCACTCAGT CCGATCCTGC CGACAGCAAT
151 CCGCACCCG AGGCCGGCGA AACCGCGCA ACGGAAAGCC AAACGGCAAA
201 CACGGCACAA ACCCCTGCCT TGAATCCGC CGCCGAAAC GGGGAAACCG
251 CGGCCGACAA ACCGCAAGGAC TTGGCAGGCG AAGACAAGCC TTCTGCCGCC
301 GACAGCGAAA TCAGCGAGCC TGA AACGTA GCGCGCCGC TGGTGCTGAT
351 TAACGACCGG CTCGAAGACA GCAACATCAA AGGTTTGAA GAATCCGAGA
401 AACTGCAACA GGCAGAAACC GCCAAACCG AACCGAAGCA GGCAAAACAA
451 CGCGCTGCCG AAAAAGTGC GGCAACTGCC GACAGTACGG ATACGGTAGC
501 GGTTGAAAA CCGAAACGCA CTGCCGAACC CAAACCGCAA AAAGCGGAAC
551 GCACTGCCGA AGCCAAGCCC AAAGCCAAAG AAACCAAAAC CGCCGAAAAA
601 GTTGCCGACA AACCGAAAC TGCTGCCGAA AAAACCAAA CCGGATACGGC
651 AAATCCGAC AGCGCGGTA AAGAAGCGAA AAAAGCCGAC AAGGCTGAAG
701 GCAAAAAGAC AGCCGAAAAA GACCGTTCGG ACGGCAAAAA ACACGAAACG

```

q746.ppt

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2553>:

m746.seq

1	ATGTCGGA	ACAAACAAA	CGAAGTCTG	AGCGGTACG	AACAACCTCA
51	ACGGCGCAAC	CGCGCGCGCC	TCGTAAACGGC	AAGTTGCCTG	GTTCGCGCCT
101	CTCTGATCCT	GCTGGCAGC	CCCTTCAGTT	CCGGCCCTGC	CGAACAGACT
151	CGCGCGGAAA	CGACGGCGGT	AGAAAACAAA	CGCGCAGTGC	CGGCAACAAAC
201	CCCTGCCTTG	AAATCGCCGC	CCGACAACAC	GCAGCACTTG	GCAGGCGAAG
251	ACAAGCCTTC	TGCCCGCCAG	AGCGAAATCA	CGAGCGCTGA	AAACGTAGGC
301	CGCGCGCTGG	TGCTGATTAA	CGACGGCTCT	GAGACAGACA	ACATCAACAGG
351	TTTGGAGACA	TCCGAGAACT	TGCAACAGGC	AGAAACCGCC	AAAACCGCAC
401	CGAAGCAGGC	ACAGAAACGC	GTGTCCGAAA	AAGTCGCGC	AACTGCGCAC
451	AGTACGGATA	CGGTAGCGGT	TGAAAACACG	AAACGCATCT	CCGAAACAAA
501	ACCGCAAAAA	GCGGAACGCA	CTGCCAAAGC	CAAGCCCAAA	GCCAAAGAAA
551	CCAAACCCGC	CGAAAAGATT	GCCGACAAAC	CGAAATCTGC	CGCCGGAAAA
601	ACCAAAACCGG	ATACGCGAAA	ATCCGACAGC	GCGGTAAAGC	AAGCGAAAAA
651	AGCCGACAAG	GCTGAAAGCA	AAAAAACAGC	CGAAAAAGAC	CGTTTCGGACG
701	GCAAAAAGACA	CGAAACGGGA	CAAAAACACG	ACAAGCGGGA	CAAGACCCAA
751	ACCGCCGAGA	AGAAAAATC	CGGTAAAAAC	CGCGCCATTC	AGGCAGGTTA
801	TGCCGAAAAA	GAGACCGCCT	TAAGCTTCCA	GCGCAAAATG	AAGCGCGCGG
851	GATCGTATTC	GACCATCACC	GAATATTAGA	CCGACATCCG	CAAACTTTAC
901	CGCGTCAAA	CAAGCAACTA	TAAAAACGTA	AGGGATAGCG	ACAACGCTTT
951	GAACAATAATG	CGCGTACACG	GTATCGCCGG	TCAGGTAACG	AATGAATAG

m746.pap

1	MSENKQNEVL	SGYBQQLKRRN	RRRLVTSASCL	VAASCILLAA	ALSSGPAEQT
51	AGETSGVENV	AAGAARQTPAL	KSAADVPQDL	AGEDKPSAAD	SEISEPENVG
101	APLVLINERL	EDSNIKGLEA	SEKLQQAETA	KTAGPQAKOR	AAEKVPATAD
151	STDTVAVEPK	KRTAEAKRQK	AERTAKAKPK	AKETTKKHEV	ADPKPTAAEK
201	TKPTAKASDS	AVKEAKRQAD	AESKTKTAED	RSDGKTKAET	QKTDKADTKT
251	RAKEKKSCKK	AAIQAGYAEK	ERALSILQRM	KAAIGDSTIT	EIMTDSNGYV
301	TVKSSNYKVA	RNDAERDNLKL	RVHGIGAQVT	NE*	

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 746 shows 89.9% identity over a 346 aa overlap with a predicted ORF (ORF 746) from *N. gonorrhoeae*:

m746/g746 89.9% identity in 346 aa overlap

	10	20	30	40	50	
m746.pep	MSENKQNEVL	SGYEQLKRRNRRLVTASCLVA	ASCILLAAALSSGPAEQT	----	AGETSG	
g746	MSENKQNEVL	TGYEQLKRRNRRLVTASSLVA	ASCILLAAALSSDPADSNPAPQAGETGA			
	10	20	30	40	50	60
	60	70	80	90	100	109
m746.pep	VENKAAGAA	QTPALKSAA-----	DKPQDLAGEDKPSAADSEISEPENVGAPLVLINER			
g746	TESQTANTA	QTPALKSAAENGETAADK	QPQDLAGEDKPSAADSEISEPENVGAPLVLINDR			
	70	80	90	100	110	120

1215

```

      110      120      130      140      150      160      169
m746.pep  LEDSNIKGLEASEKLQQAETAKTAPKQAKQRAAEKVPATADSTDTVAVEKPKRTAETKPQ
g746      LEDSNIKGLEASEKLQQAETAKTEPKQAKQRAAEKVSATADSTDTVAVEKPKRTAEPKPQ
           130      140      150      160      170      180

      170      180      190      200*      210      220      229
m746.pep  KAERTAKAKPKAKETKTAEKVADKPKTAAEKTTPDTAKSDSAVKEAKKADKAESKKTAEK
g746      KAERTAEAKPKAKETKTAEKVADKPKTAAEKTTPDTAKSDSAVKEAKKADKAEGKKTAEK
           190      200      210      220      230      240

      230      240      250      260      270      280
m746.pep  DRSDGKKKHETAQKTDKADKTKTAEKEKSGK---KAAIQAGYAEKERALSQRKMKAAAGID
g746      DRSDGKKKHETAQKTDKADKTKTAEKEKSGKAGKAAIQAGYAEKERALSQRKMKAAAGID
           250      260      270      280      290      300

      290      300      310      320      330
m746.pep  STITEIMTDNGKVYRVKSSNYKNARDAERDLNKL RVHGIAGQVTNEX
g746      STITEIMTDNGKVYRVKSSNYKNARDAERDLNKL RVHGIAGQVTNEX
           310      320      330      340

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2555>:

```

a746.seq
1  ATGTCCGAAA ACAAAACAAA CGAAGTCCTG AGCGGTTACG AACAACTCAA
51  ACGGCGCAAC CGCCGCCGCC TCGTAACGGC AAGTTGCCCTG GTTGCCGCCT
101 CCTGCATCCT GCTGGCAGCC GCCCTCAGTT CCGGCCCTGC CGAACAGACT
151 GCGGCGGAAA CAAGCGGCGT AGAAAACAAA GCGGCAGGTG CGGCACAAAC
201 CCCTGCCTTG AAATCCGCCG CCGACAAACC GCAGGACTTG GCAGGCGAAG
251 ACAAGCCTTC TGCCGCCGAC AGCGAAATCA GCGAGCCTGA AAACGTAGGC
301 GCGCCGCTGG TGCTGATTAA CGACCGCCTC GAAGACAGCA ACATCAAAGG
351 TTTGGAAGCA TCCGAGAAAC TGCAACAGGC AGAACCAGCC AAAACCGCAC
401 CGAAGCAGGC AAAACAACGC GCTGCCGAAA AAGTGCCGGC AACTGCCGAC
451 AGTACGGATA CGGTAGCGGT TGA AAAACCG AAACGCATG CCGAAACAAA
501 ACCGCAAAAA GCGGAACGCA CTGCCAAAGC CAAGCCCAAA GCCAAAGAAA
551 CCAAAACCGC CGAAAAAGTT GCCGACAAAC CGAAAACCTGC CGCCGAAAAA
601 ACCAAACCGG ATACGGCAAA ATCCGACAGC GCGGTAAAAG AAGCGAAAAA
651 AGCCGACAAG GCTGAAAGCA AAAAACAGC CGAAAAAGAC CGTTCGGACG
701 GCAAAAAACA CGAAACGGCA CAAAAACCG ACAAGCGGA CAAGACCAAA
751 ACCGCGGAGA AGGAAAAATC CGGTAAAAA GCCGCCATTC AGGCAGGTTA
801 TGCCGAAAAA GAACGCGCCT TAAGCCTCCA GCGCAAAATG AAGCGCGCGG
851 GTATCGATTG GACCATCACC GAAATTATGA CCGACAACGG CAAAGTTTAC
901 CGCGTCAAT CAAGCAACTA TAAAACGCA AGGGATGCCG AACGCGATTT
951 GAACAAATTG CGCGTACACG GTATCGCCGG TCAGGTAACG AATGAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2556; ORF 746.a>:

```

a746.pep
1  MSENKQNEVL SGYEQLKRRN RRRLVTASCL VAASCILLAA ALSSGPAEQT
51  AGETSGVENK AAGAAQTPAL KSAADKPQDL AGEDKPSAAD SEISEPENVG
101 APLVLINDRL EDSNIKGLEA SEKLQQAETA KTAPEKQAKQ AAEKVPTAD
151 STDTVAVEKP KRTAETKPQK AERTAKAPK AKETKTAEKV ADKPKTAAEK
201 TKPDTAKSDS AVKEAKKADK AESKRTAEKD RSDGKKHETA QKTDKADKTK
251 TAEKEKSGKK AAIQAGYAEK ERALSQRKM KAAGIDSTIT EIMTDNGKVV
301 RVKSSNYKNA RDAERDLNKL RVHGIAGQVT NE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 746 shows 99.7% identity over a 332 aa overlap with a predicted ORF (ORF 746) from *N. meningitidis*:

a746/m746; 99.7% identity in 332 aa overlap

```

      10      20      30      40      50      60
a746.pep  MSENKQNEVL SGYEQLKRRNRRRLVTASCLVAASCILLAAALSSGPAEQTAGETSGVENK
m746      MSENKQNEVL SGYEQLKRRNRRRLVTASCLVAASCILLAAALSSGPAEQTAGETSGVENK
           10      20      30      40      50      60

```


1216

	70	80	90	100	110	120
a746.pep	AAGAAQTPALKSAADKPQDLAGEDKPSAADSEISEPENVGAPLVLINDRLEDSNIKGLEA					
m746	AAGAAQTPALKSAADKPQDLAGEDKPSAADSEISEPENVGAPLVLINERLEDSNIKGLEA					
	70	80	90	100	110	120
	130	140	150	160	170	180
a746.pep	SEKLQQAETAKTAPKQAKQRAAEKVPATADSTDVAVEKPKRTAETKPKQAERTAKAKPK					
m746	SEKLQQAETAKTAPKQAKQRAAEKVPATADSTDVAVEKPKRTAETKPKQAERTAKAKPK					
	130	140	150	160	170	180
	190	200	210	220	230	240
a746.pep	AKETKTAEKVADKPKTAAEKT KPD TAKSDSAVKEAKKADKAESKKTAEKDRSDGKKHETA					
m746	AKETKTAEKVADKPKTAAEKT KPD TAKSDSAVKEAKKADKAESKKTAEKDRSDGKKHETA					
	190	200	210	220	230	240
	250	260	270	280	290	300
a746.pep	QKTDKADKTKTAEKEKSGKKAIIQAGYAEKERALS LQRKMKAAAGIDSTITEIMTDNGKVY					
m746	QKTDKADKTKTAEKEKSGKKAIIQAGYAEKERALS LQRKMKAAAGIDSTITEIMTDNGKVY					
	250	260	270	280	290	300
	310	320	330			
a746.pep	RVKSSNYKNARDAERDLNKL RVHGIAGQVTNEX					
m746	RVKSSNYKNARDAERDLNKL RVHGIAGQVTNEX					
	310	320	330			

g747.seq not found yet

g747.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2557>:

m747.seq

```

1   CTGACCCCTT GGGCGGATGC ATATGCAGAT TTGCGCGGCA AAACCAAAGT
51  GATGACGACC CAGATGGGTG CTCCCGCGA TGTGAGCAAA AGCGCCAAAG
101 GTTGGAGTGT CGGTATCGGT CTGAATGTAG GCAAACAGTT GACCGACAGC
151 GTCGGTCTCG AGTTTGATCC ATACTACCGT CACAAAACAA TCTACAAACC
201 CCGTGAGATT GTCTTGGACG GTGACAAAAC CAAATGGGC CGCTCCAAAT
251 CCAACGAGTA CGGCTTCCGC GTAGCCGCAA CGTTCTATAG TCAATTAAAA
301 TCAAAATAG

```

This corresponds to the amino acid sequence <SEQ ID 2558; ORF 747>:

m747.pep

```

1   LTPWADAYAD LRGKTKVMTT QMGASRDVSK SAKGWSVGIG LNVGKQLTDS
51  VGLEFDPYYR HKTIIKPREI VLDGDKTKMG RSKSNEYGFR VAATFYSQLK
101 SK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2559>:

a747.seq

```

1   CTAACCCCTT GGGCGGATGC ATATGCAGAT TTGCGCGGCA AAACCAAAGT
51  GATGACGACC CAGATGTGTG CTCCCGCGA TGTGAGCAAA AGCGCCAAAG
101 GTTGGAGTGT CGGTATCGGT CTGAATGTAG GCAAACAGTT GACCGACAGC
151 GTCGGTCTCG AGTTTGATCC ATACTACCGT CACAAAACAA TCTGCAAACC
201 CCGTGAGATT GTTTTGGACG GCGACAAAAC CAAATGGGC CGCTCCAAAT
251 CCAACGAGTA CGGCTTCCGC GTAACCGCAA CGTTCTATAG TCAATTAAAA
301 TCAAAGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2560; ORF 747.a>:

a747.pep

```

1   LTPWADAYAD LRGKTKVMTT QMCASRDVSK SAKGWSVGIG LNVGKQLTDS
51  VGLEFDPYYR HKTICKPREI VLDGDKTKMG RSKSNEYGFR VTATFYSQLK
101 SK*

```

Computer analysis of this amino acid sequence gave the following results:

1217

Homology with a predicted ORF from *N. meningitidis*

ORF 747 shows 97.1% identity over a 102 aa overlap with a predicted ORF (ORF 746) from *N. meningitidis*:

a747/m747 97.1% identity in 102 aa overlap

```

a747.pep      10      20      30      40      50      60
               LTPWADAYADLRGKTKVMTTQMCASRDVSKSAGWSVGIGLNVGKQLTDSVGLFDPYYR
               |||||
m747          10      20      30      40      50      60
               LTPWADAYADLRGKTKVMTTQMGASRDVSKSAGWSVGIGLNVGKQLTDSVGLFDPYYR
               |||||

a747.pep      70      80      90     100
               HKTICKPREIVLDGDKTKMGRSKSNEYGFRVTATFYSQLKSKX
               |||||
m747          70      80      90     100
               HKTIIKPREIVLDGDKTKMGRSKSNEYGFRVAATFYSQLKSKX
               |||||

```

a747/m80195

gi|150271 (M80195) outer membrane protein [*Neisseria meningitidis*] Length = 272

Score = 59.3 bits (141), Expect = 6e-09

Identities = 29/99 (29%), Positives = 51/99 (51%), Gaps = 4/99 (4%)

Query: 1 LTPWADAYADLRGKTKVNTTQMCASRDVSKSAGWSVGIGLNVGKQLTDSVGLFDPYYR 60
 + PW++ DL + K+ T +D+++ GW G+G N+GK+L +S +E P+Y+
 Sbjct: 174 INPWSEVKFDLNSRYKLNTGVNLKKDINQKTNGWGFGLGANIGKKLGESASIEAGPFYK 233

Query: 61 HKTICKPREIVL---DGD-KTKMGRSKSNEYGFRVTATF 95
 +T + E + GD + ++ EYG RV F
 Sbjct: 234 QRTYKESGEFSVTTKSGDVSLTIPKTSIREYGLRVGIKF 272

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2561>:

```

g748.seq
1 ATGAGTCAAA ACCAACC CGC ACRACCGACC AAACGCAATC TGTTCAAAAC
51 CGCCCTTGCC GTCGCGCAA TCGGCGCAAT CGGAGGTAT TTGCGCGCCA
101 AAAAACAGGG CGAAACCGCC GAACGCACCG CGGAAAGCCA ACACGCGCCC
151 CAAGCCTATC CCTGCTACGG CGAACATCAG GCAGGTATCG TTACGCGCGC
201 GCAGCGCTTT TCCATTATGT GCGCCTTGA CGTACCGCG CAAAGTGCCA
251 AGCAGCTGGA AAACCTGTTC CGCACACTGA CGGCCCGCAT CGAGTTTCTC
301 ACCCAAGCGG GAGAATACCA AGACGGCGAC GACAAACTCC CGTCAGCCGG
351 CAGCGGCATT TTGGGTAAAG CCTCAACCC CGACGGATTG ACCGTTACCG
401 TGGGGTGGG CAGCAGCCTG TTTGACGGCC GGTTCGACT CAAAGACAAA
451 AAAACGGTTC ATTTGCAGGA AATGCGCGAC TTCCCAACG ATAAGCTGCA
501 AAAAAGCTGG TCGGACGGCG ATTTGAGCCT GCAAACTGCG GCCTTCACCC
551 CCGAAACCTG CCAAACCGCC CTGCGCGACA TCATCAAACA CACCGCCCAA
601 ACCGCCGTCA TCCGCTGGAG TATCGACGGG TGGCAGCTA AATCCGAACC
651 CGGCGCGATG GCGGCGCGCA ACCTGTTGGG CTTCCGAGAC GGCACGGGCA
701 ACCCAAGGT TTCCGATCCC AAAACGCGCG ACGAGGTTT ATGACGGGG
751 GTGGCCGCCA ACAGCCTCGA CGAACCGGAG TGGCGGAAA ACGGCAGCTA
801 TCAGGCAGTC CGCCTTATCC GCCGCTTGT CGAGTTTGG GACAGGACGC
851 CGCTTCAAGA GCAAACCGAC ATTTTCGGGC GCGGAAAATA CAGCGGGGCG
901 CCGATGGACG GCAAAAAGA AGCCGACCAA CCGGATTTCG CCAAAGACCC
951 CGAGGGTGAT ATCAGCCCA AAGACAGCCA TATGCGCCTG GCGAATCCGC
1001 GCGATCCCGA ATTCCTCAA AAACACTGCC TCTTCGCGC CGCCTACAGC
1051 TATTCTCGCG GACCGCCTC AAGCGGACAG CTTGATGTCG GGCTGGTGTT
1101 CGTCTGTAT CAGGCAATC TTGCCGACGG TTTATCTTC GTGCAAAACC
1151 TCCTCAACGG CGAACCGCTG GAAGAATACA TCAGCCCTT CGGCGGCGGC
1201 TATTCTTTCG TCTTGCCCGG CGTGGGAAA GCGGATTCT TGGGACAAGG
1251 GCTCCGGGG GTATAA

```

This corresponds to the amino acid sequence <SEQ ID 2562; ORF 748.ng>:

```

g748.pep
1 MSQNQPAQPT KRNLFKTALA VGAIGAIGGY FGGKKQGETA ERTAESQHSP
51 QAYPCYGEHQ AGIVTPRQAF SIMCAIDVTA QSAKQLENLF RLTARIEFL
101 TQGEYQDGD DKLPSAGSGI LGKAFNPDGL TVTVGVGSSL FDGRFGLKDK
151 KTVHLQEMRD FPNDKLQKSW CDGDLSLQIC AFTPETCQTA LRDIKHQAQ
201 TAVIRWSIDG WQPKSEPGAM AARNLLGFRD GTGNPKVSDP KTADEVLWIG
251 VAANSLDEPE WAKNGSYQAV RLIRRFVEFW DRTPLOEQTD IFGRRKYSQA
301 PMDSKKKADQ PDFAKDPEGD ITPKDSHMRL ANPRDPEFLK KHCLFRRAYS
351 YSRGPASSGQ LDVGLVFVCY QANLADGFIF VQNLNGEPL EEYISPFGGG

```

m748.seq

1	ATGAGCAAAA	AACAACCCGC	ACAACCGACC	AGGCGCACTC	TTTTTAAAAAC
51	CGGCGATCGCA	CGCGAGGACG	TGCGGCGCAAT	CGGAGGTTAT	CTCGGCGGCA
101	AAAAACAGCGA	GCGAAACGCC	GAACGCACCG	CCGAAAGCCA	ACACTCGGCC
151	CAGGCTATC	CCTGCTACGG	CGAACATCAG	CAGGCATCG	TTACGCGCGA
201	GCAGGCGTTT	TGCATTATGT	GGCGCTTCGA	CGTAACCGCG	CAAAGTGCCG
251	AGCAGCTGGA	AAACCTGTTC	CGCACGCTGA	CCGCGCCGAT	CGAGTTTCTC
301	ACCCAAGGCG	CGGAATACCA	AGACGGCGAC	GACAAACTTC	CGCCAGCCGG
351	CAGCGGCATT	TTGGGCAAA	CGTTCAACCC	CGACGGGTG	ACCGTTACCG
401	TGGGGGTGGG	CAGCAGCCCT	TTTGACGCC	GGTTCGGACT	CAARGACAAA
451	AAACCGATTC	ATTTCAGGA	AATGCGCGAC	TTTCCAACG	ATAAGCTGCA
501	AAAAAGCTGG	TGCGAGCGCG	ATTTGAGCCT	GCAAACTGT	GCCTTCACCC
551	CGGAACAGCT	CCAAGCGCCG	CTGCGCGACA	TCATCAAACA	CACCGTCCAA
601	ACCGCGGTTA	TCCGTTGGAG	TATCAGCGG	TGCGAGCCA	AATCCGAACC
651	CGGCGCGATG	GCGGCGCGCA	ACCTGTTGGG	CTTCAGGGAC	GGCACGGGCA
701	ACCCCAAAGT	TTCGATCCCG	AAAATGCGC	ACGAGGTTTT	GTGACCGGGG
751	GTGGCGCGCA	ACAGCTCCGA	CGAACCGGAG	TGGGCGAAAA	ACGGCAGCTA
801	TCAGGCACTC	CGCCTTATCC	GGCATTGTG	CGAGTTTTGG	GACGAGGACG
851	CGCTTCAAGA	GCAAAACCGA	ATTTTCGGGG	GGCGCAAAAT	CAGCGGTCCG
901	CGAGTGGACG	GCAAAAAAGA	AGCCGACCRA	CCGGATTTTTG	CCAAAGACCC
951	CGAGGTGTAT	ATCAGCGCCA	AAGACAGCCA	TATACGCTCG	CGGAATCCCG
1001	GCATTCGCGA	ATTCTCAA	AAACACCGAC	TCTTCGCGCG	CGCCTACAGC
1051	TATTCGCGCG	GACTCGCCTC	AAGCGGACAG	CTTGATGTGC	GGCTGTGGTT
1101	GTCTGCTAT	CAGGCAAAAC	TGCGCGAGG	ATTCACTTTC	GTGCAAAAC
1151	TCCTCAACGG	CGAACCGCTG	GAAGAATACA	TCAGCCCCCT	CGGCGGCGGC
1201	TATTTCTTCG	TCTTCGCGCG	CGTGGA AAAA	GGCGGCTTTT	TGGGGCAAGG
1251	GCTGCTGGCG	GTATA			

m748 . pep

1	MSKKQPAQPT	RRTLFKTAIA	AGAVGAIGGY	LGGKKOGETA	ERTAESQHSP
51	QAYPCYGEHG	AGIVTPQQAF	SIMCAFDVTA	QSAKQLENLF	RTLTAIRIEFL
101	TGGEGYQDGD	DLKLPAGSGI	LKGANFNDLQ	TSVTGVGSSL	FDGRFGLKDK
151	KPIHLQEMRD	FSNDKLQKSW	CDGDLSLQIC	AFTPETCQAA	LDRIIKHTVY
201	TAIVIRWISD	WQKSEPGAM	AARNLLGFWD	GTGNPKVSDT	KTADEVLTWG
251	VAANSLEDEP	WAKNGSYQAV	RLRIHEVFPR	DRTPLEQEDP	IFGRRAVSYGA
301	PMDGKKEADQ	PDFAKDPEGD	ITPKDSHIRL	ANPRDPEFLK	KHRLFRAYRS
351	YSRGLASSGG	LDVLGVFVCY	QANLADGGIF	VQNLNNGEPL	EYISPFSGGG
401	YFFRLPGVGE	GGFLGOGLLG	V*		

ORF 748 shows 95.0% identity over a 421 aa overlap with a predicted ORF (ORF 748) from *N. gonorrhoeae*

m748/g748 95.0% identity in 421 aa overlap

	10	20	30	40	50	60
m748.pep	MSKKQPAQPTRRTLFKTAIAAGAVGAIGGYLGGKKQGETAERTAESQHSPOAYPCYGEHQ					
g748	MSQNQPAQPTKRNLFKTALAVGAIGAIGGYFGGKKQGETAERTAESQHSPOAYPCYGEHQ					
	10	20	30	40	50	60
m748.pep	AGIVTPQQAFSIMCAFDVTAQSAKQLENLFRILTARIEFLTQGGEYQDGGDKLPAGSGI					
g748	AGIVTPROQAFSIMCAFDVTAQSAKQLENLFRILTARIEFLTQGGEYQDGGDKLPSAGSGI					
	70	80	90	100	110	120
m748.pep	AGIVTPQQAFSIMCAFDVTAQSAKQLENLFRILTARIEFLTQGGEYQDGGDKLPAGSGI					
g748	AGIVTPROQAFSIMCAFDVTAQSAKQLENLFRILTARIEFLTQGGEYQDGGDKLPSAGSGI					
	70	80	90	100	110	120
m748.pep	LGKAFNPDLGLTVTVGVGSSSLFDGRFGLKDKKPIHLQEMRDFSNDKLQKSWCDGDSLQIC					
g748	LGKAFNPDLGLTVTVGVGSSSLFDGRFGLKDKKTVHLQEMRDFPNDKLQKSWCDGDSLQIC					
	130	140	150	160	170	180
m748.pep	LGKAFNPDLGLTVTVGVGSSSLFDGRFGLKDKKPIHLQEMRDFSNDKLQKSWCDGDSLQIC					
g748	LGKAFNPDLGLTVTVGVGSSSLFDGRFGLKDKKTVHLQEMRDFPNDKLQKSWCDGDSLQIC					
	130	140	150	160	170	180
m748.pep	AFTPETCQAALRDIKIHTVQTAVIRWSIDGWQPKSEPGAMAARNLLGFRDGTGNPKVSD					
g748	AFTPETCQAALRDIKIHTVQTAVIRWSIDGWQPKSEPGAMAARNLLGFRDGTGNPKVSD					
	190	200	210	220	230	240
m748.pep	AFTPETCQAALRDIKIHTVQTAVIRWSIDGWQPKSEPGAMAARNLLGFRDGTGNPKVSD					
g748	AFTPETCQAALRDIKIHTVQTAVIRWSIDGWQPKSEPGAMAARNLLGFRDGTGNPKVSD					

	190	200	210	220	230	240
g748	AFTPETCQTALRDI	IKHTAQTA	VIKWSIDGWQPK	SEPGAMAARNLL	GGFRDGTGNPK	VSDP
m748.pep	KTAD	EVLWTGVA	ANSLDEPEWAK	NGSYQAVRLIR	HFEVFWDRTP	LQEQETDIFGRK
g748	KTAD	EVLWTGVA	ANSLDEPEWAK	NGSYQAVRLIR	HFEVFWDRTP	LQEQETDIFGRK
m748.pep	PMDGKKEADQ	PDFAKDP	EGDITPKDSHIR	LANPRDPEFLK	KKHRLFRRAYS	YSRGLASSGQ
g748	PMDGKKEADQ	PDFAKDP	EGDITPKDSHMR	LANPRDPEFLK	KKHCLFRRAYS	YSRGPASSGQ
m748.pep	LDVGLVFV	VCYQANLADG	FIFVQNLLNGE	PLEEYISPF	GGGYFFVLP	PGVEKG
g748	LDVGLVFV	VCYQANLADG	FIFVQNLLNGE	PLEEYISPF	GGGYFFVLP	PGVGKG
m748.pep	VX					
g748	VX					

```

a748.seq
1      ATGAGCAAAA   ACCAACCCGC   ACAACCGACC   AGGCGCACTC   TTTTAAAAAC
51     CGCGATTCGCA   GCTGGAGCAG   TCGGCGCAAT   CGGAGGTTAT   CTCGGCGGCA
101    AAAAACGGGG   CGAAACCGCC   GAACGCACCG   CCGAAAGCCA   ACACTCGCCC
151    CAAGCGCTATC   CTCGTACGG   CGACATCTGA   CGAGCGATCG   TTACGCCGCA
201    GCAGGCGT*TT  TCGATTATGT   GCGCCTTCAG   CGTAAACGGC   CAAAGTGCCA
251    AGCAGCTGGA   AAACCTGTT   CGCACGCTGA   CCGCCCGCAT   CGAGTTTCTC
301    ACCCAAGGCG   GCGAAATACA   AGACGGCCAG   GACAACAT*TC  CGCCAGCCGG
351    CAGCGGCAT   TTGGGCAAA   CCTTCAACCC   CGACGGGGTT   ACCGTTACCG
401    TGGGGGTGGG   CAGCAGCCTG   TTTGACGGCC   GGTTCGGACT   CAAAGACAAA
451    AAACCGATT   ATTTGCAGGA   AATTCGGGCT   TTCTCCAACG   ATAAGCTGCA
501    AAAAACGCTGG  TCGCAGCGGC   AATTGAGCATT  GCAAA*TCGT   GCCTT*ACCC
551    CCGAAACCTG   CCAAGCCGCG   CTGGCGGACA   TCATCAAACA   CACCGTCCAA
601    ACCCGCGTTA   TCCGCTGGAG   TATCGAGTGG   TGGCAGCCTA   AATCCGAACC
651    CGGCGCGAT   CGGCGCGCA   ACCTGTTGGG   CTTCGCCGCA   GGCACGGGCA
701    ACCCCAAGT   TTCCGACCCC   AAAACTGCCG   ACGAGGTTTT   GTGGACGGGG
751    GTGGCGCGCA   ACAGCCTCGA   CGCAACCGGAG  TGGGCGAAAA   ACGGCAGCTA
801    TCAGGCAGTC   GCCTTATCC   GCGCACTTGT   TGA*TTTGG   GACAGGACGC
851    CGCTTCAAGA   GCAAAACGAC  ATTTTCGGGC   GGCCAAATA   CAGCGGCGCG
901    CCGATGGACG   GCAAAAAGA   AGCGGACCA   CCGGATTTTG   CCAAGAGCCC
951    CGAGGGGAAT   ACCACGGCCA  AAGACGCCA   TATACGCTGC  GCGAATCCGC
1001   GCGATCCCGA   GTTCCTTAA   AAACACCGGC   TCTTCGCGCG  CGCCTACAGC
1051   TATTTCGCGC   GACTCGCCTC  AAGCGGACAG  CTTGATGTCG   GGCTGTG*TT
1101   CGCTCTGCTAT  CAGGCAAAACC  TTGCGCAGCG  ATTCACTCTC  GTGCAAAACC
1151   TCCTCAAGCG   CGAAAGCCTG  GAAGAATACA   TCAGCCCTT   CGGCGGCGGC
1201   TATTTCTTCG   TCTTGCCTCG  CGTGGAAAAA   GGC*GGCTTTT  TGGGGCAAGG
1251   GCTGCTCGCC   GTATAA

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a748.pep
1  MSKNQPAQPT  RRTLFKTAIA  AGAVGAIGGY  LGGKKRGETA  ERTAESQHP
51  QAYPCYGEHQ  AKIVTPQQA  SIMCAFDVTA  QSAQLENLF  RDLTARIEFL
101  TQGGEYQDGD  DLPPAGSGI  LGKAFNDPGL  TVTVGVGSSL  PDGFRGLKDK
151  KPIHLQEMRD  FSNDKLQKSW  CDGDLSLQIC  AFTPETCQAA  LRDIHKHTVQ
201  TAVIRWSIDG  WQKPSSEGM  AARNLLGFRC  DTGNPKVSD  KTADEVLTNG
251  VAANSLEDEP  WAKNGSYQAV  RLRIHFVEFW  DRTPLEQETD  IFGRRKYSGA
301  PMDGKKEADQ  PDFAKDPEGN  TTPKDSHRL  ANPRDPEFLK  KHRLFRFRAYS
351  YSRGLASSGQ  LDVGLVFVCY  QANLADGFIF  VQNLNLGEPL  E EYISPFGGG
401  YFFVLPGVEK  GGFLGGGLLG  V*

```

Computer analysis of this amino acid sequence gave the following results:

1220

Homology with a predicted ORF from *N. meningitidis*

ORF 748 shows 99.0% identity over a 421 aa overlap with a predicted ORF (ORF 748) from *N. meningitidis*:

a748/m748 99.0% identity in 421 aa overlap

	10	20	30	40	50	60
a748.pep	MSKNQPAQPTRRTLFKTAIAAGAVGAIGGYLGGKKRGETAERTAESQHSPPQAYPCYGEHQ					
m748	MSKKQPAQPTRRTLFKTAIAAGAVGAIGGYLGGKKQGETAERTAESQHSPPQAYPCYGEHQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
a748.pep	AGIVTPQQAFSIMCAFDVTAQSAKQLENLFRTLTARIEFLTQGGGEYQDGGDKLPPAGSGI					
m748	AGIVTPQQAFSIMCAFDVTAQSAKQLENLFRTLTARIEFLTQGGGEYQDGGDKLPPAGSGI					
	70	80	90	100	110	120
	130	140	150	160	170	180
a748.pep	LGKAFNPDLTVTVGVGSSSLFDGRFGLKDKKPIHLQEMRDFSNDKLQKSWCDGDLQLQIC					
m748	LGKAFNPDLTVTVGVGSSSLFDGRFGLKDKKPIHLQEMRDFSNDKLQKSWCDGDLQLQIC					
	130	140	150	160	170	180
	190	200	210	220	230	240
a748.pep	AFTPETCQAALRDI IKHTVQTAVIRWSIDGWQPKSEPGAMAARNLLGFRDGTGNPKVSDP					
m748	AFTPETCQAALRDI IKHTVQTAVIRWSIDGWQPKSEPGAMAARNLLGFRDGTGNPKVSDP					
	190	200	210	220	230	240
	250	260	270	280	290	300
a748.pep	KTADEVLTWGVAANSLDEPEWAKNGSYQAVRLIRHFVEFWDRTPLEQETDIFGRRKYSGA					
m748	KTADEVLTWGVAANSLDEPEWAKNGSYQAVRLIRHFVEFWDRTPLEQETDIFGRRKYSGA					
	250	260	270	280	290	300
	310	320	330	340	350	360
a748.pep	PMDGKKEADQPDFAKDPEGNTTPKDSHIRLANPRDPEFLKKHRLFRRAYSYSRGLASSGQ					
m748	PMDGKKEADQPDFAKDPEGNTTPKDSHIRLANPRDPEFLKKHRLFRRAYSYSRGLASSGQ					
	310	320	330	340	350	360
	370	380	390	400	410	420
a748.pep	LDVGLVFVCYQANLADGFI FVQNLNGEPL E EYISPFGGGYFFVLP GVEKGGFLGQGLLG					
m748	LDVGLVFVCYQANLADGFI FVQNLNGEPL E EYISPFGGGYFFVLP GVEKGGFLGQGLLG					
	370	380	390	400	410	420
a748.pep	VX					
m748	VX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2567>:

g749.seq

1	ATGAGAAAAT	TCAATTGAC	CGCATTGTCC	GTGATGCTTG	CCTTGGGTTT
51	GACCGCGTGC	CAGCCGCCGG	AGGCGGAGAA	AGCCGCGCCG	GCCGCGTCCG
101	GTGAGACCCA	ATCCGCCAAC	GAAGGCGGTT	CGGTCCGTAT	CGCCGTCAAC
151	GACAATGCCT	GCGAACCGAT	GAATCTGACC	GTGCCGAGCG	GACAGGTGTG
201	GTTC AATATT	AAAAACAACA	GCGGCCGCAA	GCTCGAATGG	GAATCCTGA
251	AGGGCGTGAT	GGTGGTGGAC	GAACGCGAAA	ATATCGCCCC	GGGCGCTTTC
301	GACAAAATGA	CCGTAAccct	GCTGCCGGGC	GAATACGAAA	TGACCTGCGG
351	CCTTTTGACC	AATCCGCGCG	GCAAGCTGGT	GGTAGCCGAC	AGCGGCTTTA
401	AAGACACCGC	CAACGAAGCG	GATTTGGAAA	AACTGCCCCA	ACCGCTCGCC
451	GACTATAAAG	CCTACCTTCA	AGCGGAGGTT	AAAGAGCTGG	CGGCGAAAAC
501	CAAAACCTTT	ACCGAAGCCG	TCAAAGCAGG	CGACATTGAA	AAGGCGAAT
551	CCCTGTTTGC	CGCCACCCGC	GTCCATTACG	AACGCATCGA	ACCGATTGCC
601	GAGCTTTTCA	GCGAACTCGA	CCCCGTCA TC	GATGCGTGTG	AAGACGACTT
651	CAAAGACGGT	GCGAAAGATG	CCGGGTTTAC	CGGCTTCCAC	CGTATCGAAC
701	ACGCCCTTTG	GGTGGAAAAA	GACGTATCCG	GCGTGAAGGA	AACCGCGGCC
751	AAACTGATGA	CCGATGTCGA	AGCCCTGCAA	AAAGAAATCG	ACGCATTGGC

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801 GttccctCCG GGCAAAGTGG TCGCGGCGC GTCCGAAGT ATTGAAGAAG
851 CGCGGGGCG TAAATCAGC GCGGAAGAAG ACCgttaCAG CCACACCGAT
901 TTGAGCGACT TCCAAGCTAA TCGGACGGA TCTAAAAAA TCCTCGATT
951 GTTCCGTCCG TTGATTGAGG CAAAAACAA AGCCTTGTG GAAAAACCG
1001 ATACCAACTT CAAACAGGTC AACGAAATC TGGCGAAATA CCGCACCAA
1051 GACGGTTTTG AAACCTACGA CAAGCTGAGC GAAGCCGACC GCAAAGCATT
1101 ACAGGCTCCT ATTAACGCGC TTGCCGAAGA CCTTGCCCAA CTTCGCGGCA
1151 TACTCGGCTT GAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2568; ORF 749.ng>:

```

g749.pep
1 MRKFNLALS VMLALGLTAC QPPEAEKAAP AASGETQSAN EGGSVGIQAVN
51 DNACEPMNLT VPSGQVVFNI KNNSGRKLEW EILKGMVVD ERENIAPLS
101 DKMTVTLPLG EYEMTCGLLT NPRGKLVDAD SGFKDTANEA DLEKLQPLA
151 DYKAYVQGEV KELAAKTKTF TEAVKAGDIE KAKSLFAATR VHYERIEPIA
201 ELFSELDPMI DACEDDFKDG AKDAGFTGFH RIEHALWVEK DVSGVKETAA
251 KLMTDVEALQ KEIDALAFPP GKVVGGASEL IEEAAGSKIS GEEDRYSHTD
301 LSDFQANADG SKKIVDLFRP LIEAKNKALL EKTDTNFKQV NEILAKYRTK
351 DGFETYDKLS EADRKALQAP INALAEDLAQ LRGLGLK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2569>:

```

m749.seq
1 ATGAGAAAT TCAATTGAC CGCATTGTC GTGATGCTT CTTAGETTT
51 GACCGCGTGC CAGCCGCCG AGCGGAGAA AGCTGCGCC GCAGCGTCCG
101 GTGAGGCGCA AACCGCCAAC GAGGCGGTT CGGTCAATAT CGCCGTCAAC
151 GACAAATGCTT GCGAACCGAT GGAATGACC GTGCCGAGC GACAGGTGT
201 GTTCAATATT AAAACAACA GCGCCGCAA GCTCGAATG GAAATCCTGA
251 AAGGCGTGTAT GGTGGTGGAC GAGCGCGAA ACATCGCCC CGGACTTTCC
301 GATAAAATGA CCGTCACCT GTTCCCGGC GAATACGAAA TGACTTCCG
351 TCTTTTGACC AATCCGCGC GCAAGCTGT GGTAAACCG AGCGGCTTTA
401 AAGACACCGC CAACGAAGCG GATTTGAAA AACTGTCCA ACCGCTCGC
451 GACTATAAAG CCTACGTCA AGCGAGGTT AAAGAGCTG TGGCGAAAC
501 CAAAACCTTT ACCGAAGCG TCAAGCAGG CGACATTGA AAGGCGAAAT
551 CCCTGTTTGC CGACACCCG GTCCATTAC AACGCATCG ACCGATTGC
601 GAGCTTTTCA GCGAACTCG CCCGTCATC GATGCGCGT AAGACGACT
651 CAAAGACGGC GCGAAAGAT CCGGATTTT CGGCTTTCG CGTATCGAAT
701 ACGCCCTTTG GGTGGAATA GACGTGTCC GCGTGAAGA AATTGCAGC
751 AAAGTATGA CCGATGTCG AGCCCTGCA AAAGAAATC ACGCATTGC
801 GTTTCCTCCG GGCAAGGTG TCGCGGCGC GTCCGAATG ATTGAAGAAG
851 TGGCGGGCAG TAAATCAGC GCGGAAGAAG ACCGTACAG CCACACGAT
901 TTGAGCGACT TCCAAGCAA TGTGGACGA TCTAAAAAA TCCTCGATT
951 GTTCCGTCG CTGATCGAG CAAAAACAA AGCCTTGTG GAAAAACCG
1001 ATACCAACTT CAAACAGGTC AACGAAATC TGGCGAAATA CCGGACTAAA
1051 GACGGTTTTG AAACCTACGA CAAGCTGGC GAAGCCGACC GCAAAGCGT
1101 ACAGGCTCCT ATTAACGCGC TTGCCGAAGA CCTTGCCCAA CTTCGCGGCA
1151 TACTCGGCTT GAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2570; ORF 749>:

```

m749.pep
1 MRKFNLALS VMLALGLTAC QPPEAEKAAP AASGEAQTAN EGGSVSIQAVN
51 DNACEPMELT VPSGQVVFNI KNNSGRKLEW EILKGMVVD ERENIAPLS
101 DKMTVTLPLG EYEMTCGLLT NPRGKLVDAD SGFKDTANEA DLEKLQPLA
151 DYKAYVQGEV KELVAKTKTF TEAVKAGDIE KAKSLFADTR VHYERIEPIA
201 ELFSELDPMI DAREDDFKDG AKDAGFTGFH RIEYALWVEK DVSGVKEIAA
251 KLMTDVEALQ KEIDALAFPP GKVVGGASEL IEEVAGSKIS GEEDRYSHTD
301 LSDFQANVDG SKKIVDLFRP LIEAKNKALL EKTDTNFKQV NEILAKYRTK
351 DGFETYDKLG EADRKALQAS INALAEDLAQ LRGLGLK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 749 shows 96.1% identity over a 388 aa overlap with a predicted ORF (ORF 749) from *N. gonorrhoeae*

```

m749/g749 96.1% identity in 388 aa overlap

          10      20      30      40      50      60
m749.pep MRKFNLALS VMLALGLTACQPPEAEKAAPASGEAQTANEGGSVSIQAVNDNACEPMELT
          |||||
g749      MRKFNLALS VMLALGLTACQPPEAEKAAPASGETQSANEGGSVGIQAVNDNACEPMNLT
          10      20      30      40      50      60

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	70	80	90	100	110	120
m749.pep	VPSGQVVFNIKNNSGRKLEWEILKGMVVDERENIAPGLSDKMTVTLLPGEYENTCGLLT					
g749	VPSGQVVFNIKNNSGRKLEWEILKGMVVDERENIAPGLSDKMTVTLLPGEYENTCGLLT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m749.pep	NPRGKLVVTD SGFKDTANEADLEKLSQPLADYKAYVQGEVKELVAKTKTFTEAVKAGDIE					
g749	NPRGKLVVADSGFKDTANEADLEKLPQPLADYKAYVQGEVKELAAKTKTFTEAVKAGDIE					
	130	140	150	160	170	180
	190	200	210	220	230	240
m749.pep	KAKSLFADTRVHYERIEPIAELFSELDPVIDAREDDFKDGAAGFTGFHRIEYALWVEK					
g749	KAKSLFAATRVHYERIEPIAELFSELDPVIDACEDDFKDGAAGFTGFHRIEHALWVEK					
	190	200	210	220	230	240
	250	260	270	280	290	300
m749.pep	DVSGVKEIAAKLMTDVEALQKEIDALAFPPGKVVGGASELIEEVAGSKISGEEDRYSHTD					
g749	DVSGVKETAAKLMTDVEALQKEIDALAFPPGKVVGGASELIEEAAGSKISGEEDRYSHTD					
	250	260	270	280	290	300
	310	320	330	340	350	360
m749.pep	LSDFQANVDGSKKIVDLFRPLIEAKNKALLEKTDNFKQVNEILAKYRTKDGFTYDKLG					
g749	LSDFQANADGSKKIVDLFRPLIEAKNKALLEKTDNFKOVNEILAKYRTKDGFTYDKLS					
	310	320	330	340	350	360
	370	380	389			
m749.pep	EADRKALQASINALAEDLAQLRGILGLKX					
g749	EADRKALQAPINALAEDLAQLRGILGLKX					
	370	380				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2571>:

a749.seq

```

1  ATGAGAAAAT TCAATTGAC CGCATTGTCC GTGATGCTTG CCTTAGGTTT
51  GACCGCGTGC CAGCCGCGCG AGGCGGAGAA AGCTGCGCCG GCACGCTCCG
101 GTGAGGCGCA AACCGCCAAC GAGGGCGGTT CGGTCAGTAT CGCCGTC AAC
151 GACAATGCCT CGCAACCGAT SGAAGTACC GTGCCGAGCG GACAGGTTGT
201 GTTCAATATT AAAAACAACA GCGGCCGCAA GCTCGAATGG GAAATCCTGA
251 AAGGCGTGAT GGTGGTGGAC GAGCGCGAAA ACATCGCCCC CGGACTTTCC
301 GATAAAATGA CCGTCACCCCT GTTGCCGCGG GAATACGAAA TGACTTGGCG
351 TCTTTTGACC AATCCGCGCG GCAAGCTGGT GGTAAACGAC AGCGGCTTTA
401 AAGACACCGC CAACGAAGCG GATTGGAAA AACTGTCCCA ACCGCTCGCC
451 GACTATAAAG CCTATGTTC AAGCGAAGTC AAAGAGCTGG TGGCGAAAC
501 CAAACCTTT ACCGAAGCCC TCAAAGCAGG CGACATTGAA AAGGCGAAAT
551 CCCTGTTTGC GCACACCCGC GTCCATACG AACGCATCGA ACCGATTGCC
601 GAGCTTTTCA GCGAACTCGA CCCCGTCATC GATGCGCGTG AAGACGACTT
651 CAAAGACGGC GCGAAAGATG CCGGATTAC CGGCTTCCAC CGTATCGAAT
701 ACGCCCTTTG GGTGGAAAAA GACGTGTCCG GCGTGAAGGA AATTGCAGCG
751 AAAGTATGTA CCGATGTGTA AGCCCTGCAA AAAGAAATCG ACGCATTGGC
801 GTTTCCTCCG GCGAAGGTGG TCGGCGGGCG GTCCGAAGTG ATTGAAGAAG
851 TGGCGGGCAG TAAATCAGC GCGGAAGAAG ACCGGTACAG CCACACCGAT
901 TTGAGCGACT TCCAAGCAA TGTGGACGGA TCGAAAAAAA TCGTCGATTT
951 GTTCCGTCCG TTGATCGAGA CCAAAAACAA AGCCTTGTG GAAAAACCG
1001 ATACCAACTT CAAACAGGTC AACGAAATTC TGGCGAAATA CCGGACTAAA
1051 GACGGTTTGT AAACCTACGA CAAGCTGGGC GAAGCCGACC GCAAAGCGTT
1101 ACAGGCCTCT ATTAACGCGC TTGCCGAAGA CCTTGCCCAA CTTCGCGGCA
1151 TACTCGGCTT GAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2572; ORF 749.a>:

a749.pep

```

1  MRKENLTALS VMLALGLTAC QPPEAEKAAP AASGEAQTAN EGGSVSIAVN
51  DNACEPMELT VPSGQVVFNI KNNSGRKLEW EILKGMVVVD ERENIAPGLS
101 DKMTVTLLPG EYEMTCGLLT NPRGKLVVTD SGFKDTANEAD LEKLSQPLA
151 DYKAYVQGEV KELVAKTKTF TEAVKAGDIE KAKSLFADTR VHYERIEPIA
201 ELFSELDPVI DAREDDFKDG AKDAGFTGFH RIEYALWVEK DVSGVKEIAA
251 KLMTDVEALQ KEIDALAFPP GKVVGGASEL IEEVAGSKIS GEEDRYSHTD

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301 LSDFQANVDG SKKIVDLFRP LIETKNKALL EKTDTNFKQV NEILAKYRTK
 351 DGFETYOKLG EADRKALQAS INALAEDLAQ LRGILGLK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N meningitidis*

ORF 749 shows 99.7% identity over a 388 aa overlap with a predicted ORF (ORF 749) from *N. meningitidis*:

a749/m749 99.7% identity in 388 aa overlap

	10	20	30	40	50	60
a749.pep	MRKFNLTALS	VMLALGLTACQPPEAEKAA	PAASGEAQTANEGGSVSI	AVNDNACEPMELT		
m749	MRKFNLTALS	VMLALGLTACQPPEAEKAA	PAASGEAQTANEGGSVSI	AVNDNACEPMELT		
	70	80	90	100	110	120
a749.pep	VPSGQVVFNI	KNNSGRKLEWEILKGM	VVDERENIAPGLSDKMT	VTILLPGEYEMTCGLLT		
m749	VPSGQVVFNI	KNNSGRKLEWEILKGM	VVDERENIAPGLSDKMT	VTILLPGEYEMTCGLLT		
	130	140	150	160	170	180
a749.pep	NPRGKLVVTD	SGFKDTANEADLEKLSQ	PLADYKAYVQGEVKEL	VAKTKTFTTEAVKAGDIE		
m749	NPRGKLVVTD	SGFKDTANEADLEKLSQ	PLADYKAYVQGEVKEL	VAKTKTFTTEAVKAGDIE		
	190	200	210	220	230	240
a749.pep	KAKSLFADTR	VHYERIEPIAELFSELD	PVIDAREDDFKDGAKDAG	FTGFHRIEYALWVEK		
m749	KAKSLFADTR	VHYERIEPIAELFSELD	PVIDAREDDFKDGAKDAG	FTGFHRIEYALWVEK		
	250	260	270	280	290	300
a749.pep	DVSGVKELIA	AKLMTDVEALQKEIDAL	AFPPGKVVGASELIEE	VAGSKISGEEDRYSHTD		
m749	DVSGVKELIA	AKLMTDVEALQKEIDAL	AFPPGKVVGASELIEE	VAGSKISGEEDRYSHTD		
	310	320	330	340	350	360
a749.pep	LSDFQANVDG	SKKIVDLFRPLIETKNK	ALLEKTDITNFKQVNEI	LAKYRTKDGFTYDKLG		
m749	LSDFQANVDG	SKKIVDLFRPLIETKNK	ALLEKTDITNFKQVNEI	LAKYRTKDGFTYDKLG		
	370	380	389			
a749.pep	EADRKALQAS	INALAEDLAQLRGILGLKX				
m749	EADRKALQAS	INALAEDLAQLRGILGLKX				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2573>:

g750.seq

```

1  GTGAAACCGC GTTTTATTG GGCAGcctGC GCCGTCTGC CGGCCGCCCTG
51  TTCGCCCGAA CCTGCCCGCG AAAAAACTGT ATcgcCCGCA TCCCAAGCCG
101 CATCCACACC TGTCGCCACG CTGACCGTGC CGACCGCGCG GGGCGATGCC
151 GTTGTGCCGA AGAATCCCGA ACgcgtcgcc gtgtAcgaCt ggGCCGCCGTt
201 ggaTACGCTG ACCGAGCCGG GCGTGAATGT GGGCGCAACC ACCGCGCCGG
251 TGCGCGTGGA CTATTGCGAG CCTGCATTG ACAAGCGCGC AACGGTGGGG
301 ACGCTGTTTG AGCCCGATTG CGAATCCCTG CACCGCCACA ATCCGCAGTT
351 TGTCATTACC GCGCGGCCGG GTGCGGAAGC GTATGAACAG TTGGCGAAAA
401 ACGCGACCAC CATAGATTG ACGGTGGACA ACGGCAATAT CCGCACCAGC
451 GGCGAGAAGC AGATGGAGAC CCTGTCGCGG ATTTTCGGTA AGGAAGCGCG
501 CGTGGCGGAA TTGAATGCGC AGATTGACGC GCTGTTCCGC CAAAAGCGCG
551 AAGCCGCCAA AGGCAAAGGA CGCGGCTGG TGCTGTCGGT TACAGGCAAC
601 AAGGTGTCCG CCTTCGGCAC GCAATCGCGG TTGGCAAGTT GGATACACGG
651 CGACATCGGC CTGCCGCCCG TGGACGAATC TTACGCAAC GAAGGGCACG
701 GGCAGCCCGT TTCCTTCGAA TACATCAAAG AGAAAAACCC CGGCTGGATT
751 TTCATCATCG ACCGCACCGC CGCCATCGGG CAGGAAGGGC CGGCTGCCCT
```


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```

801 GGAAGTGTG GATAACGCGC TGGTATGCGG CACGAACGCT TGGAAAGCGCA
851 AGCAAATCAT CGTCATGCCT GCCGCGAACT ACATTGTGCG GGGCGGCGCG
901 CGGCAGTTGA TACAGGCGGC GGAACAGTTG AAGGCGGCGT TTGAAAGGCG
951 AGAACCCGTT GCGGCGCAGT AG

```

This corresponds to the amino acid sequence <SEQ ID 2574; ORF 750.ng>:

```

g750.pep
1  VKPRFYWAAC AVLPAACSPE PAAEKTVSAA SQAASTPVAT LTVPTARGDA
51  VVPKNPERVA VYDWAALDTL TEPGVNVGAT TAPVRVDYLO PAFDKAATVG
101 TLFEPDCESL HRHNPQFVIT GGPGEAYEQ LAKNATTIDL TVDNGNIRTS
151 GEKQMETLSR IFGKEARVAE LNAQIDALFA QKREAAKRG RGLVLSVTGN
201 KVSFAFGTQR LASWIHGDIQ LPPVDESLRN EGHGQPVSEF YIKEKNPGMI
251 FIIDRTAAIG QEGPAAVEVL DNALVCGTNA WKRRKQIIVM AANYIVAGGA
301 RQLIQAAEQL KAAFEKAEPV AAQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2575>:

```

m750.seq
1  GTGAAACCGC GTTTTATTG GGCAGCCTGC GCCGTCCTGC TGACCGCCTG
51  TTCGCCCGAA CCTGCCGCGC AAAAACTGT ATCCGCGCGA TCCGCATCTG
101 CCGCCACGCT GACCGTGCCG ACCGCGCGGG GCGATGCCGT TGTGCCGAAG
151 AATCCCGAAC GCGTCGCGGT GTACGACTGG GCGGCGTTGG ATACGCTGAC
201 CGAATTGGGC GTGAATGTGG GCGCAACCAC CGCGCCGGTG CGCGTGGATT
251 ATTTGCAGCC TGCATTGAC AAGGCGGCAA CGGTGGGGAC GCTGTTTCGAG
301 CCCGATTACG AAGCCCTGCA CCGCTACAAT CCTCAGCTTG TCATTACCGG
351 CCGGCCGGGC GCGGAAGCGT ATGAACAGTT AGCGAAAAAC GCGACCACCA
401 TAGATCTGAC GGTGGACAAC GGCAATATCC GCACCAGCGG CGAAAGCAG
451 ATGGAGACCT TGGCGCGGAT TTTCGGCAAG GAAGCGCGCG CGGCGGAATT
501 GAAGGCGCAG ATTGACGCGC TGTTCCGCCA AACGCGCGAA GCCGCCAAG
551 GCAAAGGACG CGGCTGGTGT CTGTCGGTTA CGGCAACAA GGTGTCCGCC
601 TTCGGCACGC AGTCGCGGTT GGCAAGTTGG ATACACGCGC ACATCGGCCT
651 ACCGCTGTGA GACGAATCTT TACGCAACGA GGGGCACGGG CAGCCTGTTT
701 CCTTCGAATA CATCAAGAG AAAAAACCCG ATTGGATTTT CATCATCGAC
751 CGTACGCGCG CCATCGGGCA GGAAGGGCCG GCGGCTGTGC AAGTATTGGA
801 TAACGCGCTG GTACGCGGCA CGAACGCTTG GAAGCGCAAG CAAATCATCG
851 TCATGCTCTC CGCGAAGTAC ATTGTCCGCG GCGGCGCGCG CGAGTTGATT
901 CAGGCGCGCG AGCAGTTGAA GGCGGCGTTT AAAAAGGCAG AACCCTTGC
951 GGCGGGGAAA AAGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2576; ORF 750>:

```

m750.pep
1  VKPRFYWAAC AVLLTACSPE PAAEKTVSAA SASAATLTVP TARGDAVVPK
51  NPERVAVYEW AALDTLTELG VNVGATTAPV RVDYLQAFD KAATVGTLEF
101 PDYEALHRYN POLVITGGPG AEAYEQLAKN ATTIDLTVDN GNIRTSGEFQ
151 METLARIFGK EARAELKAQ IDALFAQTRE AAKGKGRGLV LSVTGNKVSA
201 FGTQSRILASW IHGDI GLPPV DESLRNEGHC QPVSEFYIKE KNPDWIFIID
251 RTAAIGQEGP AAVEVDNAL VRGTNAWKRK QIIVMPAANY IVAGGARQLI
301 QAAEQKKAFF KKAEPVAAGK K*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 750 shows 93.8% identity over a 322 aa overlap with a predicted ORF (ORF 750) from *N. gonorrhoeae*

```

m750/g750 93.8% identity in 322 aa overlap

          10      20      30      40      50
m750.pep  VKPRFYWAACAVLLTACSPEPAAEKTVSAAASASA----ATLTVPTARGDAVVPKNPERVA
          |||||  :|||  |||||  |||||  |||||
g750       VKPRFYWAACAVLPAACSPEPAAEKTVSAAASQAASTPVATLTVPTARGDAVVPKNPERVA
          10      20      30      40      50      60

          60      70      80      90      100     110
m750.pep  VYDWAALDTLTELGVNVGATTAPVRVDYLOPAFDKAATVGTLFEPDYEALHRYNPQLVIT
          |||||  |||||  |||||  |||||  |||||  |||||
g750       VYDWAALDTLTEPGNVGATTAPVRVDYLOPAFDKAATVGTLFEPDCESLHRHNPQFVIT
          70      80      90      100     110     120

          120     130     140     150     160     170
m750.pep  GGPGEAYEQLAKNATTIDLTVDNGNIRTSGEKQMETLARIFGKEARAELKAQIDALFA
          |||||  |||||  |||||  |||||  |||||  |||||

```

```

g750      GGPGEAEYEQLAKNATTIDLTVDNGNI RTSSEKQMETLSRIFGKEARVAELNAQI DALFA
          130         140         150         160         170         180

m750.pep   180        190        200        210        220        230
QTREAAKGKGRGLVLSVTGNKVSAFGTQSRLASWIHGDI GLPPVDES LRNEGHGC QPVSFEE
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | :
g750       QKREAAGKGRGLVLSVTGNKVSAFGTQSRLASWIHGDI GLPPVDES LRNEGHGC QPVSFEE
          190        200        210        220        230        240

m750.pep   240        250        260        270        280        290
YIKEKNPDWIFI IDRTAAIGOE GPAAVEVL DNALVRGT NAWKRKQI IVM PPAANYIVAGGA
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | :
g750       YIKEKNPGWIFI IDRTAAIGOE GPAAVEVL DNALVC GTNAWKRKQI IVM PPAANYIVAGGA
          250        260        270        280        290        300

m750.pep   300        310        320
RQLIQAAEQLKAAFKAEPV AAGKKX
| | | | | | | | | | | : | | | | |
g750       RQLIQAAEQLKAAFKAEPV AAQX
          310        320

```

a750.seq

1	GTGAACCGC	GTTTTATTG	GGCAGCCTGC	GCCGTCCTGC	TGACCGCCTG
51	TTCCGCCGAC	CCTGCCCGCG	AAAAAACTGT	ATCCGCCCGCA	TCCGCATCTG
101	CACTCCACAT	GACCTCGCGT	ACCGCCGGGG	GCGATCGCGT	TGTGCGGAAG
151	AATCCCGAAC	GCCTGCGCGT	TACGACATGG	CGCGGCTTGG	ATACGCTGAC
201	CGAATTGGGT	GTGAATGTGG	GCGCAACAC	CGCGCCGGTG	CGCGTGGATT
251	ATTTGCACTT	TGCATTTGAC	AAGGCGCGCA	CGGTGGGGAG	CGTGTTCGAG
301	CCCGATTACG	AAGCCCTGCA	CCGCTACAAT	CTCAGACTTG	TCATTACCGG
351	CGGSCCGGG	GCGGAAGCGT	ATGAACAGTT	GGCGAAAAAC	GCGACCACCA
401	TAGATCTGAC	TGGTGACGAC	GGCAATATCG	GCACACGCGG	GCAAAAGCAG
451	ATGAGAGACT	GTGGCGGAT	TTTCGGCAAC	GAAGCGCGCG	CGCGGGAATT
501	GAAGGCGCAG	ATTGACGCGC	TGTTCCGCCA	AACGCGCGAA	GCGCGCAAAG
551	GCAAAGGACG	CGGGCTGGTG	CTGTCTGGTT	CGGGCAACAA	GGTGTCCGCC
601	TTCGGCACGC	GATCGCTGTT	TGC AAGTTTG	ATGACACGGC	ACATCGGCTT
651	ACCGCCTGTA	GACGAATCTT	GAGCAACGA	GGGCACGGG	CAGCCTGCTT
701	CCTTCGAATA	CATCAAGAG	AAAAACCCCG	ATTGGATTTT	CATCATCGAC
751	CTACCCGCGC	CCATCGGGCA	GGAAGGCGCG	GCGGCTGTCG	AAGTATTGGA
801	TGACGCGCTG	GTACGCGGCA	CGAACGCTTG	GAGGCGCAAG	CAATATCTGA
851	TCATGCGCTG	CGCGAATTAC	ATTGTCGGG	GCGGCTCGCG	GCAGTTGATT
901	CAGGCGGCGG	AGCAATTGAA	GGAGGCGTTT	GAAAGGCAG	AACCCGTTGC
951	GGCGGGGAAA	GAGTAG			

a750.pep

1	VKPRFYWAAC	AVLLTACSPE	PAAEKTVSAA	SASARTLTVP	TARGDAVVPK
51	NPRVAVYWD	AADLTLTSEL	VNVGATAPV	RDVLTQPAFD	KAATVGTGLE
101	PDYEAALHYN	PQLVITGGPG	AEAYEQLAKL	ATTIDTLVDN	GNIRTSGEKQ
151	METGLATPGK	EARAELAKLA	IDALFAQTRE	AAKKGKRGVL	LSVNTGNKVA
201	FTQSRSLASL	IHGDIILPPV	DESLRNEHGK	QPVSEFGEIK	KNPWDIFIID
251	RRTAAIGQEGP	AAEVEVLNAL	VRGTNAWKRK	QIIVMPAANY	IVAGGSRQLI
301	OAASOLKEAF	EKAEPVAAGK	E*		

Homology with a predicted ORF from *N. meningitidis*

ORF 750 shows 98.8% identity over a 321 aa overlap with a predicted ORF (ORF 750) from *N. meningitidis*:

a750/m750 98.8% identity in 321 aa overlap

	10	20	30	40	50	60
a750.pep	VKPRFYWAACAVLLTACSEPAAEKTVSAASASAATLTVP	TARGDAVVPKNPERVA	VYDW			
m750	VKPRFYWAACAVLLTACSEPAAEKTVSAASASAATLTVP	TARGDAVVPKNPERVA	VYDW			
	10	20	30	40	50	60
	70	80	90	100	110	120
a750.pep	AAALDTLTTELGVNVGATTAPVRVDYLQPAFDKAATVGT	LFE	PDY	EALHRYNPOLVIT	TGG	PG
m750	AAALDTLTTELGVNVGATTAPVRVDYLQPAFDKAATVGT	LFE	PDY	EALHRYNPOLVIT	TGG	PG

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	70	80	90	100	110	120
	130	140	150	160	170	180
a750.pep	AEAYEQLAKNATTIDLTVDNGNIRTSGEKQMETLARIFGKEARAAELKAQIDALFAQTRE					
m750	AEAYEQLAKNATTIDLTVDNGNIRTSGEKQMETLARIFGKEARAAELKAQIDALFAQTRE					
	130	140	150	160	170	180
	190	200	210	220	230	240
a750.pep	AAKGKGRGLVLSVTGNKVSFAFGTOSRLASWIHGDIGLPPVDESLRNEGHGQPVSFYEYIKE					
m750	AAKGKGRGLVLSVTGNKVSFAFGTOSRLASWIHGDIGLPPVDESLRNEGHGQPVSFYEYIKE					
	190	200	210	220	230	240
	250	260	270	280	290	300
a750.pep	KNPDWIFIIDRTAAIGQEGPAAVEVDNALVRGTNAWKRKQIIVMPAANYIVAGGSRQLI					
m750	KNPDWIFIIDRTAAIGQEGPAAVEVDNALVRGTNAWKRKQIIVMPAANYIVAGGARQLI					
	250	260	270	280	290	300
	310	320				
a750.pep	QAAEQQLKEAFEKAEPVAAGKEX					
m750	QAAEQQLKAFFKAEPVAAGKKX					
	310	320				

g751.seq not found yet

g751.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2579>:

m751.seq..

```

1  ATGGCTTGGA  GTATGTTTGC  CACAACCCAA  GCCGATAGAG  CGGTAAGGTC
51  TGCAACTGCA  CCTAAAGAAA  TGTGGTTCCA  TAAGAAGATA  ATAGATGAAA
101 AAACAGGTAA  AGTATCCTTT  GATACCAGAC  AAATTGGGTC  ATTGAATGAT
151 TTAAGCAAGG  AAGAACTGGC  AAGCATTCAA  GACACAAATG  GCAAAGTTAT
201 TACTGTGTCT  AATCCTGGTA  TTTTCAATAA  TCGAGAAGAT  TCATTAAGCA
251 ACGCAGCAAA  ACAAATCGT  AATAGTACAA  ACGGTAGTGG  TGTATTGCA
301 GTCATGAATC  CTCCAACAGG  GAAATATAAA  TCTGATTCTA  ATAACAAAAT
351 AAAAGATTTT  TTATGGCTCG  GTTCAAGTCT  TGTCTCTGAA  CTGATGTATG
401 TCGGTTACGA  CCAATTAAAT  AATAAAGTGT  TCCAAGGCTA  TTTACCCAAA
451 ACCAATTCAG  AAAAAGTCAA  TCAAGATATT  TATCGAGAGG  TTCAAAAAAT
501 GGGTAACGGC  TGGTCGGTGG  ATACCAAGTA  TCACAGTCGT  GGGGGAATTA
551 CAGCAAGCGT  TTCCTTAAAA  GATTGGGTAA  ACAATCAAAA  ACAAATGGC
601 ATTGCCCCAA  TCAGAAAAGC  ACGTTTCTAT  GGTACAGCCA  CAAATGTGCA
651 GAATGATTAC  GCCGATGTTT  TACAGAAAAA  CGGCTATACC  TATACGGGTG
701 CAGACGGCAA  AACTTATAAC  AGCGGATCCT  ACTCAATCGT  GCATGATAAA
751 GATTTTGTGG  GGAACAAATG  GATACCTTTC  TTGCTAGGAA  CCAATGACAC
801 CACACAAGGT  ACATGTAAGG  GGTGTGCTGA  TTCGCATAGC  AGTTATTTTG
851 CGGAGGTGCC  AAAAGCAGGT  ACAAAGAAT  TTGATGACTA  TGTAATAATA
901 TGGGGTGAAG  TTGAATATGA  CGCTCAAGGT  AAGCCAATTA  ACAAATCTAA
951 ACCCATACTG  GTAGAACCAA  ACAAACAAA  AGATAATGAA  AAATATGAAA
1001 AAGAAGCTTT  CTAA

```

This corresponds to the amino acid sequence <SEQ ID 2580; ORF 751>:

m751.pep..

```

1  MAWSMFATTQ  ADRAVRSATA  PKEMNFHKKI  IDEKTGKVSF  DTRQINSLND
51  LSKEBLASIQ  DTNGKVITVS  NPGIFNNRED  SLSNAAKQNR  NSTNGSGVIA
101 VMNPPTGKYK  SDSNNKIKDF  LWLGSSLVSE  LMYVGVDQLN  NKVPQGYLPK
151 TNSEKLNQDI  YREVQKMGNG  WSVDTSNHSR  GGITASVSLK  DWVNNQKQNG
201 IAPIRKARFY  GTATNVQNDY  ADVLQKNGYT  YTGADGKTYN  SGSYSIVHDK
251 DFGVGNKIWF  LLGTNDTTQG  TCKGLCYSHS  SYFAEVPKAG  TKEFDDYVKI
301 WGEVEYDAQG  KPINKSKPIL  VEPNKTNDNE  KYEKEAP*

```

a751.seq not found yet

a751.pep not found yet

g752.seq not found yet

g752.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2581>:

m752.seq..

```

1  ATGAAAATTT CCAGACCICC GGAATTTACC CTGTTGCAAC AGGAATATAT
51  GCAGCATCTC ACTGAAAGAA TGACGCAAAAT TGCCAAGCTG CTGAATTCTT
101 CCGCAAACAA TCCTGATATA GACATTCCCG ATTTTCTTAC TGAAATCAAA
151 GATTATTCAG AATTTTCCGT GACAGATGAA AATGGAACCT ACCTGCATTG
201 GGACAAATTC CGCCGGATTG ACACGGAAGA TACGCGGATG AAATGGCGCG
251 CCGTTAAGGA AAGCCGCAAA AAAATCCAAA AACCAATTGA TTTCCCGTTT
301 GAACATCAGT TTTGGTCTG CATTCCCGAC TCTTGCAGG CACGGCTTCA
351 TTTGATTGAC AAAAGCTGCG GCAGTTCTAT CGGCACGTCT AGCTTGGGTG
401 GCTTCGGCAG AAGCGAGCAA AACAGATTCT TGCTCAAGTC TCTGATTATG
451 GAAGAAGCGA TTACATCCGC CCAACTGGAA GGTGCGGCTA CCACGCGTAA
501 AGTGGCCAAG GATATGCTCA AATCGCAGCG TAAACCCAAA ACAAAAGACG
551 AAATCATGAT AGTGAACAAC TATCACTTGA TGA AAAAAGC GGTAGAATTG
601 AAAAATACGC CGTTAAGTGT TGAAATGATT TTGGATTTCG ACCGCATTGC
651 TACCAGTAAC GCTATTGAAA ACAAGGCCGA GCCCGGACAA TTCAGGCAGG
701 ATGACGAAAT CTTTATCGCC GATATCAATG GTAACAGCCT GTATCAACCA
751 CCGCGCACG GACAGGTTCA TACGCTGATG GAAGAGGTGT GTGCGTTTGC
801 CAATAATACC TATGACGGCG TGGAAAATCC GTTTATCCAT CCGGTTGTCC
851 AAGCTATTAT CTTGCATTTC CTCATCGGCT ACATCCACCC ATTTGGTGAT
901 GGCAACGGGC GGACAGCGCG GGCTTTGTTT TATTGGTTTA TGCTCAAAAA
951 CGGCTACTGG CTATTGAAAT ACATATCCAT CAGCCGTCTT CTGAAAAACG
1001 CTCTGCCCCA ATACGCCAAA TCCTATTTGT ATGCGGAAAC TGACGATTTA
1051 GATTAAACCT ATTTATCTA TTACCAATGC GATATTATCA AGCGGGCGGT
1101 TGCCGATTG GAGCACTACA TTTCCGACAA ACAAAAACAC CAACAGGAAT
1151 TCAAAGCAGC GATTGCCCAA TATACTGAAA AGATAGGAAA GTTGAACCAA
1201 CGGCAAATTG GTATCCTGCA AAAAGCAGTG GAAGAAAGCG GAAAAATCTT
1251 TACTGCACAA GAAATTGCCA ACCAATACGG CATCTCCCTG AATACTGCCC
1301 GTAGCGATT TTAGTAACTG GGAGAATATA GATTCCTAGT GCCGTTCAAA
1351 TCAGGAAATG CTTTAGAGTA TGTGCTCCT CAGGATTAT TGGAAGGTT
1401 AGAAAAAAA TAG

```

This corresponds to the amino acid sequence <SEQ ID 2582; ORF 752>:

m752.pep

```

1  MKISRPPEFT LLQOEYMQHL TERMTQIAKL LNSSANNPDI DIPDFLTEIK
51  DYSEFSVTDE NGTYLHWDKF RRIHTEDTRM KWRVAVKESRK KIQKPIDFPF
101 EHQWFECIPD SLQARLHLID KSCGSSIGTS SLGGFGRSEQ NRELLKSLIM
151 EEAITSAQLE GAATTRKVAK DMLKSQRKPK TKDEIMIVNN YHLMKKAVEL
201 KNTPLSVEMI LDHRIATSN AIENKAEPGQ FRQDDEIFIA DINGNSLYQP
251 PPHGQVHTLM EEVCAFANNT YDGVENPFH PVVQAIILHF LIGYIHPFGD
301 GNGRTARALF YWFMLKNGYW LFEYISISRL LKNAPQYAK SYLYAETDDL
351 DLTFFIYYQC DIKRAVADL EHYISDKQKH QQEFKAAIAQ YTEKIGKLNQ
401 RQIGILQKAV EESGKIETAQ EIANQYGISL NTARSDSLKL GEYRFLVFPK
451 SGNALAYVAP QDILLERLEKK *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2583>:

m752-1.seq

```

1  ATGAAAATTT CCAGACCTCC GGAATTTACC CTGTTGCAAC AGGAATATAT
51  GCAGCATCTC ACTGAAAGAA TGACGCAAAAT TGCCAAGCTG CTGAATTCTT
101 CCGCAAACAA TCCTGATATA GACATTCCCG ATTTTCTTAC TGAAATCAAA
151 GATTATTCAG AATTTTCCGT GACAGATGAA AATGGAACCT ACCTGCATTG
201 GGACAAATTC CGCCGGATTG ACACGGAAGA TACGCGGATG AAATGGCGCG
251 CCGTTAAGGA AAGCCGCAAA AAAATCCAAA AACCAATTGA TTTCCCGTTT
301 GAACATCAGT TTTGGTCTG CATTCCCGAC TCTTGCAGG CACGGCTTCA
351 TTTGATTGAC AAAAGCTGCG GCAGTTCTAT CGGCACGTCT AGCTTGGGTG
401 GCTTCGGCAG AAGCGAGCAA AACAGATTCT TGCTCAAGTC TCTGATTATG
451 GAAGAAGCGA TTACATCCGC CCAACTGGAA GGTGCGGCTA CCACGCGTAA
501 AGTGGCCAAG GATATGCTCA AATCGCAGCG TAAACCCAAA ACAAAAGACG
551 AAATCATGAT AGTGAACAAC TATCACTTGA TGA AAAAAGC GGTAGAATTG
601 AAAAATACGC CGTTAAGTGT TGAAATGATT TTGGATTTCG ACCGCATTGC

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```

651 TACCACTAAC GCTATTGAAA ACAAGGCCGA GCCCGGACAA TTCAGGCAGG
701 ATGACGAAAT CTTTATCGCC GATATCAATG GTAACAGCCT GTATCAACCA
751 CCGCCGCACG GACAGGTTCA TACGCTGATG GAAGAGGTGT GTGCGTTTGC
801 CAATAATACC TATGACGGCG TGGAAAATCC GTTTATCCAT CCGGTTGTCC
851 AAGCTATTAT CTTGCATTTC CTCATCGGCT ACATCCACCC ATTTGGTGAT
901 GGCAACGGGC GGACAGCGCG GGCTTTGTTC TATTGGTTTA TGCTCAAAAA
951 CGGCTACTGG CTATTTGAAT ACATATCCAT CAGCCGTCTT CTGAAAAACG
1001 CTCCTGCCCA ATACGCCAAA TCCTATTGTG ATGCGGAAAC TGACGATTTA
1051 GATTAACTT ATTTATCTA TTACCAATGC GATATTATCA AGCGGGCGGT
1101 TGCCGATTTG GAGCACTACA TTTCCGACAA ACAAAAACAC CAACAGGAAT
1151 TCAAGCAGC GATTGCCCAA TATACTGAAA AGATAGGAAA GTTGAACCAA
1201 CGGCAATTG GTATCCTGCA AAAAGCAGTG GAAGAAAGCG GAAAAATCTT
1251 TACTGCACAA GAAATTGCCA ACCAATACGG CATCTCCCTG AATACTGCCC
1301 GTACCGATTT GAGTAACTC GGAGAATATA GATTCCTAGT GCCGTTCAAA
1351 TCAGGAAATG CTTTAGAGTA TGTGCTCCT CAGGATTAT TGGAAGGTT
1401 AGAAAAAAA TAG

```

This corresponds to the amino acid sequence <SEQ ID 2584; ORF 752-1>:

m752-1.pep

```

1 MKISRPEFT LLQEYMQHL TERMTQIAKL LNSSANNPDI DIPDFLTEIK
51 DYSEFSVTDE NGTYLHWDKF RRIHTEDTRM KWRVAVKESRK KIQKPIDFPF
101 EHQFWFCIPD SLOARLHLID KSCGSSIGTS SLGGFGRSEQ NRELLKSLIM
151 EEATISAQLE GAATTRKVK DMLKSORKPK TKDEIMIVNN YHLMKKAVEL
201 KNTPLSVEMI LDLHRIATSN AIENKREPGQ FRQDDEIFIA DINGNSLYQP
251 PPHGQVHTLM EEVCAFANNT YDGVENPFIH PVVQAILHF LIGYIHPFGD
301 GNGRTARALF YWFMLKNGYW LFEYISISRL LKNAPAQYAK SYLYAETDDL
351 DLYFYIYQC DIKRAVADL EHYISDKQKH QQEFKAAIAQ YTEKIGKLNQ
401 RQIGILQKAV EESGKIETAQ EIANQYGISL NTARSDSLKL GEYRFLVPFK
451 SGNALYVAP QDLELERLEK

```

a752.seq not found yet

a752.pep not found yet

g753.seq not found yet

g753.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2585>:

m753.seq

```

1 ATGCCCATCA CTCCACCCTT AAACATCATC TCTCCTAAAC TCTACCCCAA
51 TGAACAATGG AACGAAAGCG AAGCACTCGG TGCCATCACT TGGCTATGGT
101 ATCAGTCGCC TACGCATCGC CAAGTACCTA TTGTGGAGAT GATGACGTAT
151 ATATTGCCCTG TGTAAAAAAA CGGGCAGTTC GCTTTGTTTT GCAAGGGTAC
201 CCAACCAATC GGTATATCT CATGGGCTTA TTTTGATGAA GTGGCGCAGG
251 CGCATTATTT AGAATCTGAC CGCCATTTGC GTGACAACAG CGATTGGAAC
301 TGTGGCGACA ATATTGGCT GATTCAATGG TTTGCGCCAT TGGGACACAG
351 TCATCAAATG CGCTCAGCTG TCGCCAGTT ATTCCTAGT ACGACAGTAC
401 CGGCCTTGTA TCATAAAGGG AGCGATAAGG GTTTGAGAAT TTTAACTTTT
451 AAAACTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2586; ORF 753>:

m753.pep

```

1 MPITPPLNII SPKLYPNEQW NESEALGAIW WLWYQSPTHR QVPIVEMMTY
51 ILPVLKNGQF ALFCKGTQPI GYISWAYFDE VAQAHYLED RHLRDNSDWN
101 CGDNIWLIQW FAPLGHSHQM RSAVRQLFPS TTVRALYHKG SDKGLRILTF
151 KT*

```

a753.seq not found yet

a753.pep not found yet

g754.seq not found yet

g754.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2587>:

```
m754.seq
1  ATGATGAAGT CTATCCTCAC CGTATCCGGA AATCGTATGC GTAAACCCAG
51  AATCACCTAT TTGGATGTTT GGGCAAACGA TGAAAGAATC GGTACTTTGG
101 AAAAGGGGGC CATGTATCGG TTCGCATACG ACAATCCCAA TTCTTCGTTG
151 CTGGGCGCTGC ATTATCAAGA CAGAAGCAAG GTATATATCA GCAACAATAT
201 GCCGCATATC TTTGCACAGT ATTTTCCGGA AGGCTTTTTC GATGCACACA
251 TCACAAGCAA ATATGCTTTT CATGATGCGC CTTTGAAGA CAATGAGATG
301 CTGCGCTTGG CAATTCTGTG CAGAGAGACT TTGGGTCGGA TACATGTGCG
351 CTGTAATGAC CCGCTTTTTA ATGAATGGAT TGACGGGTTG GAGATGAAAA
401 ATCCAAGAAT ATTGACTGAA CGGGATTGTC TGGGCATAAA TGCCCGACAG
451 GTTTTTTCAGC AATATATGCG AGAAATCTTC CATCACGGCC GTTTCGTCAG
501 TGTATCCGGG ATACAGCAGA AGATGTCCTT AGATGCCATC CGCAGAAATA
551 CCAAGCAAAC TGCCTCATAT ATTGCCAAG GTTTTGATGC ATCCGAATAT
601 CCTTGCTTGG CTGCCAATGA ATTTTATGTC ATGCAGACCA TCAACAAGC
651 CGGCATTGCC GTTGCACAGA CCAGCCTGTC GGAAGATTCA TCAGTCTTAT
701 TGGTACGTCG GTTTGATGTC AGTGAACAGG GTTATTTTTT AGGGATGGAA
751 GACTTTACCA GTCTGCGCCA GTATCGGTA GAAGATAAAT ATAAAGGCAG
801 TTATGCGGCT ATGACACAGA TTATCCGACA GATATCCGGC AGACCAGATG
851 AAGATTAAAT CCATTCTTTT AATCAGCTTG CTGCCAGTTG CATATTGAAA
901 AACGGCGATG CACACCTCAA AAATTTTCA GTACTCTATC ATGACGAATA
951 CGATGTTCGT CTTGCACCTG TCTATGATGT ATTGGATACA TCAATATACA
1001 GGGTTGGAAC ACAAGGAATT TTTGATGCTT ATGACGATAC GCTGGCATTG
1051 AACCTGACTA ACCACGGTAA GAAACATAT CCTTCCAAGA ATACATTGTT
1101 GGATTTTGCT GAGAAATATT GCGATTGGG AAGAGAAGAT GCATCCTTTA
1151 TGATAGATAC AATCGTTCAA GCTAAAGAAC AGGTTCTTGT TAAATACTCG
1201 GATGTATTGC GTGAGAATGA ATGGTTGGCG CAGAAGTGGC ATTTTATCCC
1251 GGATGAAAAT GAAGAAGGTC TACCGTTTAC ATTCGGGTAG
```

This corresponds to the amino acid sequence <SEQ ID 2588; ORF 754>:

```
m754.pep
1  MMKSILTVSG NRMKRPRITY LDVWANDERI GTLEKGAMYR FAYDNPNSSI
51  LGLHYQDRSK VYISNNMPHI FAQYFPEGFL DAHITSKYAF HDAPFEDNEM
101 LRLAILCRET LGRIHVRCND PLFNEWIDGL EMKNPRILTE RDLLGINARQ
151 VFQQYMAEIF HHGRFVSVSG IQQKMSLDAL RRNTKQTASY IAKGFDASEY
201 PCLAANEFLC MQTIKQAGIA VAQTSLSSEDS SVLLVRRFDV SEQGYFLGME
251 DFTSLRQYSV EDKYKGSYAA IAQIIRQISG RPDEDLIHFF NQLAASCILK
301 NGDAHLKNFS VLYHDEYDVR LAPVYDVLDT SIYRVGTQGI FDAYDDTLAL
351 NLTNHGKTTY PSKNTLLDFA EKYCDLGRED ASFMIDTIVQ AKEQVLVKYS
401 DVLRENEWLA QKWHFIPDEN EEGLPFTFR*
```

a754.seq not found yet

a754.pep not found yet

g755.seq not found yet

g755.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2589>:

```
m755.seq..
1  ATGAGCCGTT ACCTGATTAC CTTTGATATG GATACCAACT GCCTGAAAGA
51  CAATTACCAC GGAAATAACT ATACCAATGC CTACTCCGAT ATTAACCA
101 TCTTGGCTAG ACATGGATTT GAGAACATTC AGGGCAGTGT TTATCTAGGC
151 CGTGAAGGCA TCAGTGAAGC ACACGGAACA ATAGCCATTC AGGAACTGAC
201 CGCTCGGTTT GATTGGTTTT ACTCCTGTAT TTCAAACATT AAGTTTACC
251 GCCTTGAAAG TGATTGAAC GCACAATTTA TCGCTGATGG TGTGTATCAA
301 GCCAAACAGG CTTTCCTTCA ACGTGTTGAA CAACTTCGTA TATCCCTAAC
351 AGAAGCTGGA TTGTCTGATG AGCAAATCAA TCAGGTTCTG GAAAAACAGA
401 AATTTGAATT GGAAAGTCCT AACCTGAAAT TAAATTAA
```

1230

This corresponds to the amino acid sequence <SEQ ID 2590; ORF 755>:

```
m755.pep..
  1 MSRYLITFDM DTNCLKDNYH GNNYTNAYS D IKTILARHGF ENIQGSVYLG
 51 REGISEAHGT IAIQELTARE DWFYSCISNI KFYRLESDLN AQFIADGVYQ
101 AKQAFLLQ RVE QLRISLTEAG LSDEQINQVL EKQKFELESP NLKLN*
```

a755.seq not found yet

a755.pep not found yet

g756.seq not found yet

g756.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2591>:

```
m756.seq
  1 ATGACCGCCA ACTTTGCACA GACGCTGGTC GAAATACAGG ACAGTCTGTA
 51 CAGGGTTGTG TCAACCGTCC AATACGGGGA TGACAACCTC AAGCGGTTGA
101 CAGCGGACAA ACGGAAGCAG TATGAGTTGA ACTTCAAGAT TTCCGAGGGT
151 TCTACGCGTG TAGAGTCCGA CTTTAAAGAG ACTTTGGTTC GGTTCGGTAG
201 AGATATGCTT CAAGATATGC CCCCTAAAAT CCGTTCGGCA ACGCTGGTAG
251 CGTTGACGAC CCTGCTTGTC GGAGGGGCGT TGGGTTACGG TTATTGGAA
301 TACCTGAAGC AGGTTGCTTC GGAACGGTAT CAGACCGAGC GTCTGTATAA
351 TGCCGTCGAC CGTCTGCAG AATCCCAAGA ACGGATAACG TCCGCCATCC
401 TGAAGGGTGC TAGAGGTGCC GATTTCGTGC AAATCGGCAG ACGTTCCTAC
451 AGTAGGGAGG ATATATCGGA GGCAAATAGA CGTGCAGAGC GTGTCCCGTA
501 TGGCGCAGAG TTGGTTTCAG ACGGCAATTT TACCGCTGTT TTATCTGATA
551 TAGGGGATTA A
```

This corresponds to the amino acid sequence <SEQ ID 2592; ORF 756>:

```
m756.pep
  1 MTANFAQTLV EIQDSLRYRVV STVQYGGDNL KRLTADKRKQ YELNFKISEG
 51 STRVESDFKE TLVRFRDML ODMPPKIRSA TLVALTLLV GGALGYGYLE
101 YLKQVASEGY QTERLYNAVD RLAESQERIT SAILKGARGA DFVQIGRRSY
151 SREDISEANR RAERVYPYAE LVSDGNFTAV LSDIGD*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2593>:

```
a756.seq
  1 ATGACCGCCA ACTTTGCACA GACGCTGGTC GAAATACAGG ACAGTCTGTA
 51 NAGGGTTGTG TCAACCGTCC AATACGGGGA TGACAACCTC AAGCGGTTGA
101 CAGCGGACAA ACGGAAGCAG TATGAGTTGA ACTTCAAGAT TTCCGAGGGT
151 TCTACGCGTG TAGAGTCCGA CTTTAAAGAG ACTTTGGTTC GGTTCGGTAG
201 AGATATGCTT CAAGATATGC CCCCTAAAAT CCGTTCGGCA ACGCTGGTAG
251 CGTTGACGAC CCTGCTTGTC GGAGGGGCGT TGGGTTACGG TTATTGGAA
301 TACCTGAAGC AGGTTGCTTC GGAAGGGTAT CAGACCGAGC GTCTGTATAA
351 TGCCGTCGAC CGTCTGCAG AATCCCAAGA ACGGATAACG TCCGCCATCC
401 TGAAGGGTGC TAGAGGTGCC GATTTCGTGC AAATCGGCAG ACGTTCCTAC
451 AGTAGGGAGG ATATATCGGA GGCAAATAGA CGTGCAGAGC GTGTCCCGTA
501 TGGCGCAGAG TTGGTTTCAG ACGGCAATTT TACCGCTGTT TTATCTGATA
551 TAGGGGATTA A
```

This corresponds to the amino acid sequence <SEQ ID 2594; ORF 756.a>:

```
a756.pep
  1 MTANFAQTLV EIQDSLXRVV STVQYGGDNL KRLTADKRKQ YELNFKISEG
 51 STRVESDFKE TLVRFRDML QDMPPKIRSA TLVALTLLV GGALGYGYLE
101 YLKQVASEGY QTERLYNAVD RLAESQERIT SAILKGARGA DFVQIGRRSY
151 SREDISEANR RAERVYPYAE LVSDGNFTAV LSDIGD*
```

m756 / a756 99.5% identity in 186 aa overlap

	10	20	30	40	50	60
m756.pep	MTANFAQTLVEIQDSLRYRVVSTVQYGGDNLKRLTADKRKQYELNFKISEGSTRVESDFKE					
a756	MTANFAQTLVEIQDSLXRVVSTVQYGGDNLKRLTADKRKQYELNFKISEGSTRVESDFKE					
	10	20	30	40	50	60

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	70	80	90	100	110	120
m756.pep	TLVRFGRDMLQDMPPKIRSATLVALTTLVGGALGYGYLEYLKQVASEGYQTERLYNAVD					
a756	TLVRFGRDMLQDMPPKIRSATLVALTTLVGGALGYGYLEYLKQVASEGYQTERLYNAVD					
	70	80	90	100	110	120
	130	140	150	160	170	180
m756.pep	RLAESQERITSAILKGARGADFVQIGRRSYSREDISEANRRAERVYPYGAELVSDGNFTAV					
a756	RLAESQERITSAILKGARGADFVQIGRRSYSREDISEANRRAERVYPYGAELVSDGNFTAV					
	130	140	150	160	170	180
m756.pep	LSDIGDX					
a756	LSDIGDX					

g757.seq not found yet

g757.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2595>:

m757.seq

```

1  ATGAAAATAC TCGCTTTATT AATTGCCGCT ACCTGTGCTT TATCTGCGTG
51  TGGCAGCCAA TCTGAAGAAC AACCGGCATC TGCACAACCC CAAGAGCAGG
101 CACAATCCGA ATTAAAAACC ATGCCGGTAA GCTATACCGA CTATCAATCA
151 GCAGCCAATA AAGGGCTGAA TGACCAAAAA ACCGGTCTGA CCCTTCCTGA
201 ACATGTTGTC CCTATCGACA ATGCCGGAAG AAAGAATCTG CTGCATGACT
251 TTTCAGACGG CTCACAATC TTAACCGTTG ATACCGATAA AGCCGACAAA
301 ATTACTGCTG TCCGAGTAGT CTGGAATACA GATGCAATGC CTCAAAAAGC
351 GGAAAAACTG TCCAAAGCTG CCGCAGCCTT GATTGCGGCA ACCGCTCCGG
401 AAGACCGCAC AATGCTGCGT GATACGGCGC ACCAAATCGA AATGGCGATT
451 GACAGCCATA ATGCGCAAAA AGAGCCAACC CGAGAATGGG CGCGTGGTGG
501 GATTGCTTAT AAAGTCACTG TTACCAATTT ACCGAGCGTG GTTTTGACGG
551 CAAAAGCTGA GTAA

```

This corresponds to the amino acid sequence <SEQ ID 2596; ORF 757>:

m757.pep (lipoprotein)

```

1  MKILALLIAA TCALSACGSQ SEEQPASAQP QEQAQSELKT MPVSYTDYQS
51  AANKGLNDQK TGLTLPEHVV PIDNREGKNL LHDFSDGLTI LTVDTDKADK
101 ITAVRVVWNT DAMPQKAEL SKAAPALIAA TAPEDRTMLR DTGDQIEMAI
151 DSHNAOKEPT REWARGGIAY KVTVTNLPVS VLTAKAE*

```

a757.seq not found yet

a757.pep not found yet

g758.seq not found yet

g758.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2597>:

m758.seq

```

1  ATGAACAATC TGACCGTGTT TACCCGTTTC GATACCGATT TGGCGACGCT
51  TGCCGATGAA TTGCAATATG TGTGGGAACA CACCGCGGTT ACAGACCATC
101 AGGGCAAACCT GGTGGAAATT CCCGTCTGCT ACGGCGGCGA ATACGGCCCCG
151 GATTGGCGG AAGTCGCTGC TTTCATCAG ACGGTTATTT CCGAAATCGT
201 CCGCGGCCAT ACGGCGCAAA CTATACCGT ATTTATGATG GGCTTCCAGC
251 CCGGTTTCCC TTATCTGGGC GGCTTGCCCG AAGCATTGCA CACGCCCGGC
301 CGTGCCGTGC CGAGAACGTC CGTTCCTGCC GGTTCGGTCG GTATCGGCGG
351 CAGTCAGACC GGTGTGTATC CGTTCGCTTC GCCCGGCGGC TGGCAGATTA
401 TCGGCAGAAC CGAATTACCC TTGTTCCGAG CCGATTTGAA TCCGCCGACC
451 CTGCTGGCGG CGGGTGACCA AGTCCGCTTT GTTGAGAAA GGATTGAGCC
501 ATGA

```


1232

This corresponds to the amino acid sequence <SEQ ID 2598; ORF 758>:

```
m758.pep
  1  MNNLTVFTRF DTDLATLADE LQYVWEHTAV TDHQGKLVEI PVCYGGGEYGP
 51  DLAEVAAFHQ TVISEIVRRH TAQTYTVFMM GFQPGFPYLG GLPEALHTPR
101  RAVPRTSVPA GSVGIGGSQT GVYPFASPGG WQIIGRTELP LFRADLNPPT
151  LLAAGDQVRF VAERIEP*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2599>:

```
a758.seq
  1  ATGAACAATC TGACCGTGT CACCCGTTTC GATACCGATT TGGCGACGCT
 51  TGCCGATGAA TTGCAAIATG TGTGGGAACA CACCGCCGTT ACAGACCATC
101  AGGGCAAACCT GGTGAAATC CCCGTCTGCT ACGGCGGCGA ATACGGCCCG
151  GATTGGCGG AAGTCGCTGC TTTCCATCAG ACGGTTATTT CCGAAATCGT
201  CCGCCGCCAT ACGGCGCAA CTTATACCGT ATTTATGATG GGCTTCCAGC
251  CTGGTTTCCC TTATCTGGGC GGCTTGCCCG AAGCATTGCA CACGCCCGC
301  CGTGCCGTGC CGAGAACGTC CGTTCCTGCC GGTCGCTCG GTATCGGCGG
351  CAGTCAGACC GGTGTGTATC CGTTCGCTTC GCCCGGCGGC TGGCAGATTA
401  TCGGCAGAAC CGAATTACCC TTGTTCCGAG CCGATTTGAA TCCGCCGACC
451  CTGCTGGCGG CGGTGACCA AGTCCGCTTT GTTGCAGAAA GGATTGAGCC
501  ATGA
```

This corresponds to the amino acid sequence <SEQ ID 2600; ORF 758.a>:

```
a758.pep..
  1  MNNLTVFTRF DTDLATLADE LQYVWEHTAV TDHQGKLVEI PVCYGGGEYGP
 51  DLAEVAAFHQ TVISEIVRRH TAQTYTVFMM GFQPGFPYLG GLPEALHTPR
101  RAVPRTSVPA GSVGIGGSQT GVYPFASPGG WQIIGRTELP LFRADLNPPT
151  LLAAGDQVRF VAERIEP*
```

m758 / a758 100.0% identity in 167 aa overlap

	10	20	30	40	50	60
m758.pep	MNNLTVFTRF	DTDLATLADE	LQYVWEHTAV	TDHQGKLVEI	PVCYGGGEYGP	DLAEVAAFHQ
a758	MNNLTVFTRF	DTDLATLADE	LQYVWEHTAV	TDHQGKLVEI	PVCYGGGEYGP	DLAEVAAFHQ
	70	80	90	100	110	120
m758.pep	TVISEIVRRH	TAQTYTVFMM	GFQPGFPYLG	GLPEALHTPR	RAVPRTSVPA	GSVGIGGSQT
a758	TVISEIVRRH	TAQTYTVFMM	GFQPGFPYLG	GLPEALHTPR	RAVPRTSVPA	GSVGIGGSQT
	130	140	150	160		
m758.pep	GVYPFASPGG	WQIIGRTELP	LFRADLNPPT	LLAAGDQVRF	VAERIEP*	
a758	GVYPFASPGG	WQIIGRTELP	LFRADLNPPT	LLAAGDQVRF	VAERIEP*	

g759.seq not found yet

g759.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2601>:

```
m759.seq
  1  ATGCGCTTCA CACACACCAC CCCATTTTGT TCCGTATTGT CCACCCTCGG
 51  TCTTTTGGCC GTTTCCTCTG CTTACTCATC CATTGTCCGC AACGATGTCG
101  ATTACCAATA TTTTCGCGAC TTTGCCGAAA ATAAAGGCGC GTTCACCGTA
151  GGTGCAAGCA ATATTTCCAT CCAAGACAAG CAAGGCAAAA TATTAGGCAG
201  GGTTCTCAAC GGCATCCCCA TGCCCCGACTT CCGCGTCAGC AACCGCCAAA
251  CCGCCATCGC CACCCTGGTT CACCCCAAT ACGTCAACAG TGTCAAACAC
301  AACGTCGGCT ACGGTTCCAT ACAATTCGGC AACGACACCC AAAATCCAGA
351  AGAACAAAGC TATACCTACC GCCTCGTATC ACGCAACCCG CACCCGACT
401  ACGACTACCA CCTTCCCCGC CTCAACAAAC TGTTACCGA AATCTCACCT
```

451 ACCGCACTCA GCAGCGTACC CTTGCTTGGA AACGGCCAGC CAAAGGCCAA
 501 TGCCTACCTC GATACCGACC GCTTCCCCTA CTTTGTACGA CTCGGCTCAG
 551 GCACGCAACA AGTCCGCAAA GCAGACGGCA CGCGTACAG AACCGCCCCG
 601 GCATACCAAT ACCTGACCGG CGGCACGCGG CTGAAAGTAT TGGGGTTCCA
 651 AAACCCACGGC TTA CTGTCG GCGGCAGCCT GACCGACCAA CCCCTTAACA
 701 CCTACGCAAT CGCCGGAGAC AGCGGTTCCT CCCTGTTTGC CTTGACAAAG
 751 CATGAAAACC GCTGGGTGCT TGCGGGCGTA CTCAGCACCT ACGCCGGCTT
 801 CGATAATTTT TTCAACAAAT ACATCGTCAC GCAACCCGAA TTCATCCGTT
 851 CCACCATCCG CCAATACGAA ACCCGGCTGG ATGTCGGGCT GACCACCAAC
 901 GAACTCATAT GGCGCGACAA CGGTAATGGC AACAGCACCC TGAAGGGCT
 951 CAACGAACGC ATCACCTGCT CCATTGCAAA CCCTTCGCTT GCCCCACAAA
 1001 ACGACAGCAG GCACATGCCG TCTGAAGATG CCGGCAAAAC GCTCATCCTA
 1051 TCCAGCAGGT TCGACAACAA AACACTGATG CTGGCAGACA ATATCAACCA
 1101 AGGCGCAGGC GCATTGCTAGT TCGACAGCAA CTTACCCGTC GTCGGTAAAA
 1151 ACCACACATG GCAAGGTGCA GCGTTATCG TAGCCGACGG CAAACGCGTC
 1201 TTCTGGCAAG TCAGCAACCC CAAAGGCGAC CGGCTCTCCA AACTGGGCGC
 1251 AGGCACGCTT ATCGCCAACG GACAAGGCAT CAACCGGGC GACATCAGCA
 1301 TCGGGGAAGG CACTGTCGTA CTCGCCCAA AAGCTGCTTC AGACGGCAGC
 1351 AAACAAGCAT TCAACCAAGT CGGCATCACC AGCGGCAGGG GCACGGCCGT
 1401 CCTCGCCGAC AGCCAGCAAA TCAAACCCGA AAACCTCTAT TTCGGCTTCA
 1451 GGGCGGACG GCTCGACCTC AACGGCAACA ACCTTGCTT TACCCATATC
 1501 CGCCATGCGG ACGGCGGCGC GCAAATCGTC AATCACACCC CTGACCAAGC
 1551 CGCGACACTG ACGCTGACCG GCAACCCCGT CCTCAGTCCC GAGCATGTGG
 1601 AGTGGGTGCA ATGGGGCAAC CGTCCGCAAG GCAACGCGGC GGTTCACGAA
 1651 TACATCAACC CGCACCGBAA CCGTCGGACC GACTACTTCA TACTCAAACC
 1701 CGGCGGCAAC CCGCGCGAAT TTTTCCCGTT AAATATGAAA AACTCAACAA
 1751 GCTGGCAATT TATCGGCAAC AACAGGCAAC AGGCCGCCGA ACAAGTCGCC
 1801 CAAGCCGAAA ATGCCCGCCC CGACCTGATT ACCTTCGGCG GATACTTGGG
 1851 TGAACACGCG CAAACGGGCA AAGCCGCGCC GAGTTACAGC AAAACCAATG
 1901 AAGCAGCCAT AGAAAAAACC CGCCATATCG CAAATGCCGC CGTATACGGC
 1951 CGGCCCGAAT ACCGTTACAA CGGCGCACTC AACCTGCACT ATCGTCCCAA
 2001 ACGCACCGAC AGCAGCTGTG TGCTCAACGG CGGCATGAAC CTTAACGGGG
 2051 AAGTCTTGAT TGAGGGCGGC AATATGATTG TGTCAGGCAG GCCCGTACCC
 2101 CATGCCATAC ACCACCAGGC CAAACGCGAA CCCGTTCTTG AAAACGAATG
 2151 GACCGACGGC AGCTTCAAGG CTGCACGGTT CACCCTGCGA AACCATGCCC
 2201 GACTGACGGC AGGGCGCAAT ACCGCGCATC TGGACGGCGA CATAACCGCA
 2251 TACGATCTGT CCGGCATCGA CCTCGGCTTT ACCCAAGGCA AAACACCGGA
 2301 ATGCTACCGC TCCTACCATG GCGGCAGCAC CCACTGCACA CCCAACGCGC
 2351 TTTTAAAAAGC GAAAACTAT CTGCACTAC CTGCAACGCA AGTACGCGGC
 2401 GACATTACCC TTAACGACCG TTCAGAGCTC CGCCTGGGCA AAGCACACCT
 2451 GTAGGGCAGC ATCCGTGCCG GCAAAGACAC CGCAGTCCGC ATGGAAGCAG
 2501 ACAGCAACTG GACACTTTCC CAGTCCAGCC ACACCGGCGC ACTGACGCTT
 2551 GACGGCGCAC AAATTACCCT GAACCCCGAT TTCGCCAATA ATACACACAA
 2601 CAACCGCTTC AACACACTGA CCGTCAACGG CACACTTGAC GGGTTCGGCA
 2651 CATTCGATT CTTGACCGGC ATCGTCCGAA AACAAAATGC CCCCCCCTC
 2701 AAACCTGGAAG GGGACAGCGG CGGCGCATTC CAAATCCACG TCAAAAACAC
 2751 CGGACAAGAA CCTCAAAACA CCGAATCGCT TGCCTTGTG AGCCTCAATC
 2801 CGAAACACAG CCACCAAGCC CGATTACCCC TCCAAAACGG CTATGCCGAT
 2851 TTGGGTGCCCT ACCGCTACAT CCTCCGCAAA AACAAACAG GATACAGCCT
 2901 GTACAACCCG CTCAAAGAGG CCGAATTCAT AATTGAAGCC ACGCGTGCGG
 2951 AACATGAGCG CAACCAACAG GCATACAACC AATTACAGGC AACCGACATC
 3001 AGCAGACAGG TTCAACATGA CTCTGACGCG ACCAGGCAGG CACTACAGGC
 3051 CTGGCAGAAC AGTCAAACCG AACTTGCCCG CATCGACAGC CAAGTCCAAT
 3101 ATCTGTCCGC CCAATTGAAA CAGACAGACC CGTGACCGG CATTCTGACG
 3151 CGTGCCCAAA ACCTGTGTGC CGCACAAGGA TACAGTGGCG ATATCTGCCG
 3201 TCAGGTTGCC AAAGCCGCGG ACACGAACGA CCGTCACTC TTCGAAACCG
 3251 AACTGGATAC GTATATAGAA CGTGTAGAAA TGGCCGAAAT CGAACTTGAC
 3301 AAAGCACGGC AAGGCGGCGA TGCGCAAGCC GTCGAAACAG CCCGGCACGC
 3351 CTACCTGAAC GCACTCAACC GTCTGTCCCG ACAAATCCAC AGTTTGAAAA
 3401 CCGGCGTTGC CGGCATCCGT ATGCCGAACC TGGCCGAAT GATCAGCCGG
 3451 TCGGCCAACA CCGCGTTTC CGAACAGGCC GCCTACAATA CCGGCCGGCA
 3501 ACAGGCGGGA CGCCGCATCG ACCGCCACCT TACCGATCCG CAGCAGCAAA
 3551 ACATCTGGCT GGAACCCGGT ACGCAACAAA CCGACTACCA TAGCGGCACA
 3601 CACCGTCCCT ACCAACAAAC TACCAACTAT GCACATATCG GCATCCAAC
 3651 CGGCATCACC GACCGTCTCA GTGTGCGTAC GATTTTAACC GATGAGCGCA
 3701 CAAACAACCG TTTTGATGAA GCGGTATCCG CCCGAAACCG CAGCAACGGC

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3751 GCACATCTGT TCGTCAAAGG GGAAAACGGC GCACTCTTTG CCGCGGCAGA
3801 TTTAGGCTAC AGCAACAGCC GTACCCGATT TACCGATTAT GACGGGGCTG
3851 CCGTCCGCCC CCACGCATGG GATGCAGGCA TCAACACCGG CATCAAATC
3901 GATACCGGCA TCAACCTCAG ACCCTATGCC GGCATCCGTA TAAACCGCAG
3951 CAACGGCAAC CCGTACGTAC TCGACGGCGC AGAGATAAAC AGCCCGGCGC
4001 AAATCCAAAC CACATGGCAT GCCGGCATCC GTCTCGATAA AACCCTCGAA
4051 CTGGGTCAAG CCAAGCTGAC CCCCGCCTTC AGCAGCGATT ACTACCATAC
4101 CCGCCAAAAC AGCGGTTCCT CCCTCAGCGT CAACGACCGT ACCTTACTGC
4151 AGCAAGCCCG CCACGGCACA CTGCATACCC TGCAAAATCGA CGCCGGGATA
4201 AAAGGCTGGA ACGCCAAACT TCATGCCGCT TACGGCAAAG ACAGCAACAC
4251 CGCCCGCCAC AAACAGGCAG GAATCAAAT AGGCTACAAC TGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2602; ORF 759>:

```

m759.pep
1  MRFTHTTFFC SVLSTLGLFA VSPAYSSIVR NDVDYQYFRD FAENKGAFV
51  GASNISIQDK QGKILGRVLN GIPMPDFRVS NRQTAIATLV HPQYVNSVKH
101 NVGYGSIQFG NDTQNPEEQA YTYRLVSRNP HEDYDYHLPR LNKLVTEISP
151 TALSSVPLLG NGQPKANAYL DTDREFFYFVR LSGTQQVRK ADGTRTRTAP
201 AYQYLTGGTP LKVLGFQNHG LLVGGSLTDQ PLNTYAIAGD SGSPLFAFDK
251 HENRWVLAGV LSTYAGFDNF FNKYIVTQPE FIRSTIRQYE TRLDVGLTTN
301 ELIWRDNGNG NSTLQGLNER ITLPIANPSL APQNDSRHMP SEDAGKTLIL
351 SSRFDNKTLM LADNINQAG ALQFDSNFTV VGKNHTWQGA GVIVADGKRV
401 FWQVSNPKGD RLSKLGAGTL IANGQGINQG DISIGEGTVV LAQKAASDGS
451 KQAFNQVGIT SGRGTAVLAD SQQIKPENLY FGFRGGRLDL NGNNLAFTHI
501 RHADGGAQIV NNNPDQAATL TLTGNPVLSP EHVEWVQWGN RPQGNAAVYE
551 YINPHNRNRT DYFILKPGGN PREFFPLNMK NSTSWQFIGN NRQQAEEQVA
601 QAENARPDLI TFGGYLGENA QTGKAAPSYS KTNEAAIEKT RHIANAAVYG
651 RPEYRYNGAL NLHYRPKRTD STLLLNGGMN LNEVLIEGG NMIVSGRPVP
701 HAYDHOAKRE PVLENEWTDG SFKAARFTLR NHARLTAGRN TAHLDGDITA
751 YDLSGIDLGF TQKKTPECYR SYHSGSTHCT PNAVLKAENY RALPATQVRG
801 DITLNDREL RLKAHLYGS IRAGKDTAVR MEADSNWTL SSSHTGALT
851 DGAQITLNPD FANNTNNRF NTLTVNGTLD GFGTFRELTG IVRKQNPPL
901 KLEGDSTRGAF QIHVKNTGQE PQTTESLALV SLNPKHSHQA RETLQNGYAD
951 LGAYRYILRK NNGGYSLYNP LKEAELQIEA TRAEHERNQQ AYNQLQATDI
1001 SRQVQHSDA TRQALQAWQN SQTELARIDS QVQYLSAQLK QTDPLTGILT
1051 RAQNLCAAGG YSADICRQVA KAADTNDLTL FETELDTYIE RVEMAESELD
1101 KARQGGDAQA VETARHAYLN ALNRLSRQIH SLKTGVAGIR MPNLAEELIS
1151 SANTAVSEQA AYNTGRQAG RRIDRHLTDP QQONIWLETG TQOTDYHSGT
1201 HRPYQTTNY AHIGIQTGIT DRLSVGTILT DERTNNRFE GVSARNRSNG
1251 AHLFVKGENG ALFAAADLGY SNSRTRETDY DGAAVRRHAW DAGINTGIKI
1301 DTGINLRPYA GIRINRSNGN RYVLDGAEIN SPAQIQTWH AGIRLDKTV
1351 LGQAKLTPAF SSDYYHTRQN SGSALSVNDR TLLQQAAGT LHTLQIDAGY
1401 KGWNAKLHAA YGKDSNTARH KQAGIKIGYN W*

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2603>:

```

g760.seq (partial)
1  AACAAACGCA ACACCCGTTA CGCCGCATTG GGCAAACGCG TGATGGAAGG
51  CGTTGAGACC GAAATCAGCG GTGCGATTAC ACCGAAATGG CAAATCCATG
101 CAGGTTACAG CTATCTGCAC AGCCAAATCA AAACCGCCGC CAATCCACGC
151 GACGACGGCA TCTTCCTGCT GGTGCCCAA CACAGCGCAA ACCTGTGGAC
201 GACTTACCAA GTTACGCCCG GGCTGACCGT CGGCGCGCGC GTGAACGCGA
251 TGAGCGGCAT TACTTCATCT CCAGGGATGC ATGACGGCGG TTATGCCACG
301 TTCGATCGCA TGGCGGCATA CCGCTTCACG CCCAAGCTGA AGCTGCAAAT
351 CAATGCCGAC AACATCTTCA ACCGCCATTA CTACGCCCGC GTCGGCGGCA
401 CGAACACCTT TAACATTCCC GGTTCGGAGC GCAGCCTGAC GGCAAACCTG
451 CGTTACAGTT TTAA

```

This corresponds to the amino acid sequence <SEQ ID 2604; ORF 760.ng>:

```

g760.pep (partial)
1  NNRNTRYAAL GKRVMGCVET EISGAITPKW QIHAGYSYLH SQIKTAANPR
51  DDGIFLLVPK HSANLWTTYQ VTPGLTVGGG VNAMSGITSS AGMHAGGYAT
101 FDAMAAYRFT PKLKLQINAD NIFNRHYAR VGGTNTFNIP GSERSLTANL
151 RYSF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2605>:

```
m760.seq
1  ATGGGACAGT TTATGTCAGT TTTCCGCATC AATATGACCG CCGCCACGGT
51  TTTGGCAGCA CTCTCGTCTT CGGTTTTTGC CGCACAAACG GAAGGTTTGG
101 AAACCGTCCA TATTAAGGGT CAGCGTTCTT ACAACGCGAT TGCCACCGAG
151 AAAAAACGGC ATTACAGCTC GTTTGCCGCC ACCGTCGGTA CAAAAATCCC
201 CGCTTCTTTG CGCGAAATTC CGCAATCCGT CAGCATCATT ACCAACCAGC
251 AGGTCAAAGA CCGCAATGTT GATACGTTTG ACCAGTTGGC ACGCAAAACG
301 CCCGGCCTGC GCGTGTGAG CAACGACGAC GGACGCTCTT CGGTTTACGC
351 GCGCGGTTAC GAATACAGCG AATACAACAT CGACGGCCTG CCCGCGCAGA
401 TGCAGAGTAT CAACGGCAGC CTGCCCCAACC TGTTCGCCTT CGACCGCGTG
451 GAAGTGATGC GCGGGCCGAG CGGACTGTTC GACAGCAGCG GCGAGATGGG
501 CGGCATCGTG AATCTGGTGC GCAAACGCCC GACCAAAGCG TTCCAAGGTC
551 ATGCGGCGGC AGGTTTCGGT ACGCACAAAC AATATAAGC CGAGGCGGAC
601 GTATCGGGCA GCCTCAATTC AGACGGCAGC GTGCGCGGCC GCGTGATGGC
651 GCAGACCGTC GCGCGCTCTC CGCGTCCCGC CGAGAAAAAC AACC GGCGCG
701 AAACCTTCTA CGCGCGCGCG GATTGGGACA TCAACCCCGA TACGGTTTTG
751 GCGCGGGGCT ATCTTTACCA GCAACGCGCG CTCGCGCCGT ACAACGCGCT
801 GCCTGCCGAT GCCAATAACA AATTACCGTC CCTGCCGCAA CACGTATTTG
851 TCGGCGCGGA TTGGAACAAA TTAAAAATGC ACAGCCACGA CGTGTTCGCC
901 GATTTGAAAC ATTACTTCGG CAACGGCGGC TACGGCAAAG TCGGTATGCG
951 CTATTCGGAT CGGAAAGCCG ATTCCAATTA TACGTTTTCG GCGAGCAAAC
1001 TCAACAATAC CGGACAAGCC GACGTAGCGG GTTTGGGTAC GGACATTAAA
1051 CAAAAAGCCT TTGCGGTTGA CGCAAGTTAC AGCCGTCCGT TTGCCTTGGG
1101 CAACACCGCC AACGAATTTG TGATTGGTGC AGACTACAAC CGCTTGCGCA
1151 GTACTAATGA ACAAGGGCGT TCGACTTTGT CAAAAAGCGT CGCTTTAGAT
1201 GGTTTCCGCG CTTTGCCTTA TAACGGCATA CTTCAGAACG CCCGCGCCGG
1251 AAACAAAGGT TTCAATCACT CCGTTACCGA AGAAAACCTC GACGAAACCG
1301 GTTTGTATGC CAAGACGGTG TTCCGTCCTC TGGAAAGGTT GTCGTTGATT
1351 GCAGGCGGAC GTGTAGGACA TCACAAAATC GAGTCGGGCG ACGGCAAAAC
1401 CCTGCATAAA GCTTCGAAAA CCAAATTTAC AAGCTACGCC GGCGCGGTTT
1451 ACGATATAGA CGGCAGCAAC AGCCTGTACG CTTCCGCCTC CCAACTCTAC
1501 ACACCGCAAA CCAGCATCGG CACCGACGEC AAGCTGCTCA AACC GCGCGA
1551 AGGCAACCAG TTTGAAATCG GCTACAAAGG CAGCTACATG GACGACCGCC
1601 TCAATACCCG GGTTCGTTTC TACCGCATGA AGGATAAAAA CGCCGCGCGA
1651 CCGCTGGACT CAAACAACAA AAAAACCCTG TACGCCGCAT TGGGCAAAACG
1701 CGTGATGGAA GGTGTTGAGA CCGAAATCAG CGGCGCGATG ACACCGAAAT
1751 GGCAAATCCA TGCAGGTTAC AGCTACCTGC ACAGCCAAAT CAAAACCGCC
1801 TCCAATTTCG GCGACGAAGG CATCTTCTTG CTGATGCCCA AACACAGCGC
1851 AAACCTGTGG ACGACTTACC AAGTTACGTC CGGGCTGACC ATCGGCGGCG
1901 GCGTGAACGC GATGAGCGGC ATTACTTCAT CTGCAGGGAT ACATGCAAGC
1951 GGTTATGCCA CGTTCGATGC GATGGCGGCA TACCGCTTCA CGCCCAAACCT
2001 GAAGCTGCAA ATCAACGCCG ACAACATCTT CAACCGCAT TACTACGCCC
2051 GCGTCGGCAG CGAGAGCACC TTAAACATTC CCGGTTCCGA GCGCAGCCTG
2101 ACGGCAAACC TCGGTTACAG TTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 2606; ORF 760>:

```
m760.pep
1  MQQFMSVFRI NMTAATVLAA LSSSVFAAQT EGLETVHIKQ QRSYNAIATE
51  KNGDYSSFAA TVGTKIPASL REIPQSVSII TNQQVKERNV DTFDQLARKT
101 PGLRVLNSDD GRSSVYARGY EYSEYNIDGL PAQMOSINGT LPNLFAPDRV
151 EVMRGP SGLF DSSGEMGGIV NLVRKRPTKA FQGHAAAGFG THKQYKAED
201 VSGSLNSDGS VRGRVMAQTV GASPRPAEKN NRRETFYAAA DWDINPDTVL
251 GAGYLYQQR LAPIYNGLPAD ANNKLPSLPQ HVFVGADWNK FKMHS HDVFA
301 DLKHYFGNGG YGKVMRYSD RKADSNYTFA GSKLNNTGQA DVAGLGTDIK
351 QKFAFVDASY SRPFALGNTA NEFVIGADYN RLRSTNEQGR STLKSV ALD
401 GFRALPYNGI LQNRAGNKG FNHSVTEENL DETGLYAKTV FRPLEGLSLI
451 AGGRVGH HKI ESGDGKTLHK ASKTKFTSYA GAVYDIDGSN SLYASASQLY
501 TPQTSIGTDG KLLKPREGNQ FEIGYKGSYM DDRLNTRVSF YRMKDKNAAA
551 PLDSNNK KTR YAALGKRVME GVETEISGAM TPKWQIHAGY SYLHSQIKTA
601 SNRDEGIFL LMPKHSANLW TTYQVTSGLT IGGGVNAMSG ITSSAGIHAG
651 GYATFDAMAA YRFTPKLKLQ INADNIFNRH YYARVGSEST FNIPGSERSL
701 TANLRYSF*
```

1236

m760 / g760 91.6% identity in 154 aa overlap

	530	540	550	560	570	580
m760.pep	YKGSYMDRLNTRVSYRMRKDKNAAPLDSNNKKTRYAALGKRVMEGVETEISGAMTPKW					
				:		
g760			NNRNRTRYAALGKRVMEGVETEISGAITPKW			
			10	20	30	
	590	600	610	620	630	640
m760.pep	QIHAGYSYLHSQIKTASNSRDEGIFLLMPKHSANLWTTYQVTSGLTIGGGVNAMSGITSS					
g760	QIHAGYSYLHSQIKTAAANPRDDGIFLLVPKHSANLWTTYQVTPGLTVGGGVNAMSGITSS					
	40	50	60	70	80	90
	650	660	670	680	690	700
m760.pep	AGIHAGGYATFDAMAAYRFTPKLKLQINADNIFNRHYARVGSESTENIPGSESLTANL					
	:					
g760	AGMHAGGYATFDAMAAYRFTPKLKLQINADNIFNRHYARVGSTNTENIPGSESLTANL					
	100	110	120	130	140	150
	709					
m760.pep	RYSFX					
g760	RYSFX					

g761.seq not found yet

g761.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2607>:

```

m761.seq
1  ATGAAATAT  CATTTCATTT  AGCTTTATTA  CCCACGCTGA  TTATTGCTTC
51  CTTCCCTGTT  GCTGCCGCCG  ATACGCAGGA  CAATGGTGAA  CATTACACCG
101 CCACTCTGCC  CACCGTTTCC  GTGGTCGGAC  AGTCCGACAC  CAGCGTACTC
151 AAAGGCTACA  TCAACTACGA  CGAAGCCGCC  GTTACCCGCA  ACGGACAGCT
201 CATCAAAGAA  ACGCCGCAAA  CCATCGATAC  GCTCAATATC  CAGAAAAACA
251 AAAATTACGG  TACGAACGAT  TTGAGTTCCA  TCCTCGAAGG  CAATGCCGGC
301 ATCGACGCTG  CCTACGATAT  GCGCGGTGAA  AGCATTTTCC  TCGCGGGTTT
351 TCAAGCCGAC  GCATCCGATA  TTTACCGCGA  CGGCGTGCGC  GAAAGCGGAC
401 AAGTGCGCCG  CAGTACTGCC  AACATCGAGC  GCGTGGAAT  CCTGAAAGGC
451 CCGTCTTCCG  TGCTTTACGG  CCGCACCAAC  GCGCGCGGCG  TCATCAACAT
501 GGTCAGCAAA  TACGCCAACT  TCAAACAAAG  CCGCAACATC  GGAGCGGTTT
551 ACGGCTCATG  GGCAAAACGC  AGCCTGAATA  TGGACATTAA  CGAAGTGCTG
601 AACAAAAACG  TCGCCATCCG  TCTCACCGGC  GAAGTCGGGC  GCGCCAATTC
651 GTTCCGCAGC  GGCATAGACA  GCAAAAATGT  CATGGTTTCG  CCCAGCATTG
701 CCGTCAAAC  CGACAACGGC  TTGAAGTGGA  CGGGGCAATA  CACCTACGAC
751 AATGTGGAGC  GCACGCCGGA  CCGCAGTCCG  ACCAAGTCCG  TGTACGACCG
801 CTTCCGACTG  CCTTACCGCA  TGGGGTTCGC  CCACCGGAAC  GATTTTGTCG
851 AAGACAAGCT  GCAAGTTTGG  CGTTCGACC  TTGAATACGC  CTTCAACGAC
901 AAATGGCGTG  CCCAATGGCA  GCTCGCCAC  CGCACGGCGG  CGCAGGATTT
951 TGATCATTTC  TATGCAGGCA  GCGAAAATGG  CAACTTAATC  AAACGTAAC
1001 ACGCCTGGCA  GCAGACCGAC  AACAAAACCC  TGTCGTCCAA  CTTAACGCTC
1051 AACGGCGACT  ACACCATCGG  CCGTTTGA  AACCACCTGA  CCGTAGGCAT
1101 GGATTACAGC  CGCGAACACC  GCAACCCGAC  ATTGGGTTTC  AGCAGCGCCT
1151 TTTCCGCCTC  CATCAACCCC  TACGACCGCG  CAAGCTGGCC  GGCTTCGGGC
1201 AGATTGCAGC  CTATTCTGAC  CCAAAAACGC  CACAAAGCCG  ACTCTACGG
1251 CATCTTTGTG  CAAAACATCT  TCTCCGCCAC  GCCCGATTG  AAATTCGTCC
1301 TCGGCGGCCG  TTACGACAAA  TACACCTTTA  ATTCGGA  CAAACTCACC
1351 GGCAGCAGCC  GCCAATACAG  CGGACACTCG  TTCAGCCCCA  ACATCGGCGC
1401 AGTGTGGAAC  ATCAATCCCG  TCCACACACT  TTACGCCTCG  TATAACAAAG
1451 GCTTCGGGCC  TTATGGCGGA  CGCGGCGGCT  ATTTGAGCAT  CGATACGTTG
1501 TCTTCGCGCG  TGTTCAACGC  CGACCCGAG  TACACCCGCC  AATACGAAAC
1551 CGGCGTGAAA  AGCAGTGGC  TGGACGACCG  CCTCAGCACT  ACGTTGTCTG
1601 CCTACCAAAT  CGAACGCTTC  AATATCCGCT  ACCGCCCCGA  TCCAAAAAAC
1651 AACCTTATA  TTTATGCGGT  TAGCGGCAAA  CACCGTTCGC  GCGGCGTGGA

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1701 ATTTGTCGCC ATCGGGCAAA TCATCCCCAA AAAACTCTAT CTGCGCGGTT
1751 CGTTGGGCGT GATGCAGGCG AAAGTCGTTG AAGACAAAGA AAATCCCGAC
1801 CGAGTGGGCA TCCATTGAA TAATACCAGC AACGTTACCG GCAACCTGTT
1851 TTTCCGTTAT ACCCGGACCG AAAACCTCTA CGGCGAAATC GGCCTAACCG
1901 GTACAGGCAA ACGCTACGGT TACAACCTAA GAAATAAAGA AGTGACTACG
1951 CTTCCAGGCT TTGCCGAGT TGATGCCATG CTTGGCTGGA ACCATAAAAA
2001 TGTTAACGTT ACCTTTGCCG CAGCCAATCT GCTCAATCAA AAATATTGGC
2051 GTTCGGACTC TATGCCGGGT AATCCGCGCG GCTATACTGC CCGGGTAAAT
2101 TACCGTTTCT GA

```

This corresponds to the amino acid sequence <SEQ ID 2608; ORF 761>:

```

m761.pep
1 MKISFHLALL PTLIIASFPV AAADTDQNGE HYTATLPTVS VVGQSDTSVL
51 KGYINYDEAA VTRNGQLIKE TPQTIDTLNI QKNKNYGTND LSSILEGNAG
101 IDAAYDMRGE SIFLRGFQAD ASDIYRDGVR ESGQVRRSTA NIERVEILKG
151 PSSVLYGRTN GGGVINMVSX YANFKQSRNI GAVYGSWANR SLNMDINEVL
201 NKNVAIRLTG EVGRANSFRS GIDSKNMVVS PSITVKLDNG LKWTGQYTYD
251 NVERTPDRSP TKSVDREGL PYRMGFAHRN DFKVDKLQVW RSDLEYAFND
301 KWARQWQLAH RTAAQDFDHF YAGSENGNLI KRNYAWQQTQ NKTLSNLTL
351 NGDYITIGRFE NHLTVGMDYS REHRNPTLGF SSAFSASINP YDRASWPASG
401 RLQPILTQNR HKADSYGIFV QNIFSATPDL KFLVGGRYDK YTFENSEKLT
451 GSSRQYSQHS FSPNIGAVWN INPVHTLYAS YNKGFPYGG RGGYLSIDTL
501 SSAVFNDADPE YTRQYETGVK SSWLDDRLST TLSAYQIERF NIRYRDPKPN
551 NPYIYAVSGK HRSRGVLSA IGQIIPKKLY LRGS LGVMQA KVVEDKENPD
601 RVGIHLNNTS NVTGNLFFRY TPTENLYGEI GVTGTGKRYG YNSRNKEVTT
651 LPGAARVDAM LGWNHKNVNV TFAANLLNQ KYWRSDSMPG NPGYTARVN
701 YRF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2609>:

```

a761.seq
1 ATGAAATAT CATTTCATT AGCTTTATTA CCCACGCTGA TTATTGCTTC
51 CTTCCTGTT GTCGCCGCG ATACGCAGGA CAATGGTGAA CATTACACCG
101 CCACTCTGCC CACCGTTTCC GTGGTCGGAC AGTCCGACAC CAGCGTACTC
151 AAAGGCTACA TCAACTACGA CGAAGCCGCC GTTACCCGCA ACGGACAGCT
201 CATCAAAGAA ACGCCGCAAA CCATCGATAC GCTCAATATC CAGAAAAACA
251 AAAATTACGG CACGAACGAT TTGAGTTCCA TCCTCGAAGG CAATGCCGGC
301 ATCGACGCGC CCTACGATAT GCGCGGCGAA AGCATTTTCC TCGCGCGCTT
351 TCAAGCCGAC GCATCTGATA TTTACCGCGA CGGCGTACGC AAAAGCGGGC
401 AGGTGCGCGC TAGCACCGCC AACATCGAGC GCGTGGAAT CCTGAAGGT
451 CCGTCTCCG TGCTTTATGG GCGTACCAAC GCGGCGGGT TCATCAACAT
501 CCGTCAGCAA TACGCCAACT TCAACAAAG CCGTAATATC GGTACGGTTT
551 ATGGTTCGTG GGCAACCGC AGCCTGAATA TGGACATCAA CGAAGTGCTG
601 AAAAAAAGC TCGCCATCCG TCTCACCAGC GAAGTCGGGC GCGCCAATTC
651 GTTCCGAGC GGCATAGACA GCAAAAATGT CATGGTTTCG CCCAGCATTA
701 CCGTCAAAC CEACAACGGC TTGAAGTGGA CGGGGCAATA CACCTACGAC
751 AATGTGGAGC GCACGCCCGA CCGCAGTCCG ACCAAGTCCG TGTACGACCG
801 CTTCGGACTG CCTTACCGCA TGGGGTTCGC CCACCGGAAC GATTTTGTC
851 AAGACAAGCT GCAAGTTTGG CGTTCGGACC TTGAATACGC CTTCACGAC
901 AAATGGCGTG CCCAATGGCA GCTCGCCAC CGCACGGCGG CGCAGGATT
951 TGATCATTTT TATGCAGGCA GCGAAAATGG CAACTTAATC AAACGTAAT
1001 ACGCCTGGCA GCAGACCGAC AACAAAACCC TGTCGTCCAA CTTAACGCTC
1051 AACGGCGACT ACACCATCGG CCGTTTGTAA AACCACCTGA CCGTAGGCAT
1101 GGATTACAGC CGCGAACACC GCAACCCGAC ATTGGGTTTC AGCAGCGCCT
1151 TTTCCGCTC CATCAACCCC TACGACCGCG CAAGCTGGCC GGCTTCGGGC
1201 AGATTGCAGC CTATTCTGAC CCAAAACCGC CACAAAGCCG ACTCCTACGG
1251 CATCTTTGTG CAAAACATCT TCTCCGCCAC GCCGATTTCG AAATTCGTCC
1301 TCGGCGGCGG TTACGACAAA TACACCTTTA ATTCGAAAA CAACTCACC
1351 GGCAGCAGCC GCAATACAG CGGACACTCG TTCAGCCCCA ACATCGGCGC
1401 AGTGTGAAC ATCAATCCCG TCCACACACT TTACGCTCG TATAACAAAG
1451 GCTTCGCGCC TTATGGCGGA CGCGGCGGCT ATTTGAGCAT CGATACGTTG
1501 TCTTCGCGCG TGTTCACGCG CGACCCGAG TACACCCGCC AATACGAAAC
1551 CGGCGTGAAA AGCAGTTGGC TGGACGACCG CCTCAGCACT ACCTGTCTG
1601 CCTACCAAAT CGAACGCTTC AATATCCGCT ACCGCCCCGA TCCAAAAAAC
1651 AACCCTTATA TTTATCGGCT TAGCGGCAAA CACCGTTCGC GCGCGTGGA
1701 ATTGTCCGCC ATCGGGCAAA TCATCCCCAA AAAACTCTAT CTGCGCGGTT

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1751 CGTTGGGCGT GATGCAGGCG AAAGTCGTTG AAGACAAAGA AAATCCCGAC
1801 CGAGTGGGCA TCCATTTGAA TAACACCAGC AACGTTACCG GCAACCTGTT
1851 TTTCCGTTAT ACCCCGACCG AAAACCTCTA CGGCGAAATC GGCCTAACCG
1901 GTACAGGCAA ACGCTACGGT TACGACTCAA GAAATAAAGA AGTGACTACG
1951 CTTCCAGGCT TTGCCGAGT TGATGCCATG CTTGGCTGGA ACCATAAAAA
2001 TGTTAACGTT ACCTTTGCCG CAGCCAATCT GTTCAATCAA AAATATTGGC
2051 GTTCGACTC TATGCCGGT AATCCGCGC GCTATACTGC CCGGGTAAAT
2101 TACCGTTTCT GA

```

This corresponds to the amino acid sequence <SEQ ID 2610; ORF 761.a>:

```

a761.pep
1  MKISFHLALL PTLIIASFPV AAADTQDNGE HYTATLPTVS VVGQSDTSVL
51  KGYINYDEAA VTRNGQLIKE TPQTIØTLNI QKNKNYGTND LSSILEGNAG
101 IDAAYDMRGE SIFLRGFQAD ASDIYRDGVR ESGQVRRSTA NIERVEILKG
151 PSSVLYGRTN GGGVINMVSX YANFKQSRNI GTVYGSWANR SLNMDINEVL
201 NKNVAIRLTG EVGRANSFRS GIDSKNVMVS PSITVKLDNG LKWTGQYTYD
251 NVERTPDRSP TKSVDYDRFGL PYRMGFAHRN DFVKDKLQVW RSDLEYAFND
301 KWRAQWQLAH RTAAQDFDHF YAGSENGNLI KRNYAQQTØ DNKTLSNLT
351 NGDYTIGREF NHLTVGMDYS REHRNPTLGF SSAFSASINP YDRASWPASG
401 RLQPILTQNR HKADSYGIFV QNIFSATPDL KFLVGGRYDK YTFENSENKL
451 GSSRQYSGHS FSPNIGAVWN INPVHTLYAS YNKGFAFYGG RGGYLSIDTL
501 SSAVENADPE YTRQYETGVK SSWLDDRLST TLSAYOIERF NIRYRPPDKN
551 NPYIYAVSGK HRSRGVELSA IGQIIPKKLY LRGSILGVMQA KVEDKENPD
601 RVGIHLNNTS NVTGNLFFRY TPTENLYGEI GVTGTGKRYG YDSRNKEVTT
651 LPGFARVDAM LGWNHKNVNV TFAANLNFQ KYWRSDSMPG NPRGYTARVN
701 YRF*

```

m761 / a761 99.6% identity in 703 aa overlap

	10	20	30	40	50	60
m761.pep	MKISFHLALLPTLIIASFPVAAADTQDNGEHYTATLPTVSVVVGQSDTSVLKGYINYDEAA					
a761	MKISFHLALLPTLIIASFPVAAADTQDNGEHYTATLPTVSVVVGQSDTSVLKGYINYDEAA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m761.pep	VTRNGQLIKETPQTIØTLNIQKNKNYGTNDLSSILEGNAGIDAAYDMRGESIFLRGFQAD					
a761	VTRNGQLIKETPQTIØTLNIQKNKNYGTNDLSSILEGNAGIDAAYDMRGESIFLRGFQAD					
	70	80	90	100	110	120
	130	140	150	160	170	180
m761.pep	ASDIYRDGVRESGQVRRSTANIERVEILKGPSSVLYGRTNGGGVINMVSXYANFKQSRNI					
a761	ASDIYRDGVRESGQVRRSTANIERVEILKGPSSVLYGRTNGGGVINMVSXYANFKQSRNI					
	130	140	150	160	170	180
	190	200	210	220	230	240
m761.pep	GAVYGSWANRSLNMDINEVLNKNVAIRLTGEVGRANSFRSGIDSKNVMVSPSITVKLDNG					
a761	GTVYGSWANRSLNMDINEVLNKNVAIRLTGEVGRANSFRSGIDSKNVMVSPSITVKLDNG					
	190	200	210	220	230	240
	250	260	270	280	290	300
m761.pep	LKWTGQYTYDNVERTPDRSPKSVYDRFGLPYRMGFAHRNDFVKDKLQVWRSLEYAFND					
a761	LKWTGQYTYDNVERTPDRSPKSVYDRFGLPYRMGFAHRNDFVKDKLQVWRSLEYAFND					
	250	260	270	280	290	300
	310	320	330	340	350	360
m761.pep	KWRAQWQLAHRRTAAQDFDHFYAGSENGNLIKRNIAWQQTØDNKTLSNLTNGDYTIGREF					
a761	KWRAQWQLAHRRTAAQDFDHFYAGSENGNLIKRNIAWQQTØDNKTLSNLTNGDYTIGREF					
	310	320	330	340	350	360
	370	380	390	400	410	420

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```

m761.pep      NHLTVGMDYSREHRNPTLGFSSAFSASINPYDRASWPASGRLQPILTQNRHKADSYGIFV
|||||
a761          NHLTVGMDYSREHRNPTLGFSSAFSASINPYDRASWPASGRLQPILTQNRHKADSYGIFV
              370      380      390      400      410      420

              430      440      450      460      470      480
m761.pep      QNIFSATPDLKFVLGGRYDKYTFNSENKLTGSSRQYSGHSFSPNIGAVWNINPVHTLYAS
|||||
a761          QNIFSATPDLKFVLGGRYDKYTFNSENKLTGSSRQYSGHSFSPNIGAVWNINPVHTLYAS
              430      440      450      460      470      480

              490      500      510      520      530      540
m761.pep      YNKGFPYGGGGYLSIDTLSSAVFNADPEYTRQYETGVKSSWLDRLSTTSLAYQIERF
|||||
a761          YNKGFPYGGGGYLSIDTLSSAVFNADPEYTRQYETGVKSSWLDRLSTTSLAYQIERF
              490      500      510      520      530      540

              550      560      570      580      590      600
m761.pep      NIRYRPDPKNNPYIYAVSGKHSRGVELSAIGQIIPKKLYLRGSLGVMQAKVVEDKENPD
|||||
a761          NIRYRPDPKNNPYIYAVSGKHSRGVELSAIGQIIPKKLYLRGSLGVMQAKVVEDKENPD
              550      560      570      580      590      600

              610      620      630      640      650      660
m761.pep      RVGIHLNNTSNVTGNLFFRYTPTENLYGEIGVTGTGKRYGYSRNKEVTTLPGFARVDAM
|||||
a761          RVGIHLNNTSNVTGNLFFRYTPTENLYGEIGVTGTGKRYGYDSRNKEVTTLPGFARVDAM
              610      620      630      640      650      660

              670      680      690      700
m761.pep      LGWNHKNVNVTFAAANLLNQKYWRSDSMPGNRPGYTARVNYRFX
|||||
a761          LGWNHKNVNVTFAAANLLNQKYWRSDSMPGNRPGYTARVNYRFX
              670      680      690      700

g762.seq Not yet found
g762.pep Not yet found

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2611>:

```

m762.seq
1  ATGAAGTGGT TATTAAATAT GATAATGAGA CCTATTAAAT TTAGTATGGT
51  AAATACGTTA TTATTTATTG TTATATGTAG TTCATTTTTT GATCTGCTCG
101 TTCAATTATG TACAATTTTA TTTCATAGCC AAAAAATATA CTTTATTACA
151 TTATTTTAT TATTTATTTT TAATTTTGTT ACAAATCTA TCTATATGGC
201 AATTATTTAT CCTATTTTAT ATTTTTTTAC GATAAAAAA TATTATCCTT
251 ACTCTAGGAA AGTGATAATT CTATTATCAT TAGCATTATC TATATATTTT
301 AGTTTTATGG ACTTTTACTT TTTTCCATA TATTCAGATA ACCTTAGCTA
351 TGAAACGGAG CCTTTACATT TATACATCCC TATTATTATT AATTTTTCCT
401 CACTTTTAGT TTCTAATTTT ATTTTATCTT TTATCAACAA GTAA

```

This corresponds to the amino acid sequence <SEQ ID 2612; ORF 762>:

```

m762.pep
1  MKWLLNMIMR PIKFSMVNTL LFIVICSSFF DLLVQLCTIL FHSQKIYFIT
51  LLLFIENFV TKSIYMAIIY PILYFTIKK YYPYSRKVII LLSLALSIYF
101 SEMDFYFFSI YSDNLSYETE PLHLIPIII NFFSLVSNF ILSFINK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2613>:

```

a762.seq
1  ATGAAGTGGT TATTAAATAT GATAATGAGA CCTATTAAAT TTAGTATGGT
51  AAATACGTTA TTATTTATTG TTATATGTAG TTCATTTTTT GATCTGCTCG
101 TTCAATTATG TACAATTTTA TTTCATAGCC AAAAAATATA CTTTATTACA
151 TTATTTTAT TATTTATTTT TAATTTTGTT ACAAATCTA TCTATATGGC
201 AATTATTTAT CCTATTTTAT ATTTTTTTAC GATAAAAAA TATTATCCTT
251 ACTCTAGGAA AGTGATAATT CTATTATCAT TAGCATTATC TATATATTTT

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1240

301 AGTTTATGG ACTTTACTT TTTTCCATA TATTCAGATA ACCTTAGCTA
 351 TGAACGGAG CCTTTACATT TATACATCCC TATTATTATT AATTTTTTCT
 401 CACTTTTAGT TTCTAATTTT ATTTTATCTT TTATCAACAA GTAA

This corresponds to the amino acid sequence <SEQ ID 2614; ORF 762.a>:

a762.pep
 1 MKWLLNMIMR PIKFSMVNTL LFIVICSSFF DLLVQLCTIL FHSQKIYFIT
 51 LFLLEIFNFV TKSIIYMAIIY PIIYFFTIKK YYPYSRKVII LLSLALSIYF
 101 SFMDYFFFSI YSDNLSYETE PLHLYIPIII NFFSLLVSNF ILSFINK*

m762 / a762 100.0% identity in 147 aa overlap

	10	20	30	40	50	60
m762.pep	MKWLLNMIMRPIKFSMVNTLLFIVICSSFFDLLVQLCTILFHSQKIYFITLFLLEIFNFV					
a762	MKWLLNMIMRPIKFSMVNTLLFIVICSSFFDLLVQLCTILFHSQKIYFITLFLLEIFNFV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m762.pep	TKSIYMAIIYPILYFFTIKKYYPYSRKVIIILLSLALSIYFSFMDYFFFSIYSDNLSYETE					
a762	TKSIYMAIIYPILYFFTIKKYYPYSRKVIIILLSLALSIYFSFMDYFFFSIYSDNLSYETE					
	70	80	90	100	110	120
	130	140				
m762.pep	PLHLYIPIIIINFFSLLVSNFILSFINKX					
a762	PLHLYIPIIIINFFSLLVSNFILSFINKX					
	130	140				

g763.seq not yet found

g763.pep not yet found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2615>:

m763.seq
 1 ATGACATTGC TCAATCTAAT GATAATGCAA GATTACGGTA TTCCCGTTTG
 51 CCTGACACTG ACGCCCTATT TGCAACATGA ACTATTTTCG GCTATGAAAT
 101 CCTATTTTTC CAAATATATC CTACCCGTTT CACTTTTAC CTGCCACTA
 151 TCCCTTTCCC CATCCGTTTC GGCTTTTACG CTGCCTGAAG CATGGCGGGC
 201 GGGCGAGCAA CATTGCGCTG ATTTTCAAGC GTCCCATTAC CAGCGTGATG
 251 CAGTGCAGCG ACGGCAACAA CAAGCCAAGG CCGCATTCCT TCCCCATGTA
 301 TCCGCCAATG CCAGCTACCA GCGCCAGCCG CCATCGATT TTTCCACCCG
 351 CGAAACACAG GGATGGAGCG TGCAGGTGGG ACAAACCTTA TTTGACGCTG
 401 CCAAATTTGC ACAATACCGC CAAAGCAGGT TCGATACGCA GGCTGCAGAA
 451 CAGCGTTTCG ATGCGGCACG CGAAGAATTG CTGTTGAAAG TTGCCGAAAG
 501 TTATTTCAAC GTTTTACTCA GCGAGACAC CGTTGCCGCC CATGCGGCGG
 551 AAAAAGAGGC TTATGCCAG CAGGTAAGGC AGGCGCAGGC TTTATTCAAT
 601 AAAGGTGCTG CCACCGCGCT GGATATTAC GAAGCCAAAG CCGGTTACGA
 651 CAATGCCCTG GCCCAAGAAA TCGCCGTATT GGCTGAGAAA CAAACCTATG
 701 AAAACCAAGT GAACGACTAC ACCGACCTGG ATAGCAAACA AATCGAGGCC
 751 ATAGATACCG CCAACCTGTT GGCACGCTAT CTGCCCAAGC TGGAACGTTA
 801 CAGTCTGGAT GAATGGCAGC GCATTGCCTT ATCCAACAAT CATGAATACC
 851 GGATGCAGCA GCTTGCCCTG CAAAGCAGCG GACAGGCGCT TCGGGCAGCA
 901 CAGAACAGCC GCTATCCAC CGTTTCTGCC CATGTCGGCT ATCAGAATAA
 951 CCTCTACACT TCATCTGCGC AGAATAATGA CTACCACTAT CGGGGCAAG
 1001 GGATGAGCGT CGGCGTACAG TTGAATTTGC CGCTTTTATC CGGCGGAGAA
 1051 TTGTCGGGCA AAATCCATGA AGCCGAAGCG CAATACGGGG CCGCCGAGC
 1101 ACAGCTGACC GCAACCGAGC GGCACATCAA ACTCGCCGTA CGCCAGGCTT
 1151 ATACCGAAAG CGGTGCGGCG CGTTACCAA TCATGGCGCA AGAACGGGTT
 1201 TTGGAAAGCA GCCGTTTGAA ACTGAAATCG ACCGAAACCG GCCAACAATA
 1251 CGGCATCCGC AACCGGCTGG AAGTAATACG GCGCGGCGAG GAAGTCGCCC
 1301 AAGCAGAACA GAACTGGCT CAAGCACGGT ATAAATTCAT GCTGGCTTAT
 1351 TTGCGCTTGG TGAAGAGAG CGGTTAGGG TTGGAACCG TATTTCGCGA
 1401 ATAA

1241

This corresponds to the amino acid sequence <SEQ ID 2616; ORF 763>:

```
m763.pep
1  MTLNLNLMIMQ DYGISVCLTL TPYLQHELFS AMKSYFSKYI LPVSLFTLPL
51  SLSPSVSAFT LPEAWRAAQO HSADFQASHY QRDVAVRARQQ QAKAAFLPHV
101 SANASYQRQP PSISSTRETQ GWSVQVGQTL FDAAKFAQYR QSRFDTQAAE
151 QRFDAAREEL LLKVAESYFN VLLSRDTVAA HAAEKEAYAQ QVRQAQALFN
201 KGAATALDIH EAKAGYDNAL AQEIAVLAEK QTYENQLNDY TDLDKQIEA
251 IDTANLLARY LPKLERYSLD EWQRIALSNN HEYRMOQLAL OSSGOALRAA
301 QNSRYPTVSA HVGYNQNNLYT SSAQNNDYHY RGKGMVGVQ LNLPLYTGGE
351 LSGKIHEAEA QYGAAEAQLT ATERHIKLAV RQAYTESGAA RYQIMAQERV
401 LESSRLKLKS TETGQQYGIR NRLEVIRARQ EVAQAEQKLA QARYKFMLAY
451 LRLVKESGLG LETVFAE*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2617>:

```
a763.seq
1  ATGACATTGC TCAATCTAAT GATAATGCAA GATTACGGTA TTTCCGTTTG
51  CCTGACACTG ACGCCCTATT TGCAACATGA ACTATTTTTCG GCTATGAAAT
101 CCTATTTTTC CAAATATATC CTACCCGTTT CACTTTTTCAC CTTGCCACTA
151 TCCCTTTTCC CATCCGTTTC GGCTTTTACG CTGCCTGAAG CATGGCGGGC
201 GGCGCAGCAA CATTCGGCTG ATTTTCAAGC GTCCCATTAAC CAGCGTGATG
251 CAGCGTCCGC ACGGCAACAA CAAGCCAAGG CCGCATTCTT TCCCATGTA
301 TCCGCCAATG CCAGCTACCA GCGCCAGCCG CCATCGATTT CTTCACCCCG
351 CGAAACACAG GGATGGAGCG TGCAGGTGGG ACAAACCTTA TTGACGCTG
401 CCAAATTTGC ACAATACCGC CAAAGCAGGT TCGATACGCA GGCTGCAGAA
451 CAGCGTTTCG ATGCGGCACG CGAAGAATTG CTGTTGAAAG TTGCCGAAAG
501 TTATTTCAAC GTTTTACTCA GCCGAGACAC CGTTGCCGCC CATGCGCGCG
551 AAAAAGAGGC TTATGCCCGC CAGGTAAGGC AGGCGCAGGC TTTATTCAAT
601 AAAGGTGCTG CCACCGCGCT GGATATTCAC GAAGCCAAAG CCGGTTACGA
651 CAATGCCCTG GCCCAAGAAA TCGCGTATT GGCTGAGAAA CAAACCTATG
701 AAAACCAAGT GAACGACTAC ACCGGCCTGG ACAGCAAACA AATCGAGGCC
751 ATAGATACCG CCAACCTGTT GGCACGCTAT CTGCCAAGC TGAACGTTA
801 CAGTCTGGAT GAATGGCAGC GCATTGCCTT ATCCAACAAT CATGAATACC
851 GGATGCAGCA GCTTGCCCTG CAAAGCAGCG GACAGGCGCT TCGGGCAGCA
901 CAGAACAGCC GCTATCCAC CGTTTCTGCC CATGTCGGCT ATCAGAATAA
951 CCTCTACACT TCATCTGCGC AGAATAATGA CTACCACTAT CGGGGCAAAG
1001 GGATGAGCGT CGGCGTACAG TTGAATTTGC CGCTTTATAC CGGCGGAGAA
1051 TTGTCGGGCA AAATCCATGA AGCCGAAGCG CAATACGGGG CTGCCGAAGC
1101 ACAGCTGACC GCAACCGAGC GGCACATCAA ACTCGCCGTA CGCCAGGCTT
1151 ATACCGAAAG CGCTCGGGCG CGTTACCAA TCATGGCGCA AGAACGGGTT
1201 TTGGAAAGCA GCCGTTTGAA ACTGAAATCG ACCGAAACCG GCCAACAATA
1251 CGGCATCCGC AACCGGCTGG AAGTAATACG GGCGCGGCAG GAAGTCGCCC
1301 AAGCAGAAAC GAAACTGGCT CAAGCACGGT ATAAATTCAT GCTGGCTTAT
1351 TTGCGCTTGG TGAAAGAGAG CGGTTAGGG TTGGAACCGG TATTTGCGGA
1401 ATAA
```

This corresponds to the amino acid sequence <SEQ ID 2618; ORF 763.a>:

```
a763.pep
1  MTLNLNLMIMQ DYGISVCLTL TPYLQHELFS AMKSYFSKYI LPVSLFTLPL
51  SLSPSVSAFT LPEAWRAAQO HSADFQASHY QRDVAVRARQQ QAKAAFLPHV
101 SANASYQRQP PSISSTRETQ GWSVQVGQTL FDAAKFAQYR QSRFDTQAAE
151 QRFDAAREEL LLKVAESYFN VLLSRDTVAA HAAEKEAYAQ QVRQAQALFN
201 KGAATALDIH EAKAGYDNAL AQEIAVLAEK QTYENQLNDY TDLDKQIEA
251 IDTANLLARY LPKLERYSLD EWQRIALSNN HEYRMOQLAL OSSGOALRAA
301 QNSRYPTVSA HVGYNQNNLYT SSAQNNDYHY RGKGMVGVQ LNLPLYTGGE
351 LSGKIHEAEA QYGAAEAQLT ATERHIKLAV RQAYTESGAA RYQIMAQERV
401 LESSRLKLKS TETGQQYGIR NRLEVIRARQ EVAQAEQKLA QARYKFMLAY
451 LRLVKESGLG LETVFAE*
```

m763 / a763 99.8% identity in 467 aa overlap

```

          10      20      30      40      50      60
m763.pep  MTLNLNLMIMQDYGISVCLTLTPYLQHELFSAMKSYFSKYILPVSLFTLPLSLSPSVSAFT
          |||||
a763      MTLNLNLMIMQDYGISVCLTLTPYLQHELFSAMKSYFSKYILPVSLFTLPLSLSPSVSAFT
          10      20      30      40      50      60
```

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	70	80	90	100	110	120
m763.pep	LPEAWRAAQHSADFQASHYQRDAVRARQQQAKAFLPHVSANASYQRQP	PSISSTRETQ				
a763	LPEAWRAAQHSADFQASHYQRDAVRARQQQAKAFLPHVSANASYQRQP	PSISSTRETQ				
	70	80	90	100	110	120
	130	140	150	160	170	180
m763.pep	GWSVQVGQTLFDAAKFAQYRQSRFDTQAAEQRFDAAREELLKVAESYFNVLLSRDTVAA					
a763	GWSVQVGQTLFDAAKFAQYRQSRFDTQAAEQRFDAAREELLKVAESYFNVLLSRDTVAA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m763.pep	HAAEKEAYAQQVRQAQALFNKGAATALDIHEAKAGYDNALAQEI	IAVLAEKQTYENQLNDY				
a763	HAAEKEAYAQQVRQAQALFNKGAATALDIHEAKAGYDNALAQEI	IAVLAEKQTYENQLNDY				
	190	200	210	220	230	240
	250	260	270	280	290	300
m763.pep	TGLDSKQIEAIDTANLLARYLPKLERYSLDEWQRIALSNNHEYRMQQLALQSSGQALRAA					
a763	TGLDSKQIEAIDTANLLARYLPKLERYSLDEWQRIALSNNHEYRMQQLALQSSGQALRAA					
	250	260	270	280	290	300
	310	320	330	340	350	360
m763.pep	QNSRYPTVSAHVGYNQNNLYTSSAQNNDYHYRGKGM	SVGVQLNPL	PLYTG	GELSGKIHEAEA		
a763	QNSRYPTVSAHVGYNQNNLYTSSAQNNDYHYRGKGM	SVGVQLNPL	PLYTG	GELSGKIHEAEA		
	310	320	330	340	350	360
	370	380	390	400	410	420
m763.pep	QYGAAEAQLTATERHIKLAVRQAYTESGAARYQIMAQERVLE	SSRLK	LKSTETGQ	QY	GIR	
a763	QYGAAEAQLTATERHIKLAVRQAYTESGAARYQIMAQERVLE	SSRLK	LKSTETGQ	QY	GIR	
	370	380	390	400	410	420
	430	440	450	460		
m763.pep	NRLEVIRARCEVAQAEQKLAQARYKFMLAYLRLVKESGLG	LET	VF	AE		
a763	NRLEVIRARCEVAQAEQKLAQARYKFMLAYLRLVKESGLG	LET	VF	AE		
	430	440	450	460		

1243

g764.seq not found yet

g764.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2619>:

```

m764.seq
1   ATGTTTTTCT CCGCCCTGAA ATCCTTTCTT TCTCGATACA TTACTGTATG
51  GCGCAATGTT TGGGCGGTGC GCGACCAATT GAAACCGCCC AAACGCACGG
101 CGGAAGAACA GCGCTTTTGT CCCGCGCATT TGGAACTGAC CGATACGCCG
151 GTCTCTGCCG CTCCGAAATG GCGGCGCGCT TTTATTATGG CGTTTGCCTG
201 TTTGGCTTTG TTGTGGTCCT GGTTCGGCAA AATCGATATT GTGGCGGCGG
251 CTTCGGGCAA AACGGTGTCT GCGGGGCGCA GCAAAACCAT CCAGCCGCTG
301 GAAACGGCGG TGGTTAAGGC GGTACATGTG CGCGACGGGC AGCATGTGAA
351 ACAGGGAGAA ACGCTGGCGG AACTGGAGGC TGTGGGAACA GACAGCGATG
401 TGGTGCAGTC GGAGCAGGCT TTGCAGGCTG CCCAATTGTC CAAACTGCGT
451 TATGAAGCGG TATTGGCGGC ATTGGAAAGC CGTACCGTGC CGCATATCGA
501 TATGGCGCAA GCACGGTCTT TAGGTCTCTC CGATGCCGAT GTGCAATCGG
551 CGCAGGTGTT GCGCGAGCAC CAGTATCAGG CATGGGCGGC GCAGGATGCG
601 CAATTGCAGT CGGCTTTGCG CGGCCATCAG GCGGAATTGC AGTCGGCCAA
651 GCGCGAGGAG CAGAAGCTGG TTTCGGTGGG GCGGATCGAG CAGCAGAAAA
701 CAGCAGACTA CCGCCGTTTG CGGCGCGACA ATTTTATTTT GGAACATGCG
751 TTTTGGAGC AGCAGAGCAA ATCGGTGAGC AATTGGAACG ATTTGGAAG
801 TACGCGCGGT CAGATGAGGC AGATTCAGGC GGCCATTGCA CAGGCGGAGC
851 AGAATCGGGT GCTGAATACG CAGAACCTGA AACGCGATAC GCTGGATGCG
901 CTGCGCCAGG CAAACGAACA GATTGACCAA TACCGCGGCC AAACGGATAA
951 GGCAAAGCAG CCGCAGCAGC TGATGACAAT ACAGTCGCTT GCGGACGGCA
1001 CGGTGCAGGA ATTGGCTACC TATACGGTGG GCGGTGTGGT GCAGGCTGCC
1051 CAAAAAATGA TGGTGATTGC GCCCGATGAC GACAAAATGG ACGTGGAAAGT
1101 TTTGGTATTG AACAAAGACA TCGGTTTTGT GGAACAGGGA CAGGATGCGG
1151 TGGTGAAGAT TGAGAGCTTT CCCTATACGC GCTACGGTTA TCTGACGGGC
1201 AAGGTGAAAA GTGTCAGCCA TGATGCGGTA AGCCACGAAC AGTTGGGCTT
1251 GGTTTATACG GCGGTGGTGT CGCTGGACAA ACATACCTTG AATATTGACG
1301 GCAAAGCAGT GAATCTGACG GCGGGCATGA ATGTCACGGC GGAGATTAAA
1351 ACGGGTAAAC GCGGGTGCT GATTATCTG TTAAGCCCGC TGCAAAACCA
1401 ATTGGACGAA AGCTTTAGGG AGCGATAG

```

This corresponds to the amino acid sequence <SEQ ID 2620; ORF 764>:

```

m764.pep
1   MFFSALKSFL SRYITVWRNV WAVRDQLKPP KRTAEQAFLE PAHLELTDTPE
51  VSAAPKWAAR FIMAFALLAL LWSWFGKIDI VAAASGKTVS GGRSKTIQPL
101 ETAVVKAVHV RDGQHVKGQE TLAELEAVGT DSDVVQSEQA LQAAQLSKLR
151 YEAVLAALES RTVPHIDMAQ ARSLGLSDAD VQSAQVLAQH QYQAWAAQDA
201 QLQSALRGHQ AELQSAKAQE QKLVSVGAIE QQKTADYRRL RADNFISEHA
251 FLEQSQSVS NWNLDLESTR QMRQIQAAIA QAEQNRVLNT QNLKRDLTLD
301 LRQANEQIDQ YRGQTDKAKQ RQQLMTIQSP ADGTVQELAT YTVGGVVQAA
351 QKMMVIAPDD DKMDVEVLVL NKDIGFVEQG QDAVVKIESF PYTRYGYLTG
401 KVKSVSHDAV SHEQLGLVYT AVVSLDKHTL NIDGKAVNLT AGMNVTAIEIK
451 TGKRRVLDYL LSPLQTKLDE SFRER*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2621>:

```

a764.seq (partial)
1   ATGTTTTTCT CCGCCCTGAA ATCCTTTCTT TCCCCTGACA TTACCGTATG
51  GCGCAATGTT TGGGCGGTGC GCGACCAATT GGAACCGCCC AAACGCACGG
101 CGGAAGAACA GCGCTTTTGT CCCGCGCATT TGGAACTGAC CGATACGCCG
151 GTCTCTGCCG CTCCGAAATG GCGGCGCGCT TTTATTATGG CGTTTGCCTG
201 TTTGGCTTTG TTGTGGTCCT GGTTCGGCAA AATCGATATT GTGGCGGCGG
251 CTTCGGGCAA AACGGTGTCT GCGGGGCGCA GCAAAACCAT CCAGCCGCTG
301 GAAACGGTGG TGGTTAAGGC GGTACATGTG CGCGACGGGC AGCATGTGAA
351 ACAGGGAGAA ACGCTGGCGG AACTGGAGGC TGTGGGAACA GACAGCGATG
401 TGGTGCAGTC GGAGCAGGCT TTGCAGGCTG CCCAATTGTC CAAACTGCGT
451 TATGAAGCGG TATTGGC3GC ATTGGAAAGC CGTACCGTGC CGCATATCGA
501 TATGGCGCAA GCACGGTCTT TAGGTCTCTC CGATGCCGAT GTGCAATCGG
551 CGCAGGTGTT GCGCGAGCAC CAGTATCAGG CATGGGCGGC GCAGGATGCG
601 CAATTGCAGT CGGCTTTGCG CGGCCATCAG GCGGAATTGC AGTCGGCCAA
651 GCGCGAGGAG CAGAAGCTGG TTTCGGTGGG GCGGATCGAG CAGCAGAAAA

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```

701 CAGCAGACTA CCGCCGTTTG CGGGCCGACA ATTTTATTTC GGAACATGCG
751 TTTTGGAGC AGCAGAGCAA ATCGGTCAGC AATTGGAACG ATTTGGAAG
801 TACGCGCGGT CAGATGAGGC AGATTGAGC GGCATTGCA CAGGCGGAGC
851 AGAATCGGGT GCTGAATACG CAGAACCTGA AACGCGATAC GCTGGATGCG
901 CTGCGCCAGG CAAACGAACA GATTGACCAA TACGCGGCC AAACGGATAA
951 GGCAAAGCAG CGGCAGCAGC TGATGACAAT ACAGTCGCCT GCGGACGGCA
1001 CGGTGCAGGA ATTGCCACC TATACGGTGG GCGGTGTGGT GCAGGCTGCC
1051 CAAAAATGA TGGTGGTTGC GCCCGATGAC GACAAAATGG ACGTGGAGT
1101 TTTGGTATTG AACAAAGACA TCGGTTTGT GGAACAGGGA CAGGATGCGG
1151 TGGTGAAGAT TGAGAGTTT CCCTATACG GCTACGGTTA TCTGACGGGC
1201 AAGGTGAAAA GTGTCAGCCA TGATGCGGTA AGCCACGAAC AGTTGGGCTT
1251 GGTTTATACG GCGGTGGTGT CGCTGGACAA ACATACCTTG AATATTGACG
1301 GCAAA

```

This corresponds to the amino acid sequence <SEQ ID 2622; ORF 764.a>:

```

a764.pep (partial)
1 MFFSALKSFL SRYITVWRNV WAVRDQLEPP KRTAEEOAFL PAHLELTDTP
51 VSAAPKWAAR FIMAFALLAL LWSWFGKIDI VAAASGKTVS GGRSKTIQFL
101 ETVVVKAVHV RDGQHVKGGE TLAELEAVGT DSDVVQSEQA LQAAQLSKLR
151 YEAVLAALES RTVPHIDMAQ ARSLGLSDAD VQSAQVLAQH QYQAWAAQDA
201 QLQSALRGHQ AELQSAKAE QKLVSVAIE QOKTADYRRL RADNFISEHA
251 FLEQQSKSVS NWNLESTRG QMRQIAAIA QAEQNRVLNT QNLKRDTLDA
301 LRQANEQIDQ YRGQTDKAKQ RQQLMTIQSP ADGTVQELAT YTVGGVVQAA
351 QKMMVAPDD DKMDVEVLVL NKDIGFVEQG QDAVVKIESF PYTRYGYLTG
401 KVKSVSHDAV SHEQLGLVYT AVVSLDKHTL NIDGK

```

m764 / a764 99.3% identity in 435 aa overlap

m764.pep	10	20	30	40	50	60
	MFFSALKSFLSRYITVWRNVWAVRDQLEPPKRTAEEOAFLPAHLELTDTPVSAAPKWAAR					
a764	10	20	30	40	50	60
	MFFSALKSFLSRYITVWRNVWAVRDQLEPPKRTAEEOAFLPAHLELTDTPVSAAPKWAAR					
m764.pep	70	80	90	100	110	120
	FIMAFALLALLWSWFGKIDIVAAASGKTVSGGRSKTIQPLETAVVKAVHVRDQHVKGGE					
a764	70	80	90	100	110	120
	FIMAFALLALLWSWFGKIDIVAAASGKTVSGGRSKTIQPLETVVVKAVHVRDQHVKGGE					
m764.pep	130	140	150	160	170	180
	TLAELEAVGTSDSDVVQSEQAALQAAQLSKLRYEAVLAALESRTVPHIDMAQARSLGLSDAD					
a764	130	140	150	160	170	180
	TLAELEAVGTSDSDVVQSEQAALQAAQLSKLRYEAVLAALESRTVPHIDMAQARSLGLSDAD					
m764.pep	190	200	210	220	230	240
	VQSAQVLAQHQQYQAWAAQDAQLQSALRGHQAEQKLVSVAIEQQOKTADYRRL					
a764	190	200	210	220	230	240
	VQSAQVLAQHQQYQAWAAQDAQLQSALRGHQAEQKLVSVAIEQQOKTADYRRL					
m764.pep	250	260	270	280	290	300
	RADNFISEHAFLEQQSKSVSNWNLESTRGQMRQIAAIAQAEQNRVLNTQNLKRDTLDA					
a764	250	260	270	280	290	300
	RADNFISEHAFLEQQSKSVSNWNLESTRGQMRQIAAIAQAEQNRVLNTQNLKRDTLDA					
m764.pep	310	320	330	340	350	360
	LRQANEQIDQYRGQTDKAKQRQQLMTIQSPADGTVQELATYTVGGVVQAAQKMMVAPDD					
a764	310	320	330	340	350	360
	LRQANEQIDQYRGQTDKAKQRQQLMTIQSPADGTVQELATYTVGGVVQAAQKMMVAPDD					
m764.pep	370	380	390	400	410	420
	DKMDVEVLVLNKDIGFVEQGQDAVVKIESFPYTRYGYLTGKVKSVSHDAVSHEQLGLVYT					

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|||||
a764      DKMDVEVLVLNKNKDIFVEQGDQAVVKIESFPYTRYGYLTGKVKSVSHDAVSHEQLGLVYT
              370      380      390      400      410      420

              430      440      450      460      470
m764.pep  AVVSLDKHTLNIDGKAVNLTAGMNVTAIEIKTGKRRVLDYLLSPLQTKLDESFRERX
|||||
a764      AVVSLDKHTLNIDGK
              430

```

g765.seq not yet found

g765.pep not yet found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2623>:

```

m765.seq
1  ATGTTAAGAT GCCGTCCGAA ATCCGTTTIG GATTGAGACG GCATTTTTTT
51  GAAATTTAAT TTTTAAAGGA GTAAACCTAA ATATGAAATT TCCTTCCTTC
101 CTTCTTTTAA ACGGATACTC TGCCTGTCGG CAGTAATCTC GGTATTGGGG
151 GCTTGTGCGG TCGTTGCTGA TGTTACGGT CATGATTCCG CCACAATGAA
201 CGCTGCGGCT GCCAAAGATT ATATGAAAC GGTGAGTTA AACAACTCTG
251 CCGGCAATGT CGATAACCACA TCCAGAACAG CCCGCAGGGT GCAGGCAGTA
301 TTTCGACGTA TGCTGCCTTA TGCCGATGCG GCAAATAATA CCAGCCATAA
351 GTTGTACTGG AAAATGACGG TTTTCAAAAA CGATGAGCTG AACCGTGGG
401 CAATGCCCGG TGGAAAAATG GCGTTTTATA CGGGGATAGT CGACAACTC
451 AAGCTGACCG ATGACGAAAT TGCCGCCATT ATGGGGCATG AAATGACGCA
501 CGCCTGTCAT GAACACGGTA AAAATAAGGT CGGGCAGCAA ATCTTGACCA
551 ATACGGCGGC GCAGATAGGC ACGCAGATTA TATTAGACAA AAAACCGGAT
601 ACTAATCCGG AATTGGTCGG ATTGGGTATG GATATTTTGG GGACGTACGG
651 TCTTACCTTG CCTTATAGCC GCAGCTTGGA AGAAGAAGCC GATGAGGGG
701 GAATGATGTT GATGGCGCAG GCAGGCTATC ATCCGGCGGC CGCTGTCAGG
751 GTTTGGGAAA AAATGAATCA GGAACACGAC CAAACCGCT TATTATATGC
801 TATTACCTCT ACTCATCCGA CAAACAATGC CCGTATAGAA AATCTAAAC
851 GGTGTTGCC GACCGTTATG CCGGTTTATG AGCAAAGTGT CAGAAATAAG
901 GGGCGCGTTA ATAAAAACG TCGGCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2624; ORF 765>:

```

m765.pep
1  MLRCRPKSVL DSDGIFLKFN FLRSKPKEI SFLPSFKRIL CLSAVISVLG
51  ACAVVADVYG HDSATMNAAA AKDYMKTVEL NKSAGNVDTT SRTARRVQAV
101 FRRMLPYADA ANNTSHKFDW KMTVFKNDEL NAWAMPGGKM AFYTGIVDKL
151 KLTDEIAAI MGHEMTHALH EHGKNKVQQ ILNTAAQIG TQIILDKPD
201 TNPELVGLGM DILGTYGLTL PYSRSLEEEA DEGGMLMAQ AGYHPAAVR
251 VWEKMNQEND QNGFIYATS THPTNNARIE NLKRLLTVM PVYEQSVRNK
301 GRVNRKRRR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2625>:

```

a765.seq
1  ATGTTAAGAT GCCGTCCGAA ATCCGTTTIG GATTGAGACG GCATTTTTTT
51  GAAATTTAAT TTTTAAAGGA GTAAACCTAA ATATGAAATT TCCTTCCTTC
101 CTTCTTTTAA ACGGATACTC TGCCTGTCGG CAGTAATCTC GGTATTGGGG
151 GCTTGTACGG TCGTTGCTGA TGTTACGGT CAGGATTCCG CCACAATGAA
201 TGCTGCGGCT GCCGAAGATT ATATGAAAC GGTGAGTTG AACAACTCTG
251 CCGGCAATGT CGATACTACA TCCAAACAG CCCGTAGGGT GCAGGCAGTA
301 TTTCGACGTA TGTTGCCTTA TGCCGATGCG GCAAATAATA CCGGCCATAA
351 GTTGTACTGG AAAATGACGG TTTTCAAAAA CGATGAGCTG AACCGTGGG
401 CAATGCCCGG CGGAAAAATG GCGTTTTATA CGGGGATAGT CGATAAACTT
451 AAGCTGACCG ATGGCGAAAT TGCCGCCATT ATGGGGCATG AAATGACGCA
501 TGCCCTGTCAT GAACACGGTA AAAATAAGGT CGGGCAGAAA ATCTTGACTA
551 ATATGGCGGC GCAGATAGGC ACGCAGATTA TATTAGACAA AAAACCGGAC
601 ACTAATCCGG AATTGGTCGG ATTGGGTATG GATATTTTGG GGATGTACGG
651 CATTACCTTG CCTTATAGCC GCAGCTTGGA AGAAGAAGCC GATGAGGGG
701 GAATGATGTT GATGGCGCAG GCAGGCTATC ATCCGGCAGC CGCTGTCAGG
751 GTTTGGGAAA AAATGAATCA GGAACACGAC CAAACCGCT TATTATATGC
801 TATTACCTCT ACTCATCCGA CAAACAATGC CCGTATAGAA AATCTAAAC
851 GGTGTTGCC GACCGTTATG CCGGTTTATG AGCACAGTGT TAGAAATAAG
901 GGGCGCGTTA ATAAAAACG TCGGCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2626; ORF 765.a>:

```

a765.pep
1  MLRCRPKSVL DSDGIFLKFN FLRSKPKEI SFLPSFKRIL CLSAVISVLG

```

1246

```

51  ACTVVADVYG QDSATMNAAA AEDYMKTVEL NKSAGNVDTT SKTARRVQAV
101 FRRMLPYADA ANNTGCHKFDW KMTVFKNDEL NAWAMPGGKM AFYTGIVDKL
151 KLTGDGEIAAI MGHETHALH EHGKKNVQOK ILTNMAAQIG TQIILDKKPD
201 TNPELVGLGM DILGMYGITL PYRSLEEEA DEGGMMLMAQ AGYHPAAAVR
251 VWEKMNQEND QNGFIYAIT THPTNNARIE NLKRLLPVMPVYEHVSRNK
301 GRVNKNRRR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N meningitidis*

ORF 765 shows 96.18% identity over a 309 aa overlap with a predicted ORF (ORF 765) from *N. meningitidis*:

m765 / a765 96.1% identity in 309 aa overlap

```

              10      20      30      40      50      60
m765.pep      MLRCRPKSVLSDGIFLKFNLRSKPKYEISFLPSFKRILCLSAVISVLGACAVVADVYG
a765           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
              10      20      30      40      50      60
a765           MLRCRPKSVLSDGIFLKFNLRSKPKYEISFLPSFKRILCLSAVISVLGACTVVADVYG
              10      20      30      40      50      60
m765.pep      HDSATMNAAAADYMKTVELNKSAGNVDTTSTARRVQAVFRRMLPYADAANNTSHKFDW
a765           :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a765           QDSATMNAAAADYMKTVELNKSAGNVDTTSTARRVQAVFRRMLPYADAANNTGHKFDW
              70      80      90      100     110     120
m765.pep      HDSATMNAAAADYMKTVELNKSAGNVDTTSTARRVQAVFRRMLPYADAANNTSHKFDW
a765           QDSATMNAAAADYMKTVELNKSAGNVDTTSTARRVQAVFRRMLPYADAANNTGHKFDW
              70      80      90      100     110     120
a765           QDSATMNAAAADYMKTVELNKSAGNVDTTSTARRVQAVFRRMLPYADAANNTGHKFDW
              130     140     150     160     170     180
m765.pep      KMTVFKNDELNAWAMPGGKMAFYTGIVDKLKLTDDEIAAIMGHEMTHALHEHGKKNVQOQ
a765           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a765           KMTVFKNDELNAWAMPGGKMAFYTGIVDKLKLTDGEIAAIMGHEMTHALHEHGKKNVQOK
              130     140     150     160     170     180
a765           KMTVFKNDELNAWAMPGGKMAFYTGIVDKLKLTDGEIAAIMGHEMTHALHEHGKKNVQOK
              190     200     210     220     230     240
m765.pep      ILTNAAQIGTQIILDKKPDNPELVGLGMDILGTYGLTPYRSLEEEADEGGMMLMAQ
a765           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a765           ILTNMAAQIGTQIILDKKPDNPELVGLGMDILGMYGITLPYRSLEEEADEGGMMLMAQ
              190     200     210     220     230     240
a765           ILTNMAAQIGTQIILDKKPDNPELVGLGMDILGMYGITLPYRSLEEEADEGGMMLMAQ
              250     260     270     280     290     300
m765.pep      AGYHPAAAVRVWEKMNQENDQNGFIYAITSTHPTNNARIENLKRLLPVMPVYEQSVRNK
a765           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a765           AGYHPAAAVRVWEKMNQENDQNGFIYAITSTHPTNNARIENLKRLLPVMPVYEHVSRNK
              250     260     270     280     290     300
a765           AGYHPAAAVRVWEKMNQENDQNGFIYAITSTHPTNNARIENLKRLLPVMPVYEHVSRNK
              310
m765.pep      GRVNKKRRRX
a765           |||||:|||||
a765           GRVNKNRRRX
              310

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2627>:

```

g767.seq
1  ATSAAGTTTA AACATCTGTI GCCGCTGCTG CTGTGCGCAG TGTGTGCCGC
51  GCAGGCATAT GCCCTGACGG AAGGGGAAGA CTATCTTGTG TTGGATAAAC
101 CCATTCTCTCA AGAACAGCCG GGAAAAATTG AGGTTTGGGA ATTTTTCGGC
151 TATTTTTCGCG TACATTGCCA TCATTTCGAT CCTTTGTAT TGAAGCTGGG
201 CAAGGCATTG CCGTCTGATA CTTATCTGCG GACGGAGCAC GTGGCTGGC
251 GGCTTGAAAT GCTCGGTCTG GCAAGAATGG CTGCTGCGGT CAAGCTGTGCG
301 GGTTTGAAAT ATCAGGCAAA CTCTGCTGTG TTTAAAGCAG TTTACGAACA
351 AAAAAATCCGT TTGGAAAAACA GGGCTGTTGC CGGGAATGG GCTTTATCTC
401 AAAAAAGGTTT TGACGGCAAA AAACGTATGC GCGCTATGA TTCCCCCGAA
451 GCTGCGCGCC TCGCATTAAT AATGCAGAAA CTGACGGAAC AATACGGTAT
501 TGACAGCAGC CCGACCGTTA TTGTCGGCGG AAAATACCGC GTTATCTTCA
551 ATAATGGCTT TGATGGCGGC GTTCATACGA TTAAGAATT GCTTGCCAAA
601 GTCAGGGAAG AACGCAAGCG TCAGACCCCT GCTGTACAGA AATAG

```

This corresponds to the amino acid sequence <SEQ ID 2628; ORF 767.ng>:

```

g767.pep
1  MKFKHLLPLL LSAVLSAQAY ALTEGEDYLV LDKPIPQEQP GKIEVLEFFG
51  YFCVHCHHFD PLLLLKGKAL PSDTYLRTEH VVWRPEMLGL ARMAAAVKLS

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1247

101 GLKYQANSV FKA VYEQKIR LENRAVAGKW ALSQKGFQDGK KLMRAYDSPE
 151 AAAVALKMQK LTEQYRIDST PTVIVGGKYR VIFNNGFDGG VHTIKELVAK
 201 VREERKRQTP AVQK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2629>:

m767.seq
 1 ATGAAGCTCA AACATCTGTT GCCGCTGCTG CTGTCGGCAG TGTGTCCGC
 51 GCAGGCATAT GCCCTGACGG AAGGGGAAGA CTATCTTG TGGAATAAC
 101 CCATTCTCTCA AGAACAGTCG GGTAATAATTG AGGTTTGGGA ATTTTTCGGC
 151 TATTTCTGCG TACATTGCCA TCATTTCGAT CCTTTGTTAT TGAAACTGGG
 201 CAAGGCATTG CCGTCTGATG CCTATTGAG GACGGAGCAC GTGGCTGGC
 251 AGCCTGAAAT GCTCGGTTTG GCTAGGATGG CGGCTGCCGT CAATTGTCG
 301 GGTGTGAAAT ATCAGGCAAA CCCTGCTGTG TTAAAGCAG TTTACGAACA
 351 AAAATCCGC TTGAAAACA GGTGCGTTGC CGGAAATGG GCTTTGTCTC
 401 AAAAGGCTT TGACGGCAAA AAACATGATGC GCGCTATGA TTCCCCGAA
 451 GTCGCCCGC CCGCATTAAT AATGCAGAA CTGACGGAAC AATACCGCAT
 501 CGACAGCAG CCGACCGTTA TTGTCGGCGG AAAATACCGC GTTATCTTCA
 551 ATAACGGCTT TGACGGCGGC GTTCATACGA TTAAGAATT GGTGCCAAA
 601 GTCAGGGAAG AACGCAAGCG TCAGACCCCT GCTGTACAGA AATAG

This corresponds to the amino acid sequence <SEQ ID 2630; ORF 767>:

m767.pep
 1 MKLKHLLPLL LSAVLSAQAY ALTEGEDYLV LDKPIQEQS GKIEVLEFFG
 51 YFCVHCHHFD PLLLLKLGKAL PSDAYLRTEH VVWQPEMLGL ARMAAANLS
 101 GLKYQANPAV FKA VYEQKIR LENRSVAGKW ALSQKGFQDGK KLMRAYDSPE
 151 AAAAALKMQK LTEQYRIDST PTVIVGGKYR VIFNNGFDGG VHTIKELVAK
 201 VREERKRQTP AVQK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 767 shows 95.8% identity over a 214 aa overlap with a predicted ORF (ORF 767) from *N. gonorrhoeae*

m767/g767 95.8% identity in 214 aa overlap

	10	20	30	40	50	60
g767.pep	MKFKHLLPLL LSAVLSAQAYALTEGEDYLV LDKPIQEQSGKIEVLEFFGYFCVHCHHFD					
m767	MKLKHLLPLL LSAVLSAQAYALTEGEDYLV LDKPIQEQSGKIEVLEFFGYFCVHCHHFD					
	10	20	30	40	50	60
g767.pep	PLLLKLGKALPSDYLRLTEHVVRPEMLGLARMAAAVKLSGLKYQANSVFKAVYEQKIR					
m767	PLLLKLGKALPSDAYLRTEHVVRPEMLGLARMAAANLSGLKYQANPAVFKAVYEQKIR					
	70	80	90	100	110	120
g767.pep	PLLLKLGKALPSDYLRLTEHVVRPEMLGLARMAAAVKLSGLKYQANSVFKAVYEQKIR					
m767	PLLLKLGKALPSDAYLRTEHVVRPEMLGLARMAAANLSGLKYQANPAVFKAVYEQKIR					
	70	80	90	100	110	120
g767.pep	LENRAVAGKWALSQKGFQDGKKLMRAYDSPAAAAVALKMQKLTEQYRIDSTPTVIVGGKYR					
m767	LENRSVAGKWALSQKGFQDGKKLMRAYDSPAAAAALKMQKLTEQYRIDSTPTVIVGGKYR					
	130	140	150	160	170	180
g767.pep	LENRAVAGKWALSQKGFQDGKKLMRAYDSPAAAAVALKMQKLTEQYRIDSTPTVIVGGKYR					
m767	LENRSVAGKWALSQKGFQDGKKLMRAYDSPAAAAALKMQKLTEQYRIDSTPTVIVGGKYR					
	130	140	150	160	170	180
g767.pep	VIFNNGFDGGVHTIKELVAKVREERKRQTPAVQKX					
m767	VIFNNGFDGGVHTIKELVAKVREERKRQTPAVQKX					
	190	200	210			
g767.pep	VIFNNGFDGGVHTIKELVAKVREERKRQTPAVQKX					
m767	VIFNNGFDGGVHTIKELVAKVREERKRQTPAVQKX					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2631>:

a767.seq
 1 ATGAAGCTCA AACATCTGTT GCCGCTGCTG CTGTCGGCAG TGTGTCCGC
 51 GCAGGCATAT GCCCTGACGG AAGGGGAAGA CTATCTTG TGGAATAAC
 101 CCATTCTCTCA AAAACAGTCG GGCATAATTG AGGTTTGGGA ATTTTTCGGC
 151 TATTTCTGCG TACATTGCCA TCATTTCGAT CCTTTGTTAT TGAAATTGGG
 201 CAAGGCATTG CCGTCTGATG CCTATTTAAG GACGGAGCAC GTGGCTGGC
 251 AGCCTGAAAT GCTCGGCTCG GCAAGAATGG CTGTCGCCGT CAACCTGTCA
 301 GGTGTGAAAT ATCAGGCAAA CCCTGCCGTG TTAAAGCAG TTTACGAACA
 351 AAAATCCGC TTGAAAACA GGTGCGTTGC CGAATAATGG GCTTTGTCTC
 401 AAAAGGCTT TGACGGCAAA AAACATGATGC GCGCTACGA CTCTCCTGCG

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451 GCAGCGGCTG CTGCATCAAA AATGCAGCAA TTGACGGAAC AGTACCGCAT
501 CGACAGTACG CCGACCGTTG TCGTCGGCGG AAAATACCGC GTTATCTTCA
551 ATAATGGCTT TGACGGCGGT GTTCATACGA TTAAAGAATT GGTGCCAAA
601 GTCAGGGAAG AACGCAAGCG TCAGACCCCT GCTGTACAGA AATAG

```

This corresponds to the amino acid sequence <SEQ ID 2632; ORF 767.a>:

```

a767.pep
  1 MKLKHLPLLL LSAVLSAQAY ALTEGEDYLV LDKPIPQKQS GKIEVLEFFG
  51 YFCVHCHHFD PLLLLKLGKAL PSDAYLRTEH VVWQPEMLGL ARMAAAVKLS
 101 GLKYQANPAV FKAVYEQKIR LENRVAEKW ALSQKGFQK KLMRAYDSPA
 151 AAAAASKMQQ LTEQYRIDST PTVVVGKYYR VIFNNGFDGG VHTIKELVAK
 201 VREERKRQTP AVQK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 767 shows 96.7% identity over a 214 aa overlap with a predicted ORF (ORF 767) from *N. meningitidis*:

m767/a767 96.7% identity in 214 aa overlap

```

              10      20      30      40      50      60
a767.pep    MKLKHLPLLLSAVLSAQAYALTEGEDYLVLDKPIPQKQSGKIEVLEFFGYFCVHCHHFD
              |||||
m767        MKLKHLPLLLSAVLSAQAYALTEGEDYLVLDKPIPQKQSGKIEVLEFFGYFCVHCHHFD
              10      20      30      40      50      60

              70      80      90      100     110     120
a767.pep    PLLLLKLGKALPSDAYLRTEHVWVWQPEMLGLARMAAAVKLSGLKYQANPAVFKAVYEQKIR
              |||||
m767        PLLLLKLGKALPSDAYLRTEHVWVWQPEMLGLARMAAAVNLSGLKYQANPAVFKAVYEQKIR
              70      80      90      100     110     120

              130     140     150     160     170     180
a767.pep    LENRVAEKWALSQKGFQKGLMAYDSPAASAAASKMQQLTEQYRIDSTPTVVVGKYYR
              |||||
m767        LENRSVAGKALSQKGFQKGLMAYDSPAASAAALKMQKLTEQYRIDSTPTVIVVGKYYR
              130     140     150     160     170     180

              190     200     210
a767.pep    VIFNNGFDGGVHTIKELVAKVREERKRQTPAVQKX
              |||||
m767        VIFNNGFDGGVHTIKELVAKVREERKRQTPAVQKX
              190     200     210

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2633>:

```

g768.seq
  1 ATGAATATCA AACAAATGAT TACCGCCGCA CTCATTGCCT CAGCCGCCTT
  51 TGCCACGCAG GCAGCCCCGC AAAAACCCTG ATCCGCCGCC CAAACCGCGC
 101 AACATTCAGC CGTTTGGATC GATGTCCGTT CCGAACAGGA ATTTAGCGAA
 151 GGTCAATTGC ACAACGCGGT CAACATCCCC GTCGACCAAA TCGTCCGCCG
 201 CATATACGAA GCCGCGCCCG ACAAGACAC GCCGGTCAAC CTCTACTGCC
 251 GCAGCGGACG GCGTGCCGAA GCCGCCCTTC AAGAGCTGAA AAAAGCAGGT
 301 TATACAAATG TTGCCAATCA CGGCGGTTAT GAAGACCTGC TCAAAAAGG
 351 GATGAAATGA

```

This corresponds to the amino acid sequence <SEQ ID 2634; ORF 768.ng>:

```

g768.pep
  1 MNIKQLITAA LIASAAFATQ AAPQKPVSA QTAQHSAVWI DVRSEQEFSE
  51 GHLHNAVNIQ VDQIVRRIE AAPDKDTPVN LYCRSGRAE AALQELKAG
 101 YTNVANHGGY EDLLKGMK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2635>:

```

m768.seq
  1 ATGAATATCA AACACCTGAT TACCGCCGCA CTCATTGCCT CAGCCGCCTT
  51 TGCCGCGCAG GCAGCCCCGC AAAAACCCTG ATCCGCCGCC CAAACCGCGC
 101 AACATCCGGC CGTTTGGATC GATGTCCGTT CCGAACAGGA ATTTAGCGAA
 151 GGCATTTCG ACAACGCGGT CAACATCCCC GTCGACCAAA TCGTCCGCCG
 201 CATACACGAA GCCGCGCCCG ACAAGACAC GCCGGTCAAC CTCTACTGCC

```

1249

251 GCAGCGGACG GCGTGCCGAA GCCGCCCTTC AAGAGCTGAA AAAAGCAGGT
 301 TATACAAATC TTGCCAATCA CGCGCGTTAT GAAGACCTGC TCAAAAAAGG
 351 GATGAAATGA

This corresponds to the amino acid sequence <SEQ ID 2636; ORF 768>:

m768.pep
 1 MNIKHLITAA LIASAAFAAQ AAPOKPVSA QTAQHPAVWI DVRSEQEFSE
 51 GHLHNAVNI PVDQIVRRIHE AAPDKDTPVN LYCRSGRRAE AALQELKEAG
 101 YTNVANHGGY EDLLKKG MK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 768 shows 96.6% identity over a 119 aa overlap with a predicted ORF (ORF 768) from *N. gonorrhoeae*

m768/g768 96.6% identity in 119 aa overlap

	10	20	30	40	50	60
g768.pep	MNIKGLITAA	LIASAAFAAQ	AAPOKPVSA	QTAQHPAVWI	DVRSEQEFSE	GHLHNAVNI P
m768	MNIKHLITAA	LIASAAFAAQ	AAPOKPVSA	QTAQHPAVWI	DVRSEQEFSE	GHLHNAVNI P
	10	20	30	40	50	60
	70	80	90	100	110	120
g768.pep	V	DQIVRRIE	EAAPDKDTP	VNLYCRSGRRAE	AALQELKKAGY	TNVANHGGYEDLLKKG MKX
m768	V	DQIVRRIE	EAAPDKDTP	VNLYCRSGRRAE	AALQELKKAGY	TNVANHGGYEDLLKKG MKX
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2637>:

a768.seq
 1 ATGAATATCA AACACCTGAT TACCGCCGCA CTCATTGCCT CAGCCGCCTT
 51 TGCCGCGCAG GCAGCCCCGC AAAAACCCTG ATCCGCCGCC CAAACCGCGC
 101 AACATTCAGC CGTTTGATC GATGTCCGCA GCGAACAGGA ATTTAGCGAA
 151 GGTCAATTGC ACAACGCGGT CAACATCCCC GTCGACCAAA TCGTCCGCCG
 201 CATAACGAA GCCGCGCCCG ACAAGACAC GCCGGTCAAC CTCTACTGCC
 251 GCAGCGGACG GCGTGCCGAA GCCGCCCTTC AAGAACTGAA AAAAGCAGGC
 301 TATACGAATG TTGCCAATCA CGCGCGTTAT GAAGACCTGC TCAAAAAAGG
 351 GATGAAATGA

This corresponds to the amino acid sequence <SEQ ID 2638; ORF 768.a>:

a768.pep
 1 MNIKHLITAA LIASAAFAAQ AAPOKPVSA QTAQHPAVWI DVRSEQEFSE
 51 GHLHNAVNI PVDQIVRRIHE AAPDKDTPVN LYCRSGRRAE AALQELKKAG
 101 YTNVANHGGY EDLLKKG MK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 768 shows 99.2% identity over a 119 aa overlap with a predicted ORF (ORF 768) from *N. meningitidis*:

m768/a768 99.2% identity in 119 aa overlap

	10	20	30	40	50	60
a768.pep	MNIKHLITAA	LIASAAFAAQ	AAPOKPVSA	QTAQHPAVWI	DVRSEQEFSE	GHLHNAVNI P
m768	MNIKHLITAA	LIASAAFAAQ	AAPOKPVSA	QTAQHPAVWI	DVRSEQEFSE	GHLHNAVNI P
	10	20	30	40	50	60
	70	80	90	100	110	120
a768.pep	V	DQIVRRIE	EAAPDKDTP	VNLYCRSGRRAE	AALQELKKAGY	TNVANHGGYEDLLKKG MKX
m768	V	DQIVRRIE	EAAPDKDTP	VNLYCRSGRRAE	AALQELKKAGY	TNVANHGGYEDLLKKG MKX
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2639>:

g769.seq

```

1   TTGATAATGG TTATTTTITA TTTTATTTT TGTGGGAAGA CATTTATGCC
51  TGCACGAAAC AGATGGATGC TGCTGCCTTT ATTGGCAAGC GCGGCATACG
101 CCGAAGaAAC ACCgtgCGAA CCGGATTGA GAAGCCGTCC CGAGTTCAGG
151 CTTCATGAAG CGGAGGTCAA ACCGATCGAC AGGAGAGAAG TACCGGGGCA
201 GGTGCGGGAA AAAGGAAAAG TTTTGCAGGT TGACGgcGAA ACCCTGCTGA
251 AAAATCCCGA ATTGTTGTCG CGTGCCATGT ATTCCGCAGT GGTCTCAAAC
301 AATATTGCCG GTATCCGCGT GATTTTGCCG ATTTACCTAC AACAGGCGCG
351 GCAGGATAAG ATGTTGGCAC TTTATGCACA AGGGATTTTG GCGCAGGCAG
401 AGGGCAGGGT GAAGGAGGCG GTTCCCATT ACCGGGAATT GATTGCCGCC
451 CAACCCGACG CGCCCGCCGT CCGTATGCGT TTGGCGGCGG CATTGTTTGA
501 AGACAGGCAG AACGAGGCGG CGGCAGACCA GTTCGACCCG CTGAAACAG
551 AAGATCTGCC GCCGAGCTT ATGGAGCAGG TCGAGCTGTA CCGCAAGGCA
601 TTGCGCGAAC GCGATGCGTG GAAGSTAAAC GCGGGTTTCA GCGTTACCCG
651 CGAACACAAT ATCAACCAAG CCCCNAACA GCAGCAGTAC GGCAATTGGA
701 CTTTCCCGAA ACAGGTGGAC GGCAGGCAG TCAATTACCG GTTCGGCGCG
751 GAGAAATAAT GGTGCTGAA AACCGCTGG TACACGACGG CGGGCGGCGA
801 CGTGTCGCGC AGGGTTTATC CGGGGAATAA GAAATTCAAC GATATGACGG
851 CAGGTGTTTC CGGCGGCATC GGTTTTGCCG ACCGGCGTAA AGATGTCGGG
901 CTGGCAGTGT TCCACGAACG CCGCACCTAC GGCAACGACG CTTATTCTTA
951 CGCCAACGGC GCACGCCTTT ATTTCAACCG TTGGCAAAAC CCGAGATGGC
1001 AAACGCTGTC TTCGGCGGAG TGGGGGCGTT TGAAGAATAC GCGCCGGCGG
1051 CGTTCCGACA ATACCCATTT GCAAATTTCC AATTGCTGGT TGTTTTACCG
1101 GAATGCGCGC CAATATTGGA CGGGCGGTTT GGATTTTAC CCGCAGCGCA
1151 ACCCCGCCGA CCGTGGCGAC AATTTCAACC GTTACGGCCT GCGCTTTGCC
1201 TGGGGGCGAG AATGGGGCGG CAGCGGCTGT TCTTCGCTGT TCGGCTCGG
1251 CGTGGCGAAA CGGCATTATG AAAAACCCGG CTCTTCAGC AGTTTAAAG
1301 GGGAAAGGCG CAGGGATAAA GAATCGGACA CATCTTGAG CCTTTGGCAC
1351 RSDNTHLQIS NSLVFYRNAR QYWTGGLDFY RERNPADRGD NFNRYGLRFA
1401 CGAAACGTGG AGCAACGATG TGTAAACGA ATACGAGAAA AACAGGGCGT
1451 TTGTCGAGST TAACAAACG TTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2640; ORF 769.ng>:

g769.pep

```

1   LIMVIFYFYF CGRTFMPARN RMMLPLLAS AAYAETPCE PDLRSRPEFR
51  LHEAEVKPID REKVPQVRE KGKVLQVDGE TLLKNPELLS RAMYSAVVSN
101 NIAGIRVILP IYLQARQDK MLALYAQGIL AQAEGRVKEA VSHYRELIAA
151 QPDAPAVRMR LAAALFEDRQ NEAADQFDR LKTEDLPPQL MEQVELYRKA
201 LREERDAWKVN GGFSVTREHN INQAPKQQQY GNWTFPKQVD GTAVNYRFGA
251 EKKWSLKNWG YTTAGGDVSG RVYPGNKKFN DMTAGVSGGI GFADRRKDVG
301 LAVFHERRTY GNDAYSANG ARLYFNRWQT PRWQLSSAE WGRLLKNTRRA
351 RSDNTHLQIS NSLVFYRNAR QYWTGGLDFY RERNPADRGD NFNRYGLRFA
401 WQEWGSGSL SSLFRLGVAK RHYEKPFFS SPKGERRRDK ESDTSLSLWH
451 RALHFKGITP RLTLSHRETW SNDVFNEYEK NRAFVEFNKT F*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2641>:

m769.seq

```

1   TTGATAATGG TTATTTTITA TTTTGTGGG AAGACATTTA TGCCTGCACG
51  AAACAGATGG ATGCTGCTGC TGCCTTTATT GGCAAGCGCG GCATATGCCG
101 AAGAAACACC GCGCGAACCG GATTTGAGAA GCCGTCCCGA GTTCAGGCTT
151 CATGAAGCGG AGGTCAAACC GATCGACAGG GAGAAGGTGC CGGGGCGAGT
201 GCGGGAATAA GGAAGGTTT TGCAGATTGA CGCGAAACC CTGCTGAAAA
251 ATCCCGAATT GTTGTCCTCG CCGATGTATT CCGCAGTGGT CTCAAACAAT
301 ATTGCCGGTA TCCGCGTTAT TTGCGGATT TACCTACAAC AGGCGCAGCA
351 GGATAAGATG TTGGCACTTT ATGCACAAGG GATTTTGCGC CAGGCAGACG
401 GTAGGGTGAA GGAGGCGATT TCCATTACC GGGAATTGAT TGCCGCCCAA
451 CCCGACGCGC CGGCGTCCG TATGCGTTG CGGCGAGCAT TGTTTGAAAA
501 CAGGCAGAAC GAGGCGGCGG CAGACCAGTT CGACCGCTG AAGGCGGAAA
551 ACCTGCCGCC GCAGCTGATG GAGCAGGTGC AGCTGTACCG CAAGGCATTG
601 CGCGAACGCG ATGCGTGGAA GGTAAATGCG GGCTTCACG TCACCCGCGA
651 ACACAATATC AACCAAGCCC CGAAACGGCA GCAGTACGGC AAATGGACTT
701 TCCCGAAACA GGTGGACGGC ACGGCGGTCA ATTACCGGCT CGGCGCGGAG
751 AAAAATGGT CGCTGAAAA CGGCTGGTAC ACGACGGCGG GCGGCGACGT
801 GTCCGGCAGG GTTTATCCGG GGAATAAGAA ATTCACGAT ATGACGGCAG
851 GCTTTTCCTC CGGCATCGGT TTGCGCGACC GCGCAAGA GAAGGCGGTG
901 GCAGTGTTC ACGAACGCG CACCTACGGC AACGACGCT ATTCTTACAC
951 CAACGGCGCA CGCCTTTATT TCAACCGTGC GCAACCCCG AAATGGCAAA
1001 CTTGTCTTTC GCGGAGTGG GGGCGTTGA AGAATACGCG CCGGCGCGGT
1051 TCCGACAATA CCCATTGCA AATTTCCAAT TCGCTGGTGT TTTACCGGAA
1101 TCGCGGCCAA TATTGGATGG GCGGTTTGA TTTTACCGC GAGCGCAACC
1151 CGGCCGACCG GGGCGACAAT TTCAACCGTT ACGGCTGCG CTTTGCCTGG
1201 GGGCAGGAAT GGGGCGGCG CCGCTGTCT TCGCTGTTC GCCTCGGCGC

```

m769 . pep

1	LINVIIFYCQ	KTFMPARNRW	MLLLPIILASA	AYAETPREP	DLRSRPEFRL
51	HEAEVQIPDR	EYQVQGVREK	GKVLQIDGET	LLKNPELLSR	AMYSAVSVNN
101	IAGRVILPI	KLQQAQQDKM	LALYAQGGILA	LDNNGQKEI	SHYRELIAAQ
151	PDAPAVRMRL	AAALFENRQN	EAAADQDFDL	KAENLPPQKI	EQVELYRKAL
201	RERDAWKVNG	GFSVTREHNI	NQAPKRQYQG	KWTFPKQVDG	TAVNYRLGAE
251	KKWSLKNGWY	TAGGDDVSGR	VYPKNKKEND	MTAGVSGGIG	FADRRKDLAGL
301	AVFHERTYRI	NDAYSYTINGA	RLYFNRRWQT	KWQTLSSAEW	GRLKNTRRAR
351	SDNTHLQISN	SLVRYRNARQ	YWMGGDLFFYR	ERNPADRRGN	FNRYGLRFAW
401	GQEWGGSGLS	SLFLRLGAAKR	HYEKPGRFFSG	FKGERRDDKE	LNTSLSLWHR
451	ALHFKGITPR	LTLSHRETRS	NDVFNHEYKRN	RAFVEFNKTF	*

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 769 shows 95.1% identity over a 492 aa overlap with a predicted ORF (ORF 769) from *N. gonorrhoeae*

m769/g769 95.1% identity in 492 aa overlap

	10	20	30	40	50	59
g769.pep	LIMVIFYFYFCGKTFMPARNRWMLL	-PLLASAAYAEETPCEPDLRSRPF	EFRLHEAEVKPI			
m769	LIMVIFY--FCGKTFMPARNRWMLL	LLPLLASAAYAEETPREPDLRSRPF	EFRLHEAEVKPI			
	10	20	30	40	50	
g769.pep	60	70	80	90	100	110
	DREKVP	GGVREK	GKVLQVD	GETLLK	NPELLSR	AMYSAVV
	SNNIAGIRVILPIYL	QQARQD				
m769	DREKVP	GGVREK	GKVLQID	GETLLK	NPELLSR	AMYSAVV
	SNNIAGIRVILPIYL	QQAQD				
	60	70	80	90	100	110
g769.pep	120	130	140	150	160	170
	KMLALYA	QGILAQ	AEGRVKE	AVSHYREL	IAAQPD	APAVRM
	LALAAALF	FEDRQNE	AAADQFD			
m769	KMLALYA	QGILAQ	ADGRVKE	AVSHYREL	IAAQPD	APAVRM
	LALAAALF	ENRQNE	AAADQFD			
	120	130	140	150	160	170
g769.pep	180	190	200	210	220	230
	RLKTEDL	PPQLMEQ	VELYRK	ALRERDA	WKVNGG	FSVTR
	REHNNIN	QAPKQO	QYGNW	TFFPKQV		
m769	RLKAENL	PPQLMEQ	VELYRK	ALRERDA	WKVNGG	FSVTR
	REHNNIN	QAPKQO	YGKWT	FFPKQV		
	180	190	200	210	220	230
g769.pep	240	250	260	270	280	290
	DGTAVNY	RFGAEK	KWSLKN	GWYTTAG	GDVSGR	VYPGNK
	KFFNDMT	AGVSGG	IGFADRR	KDV		
m769	DGTAVNY	RLGAEK	KWSLKN	GWYTTAG	GDVSGR	VYPGNK
	KFFNDMT	AGVSGG	IGFADRR	KDA		
	240	250	260	270	280	290
g769.pep	300	310	320	330	340	350
	GLAVFHER	TYGNDAY	SYANGAR	LYFNRWQ	TPRWQ	TLSSAE
	WGLKNT	FRARSD	NTHLQI			
m769	GLAVFHER	TYGNDAY	SYTNGAR	LYFNRWQ	TPKWQ	TLSSAE
	WGLKNT	FRARSD	NTHLQI			
	300	310	320	330	340	350
g769.pep	360	370	380	390	400	410
	SNSLVFY	RNARQY	WTGGLD	FYRERN	PADRGD	NFNRYG
	LRFAWG	QEWGGS	GLSSL	RLGVA		
m769	SNSLVFY	RNARQY	WMGGLD	FYRERN	PADRGD	NFNRYG
	LRFAWG	QEWGGS	GLSSL	RLRLGAA		
	360	370	380	390	400	410
g769.pep	420	430	440	450	460	470
	KRHYEKP	PGFFSS	FKGERR	RDKESD	TSLSLW	HRALHF
	KGITPR	LTLSH	RETWS	NDVFNE		
m769	KRHYEKP	PGFFSS	FKGERR	RDKESD	TSLSLW	HRALHF
	KGITPR	LTLSH	RETWS	NDVFNE		
	420	430	440	450	460	470

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```

m769      KRHYEKPGFFSGFKGERRRDKELNTSLSLWHRALHFKGITPRLLTSLHRETRSNDVFNEYE
          420      430      440      450      460      470

          480      490
g769.pep  KNRAFVEFNKTFX
          |||||
m769      KNRAFVEFNKTFX
          490

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2643>:

```

a769.seq
1  TTGATAATGG TTATTTTITA TTTTGTGGG AAGACATTTA TGCCTGCCAG
51  AAACAGATGG ATGCTGCTGC TGCCTTTATT GGCAAGCGCG GCATATGCCG
101 AAGAAACACC GCGCGAACCG GATTTGAGAA GCCGTCCCGA GTTCAGGCTT
151 CATGAAGCGG AGGTCAAACC AATCGACAGG GAGAAGGTAC CGGGGCAGGT
201 CGGGGAAAAA GGAAAAGTTT TGCAGATTGA CGGCGAAACC CTGCTGAAAA
251 ATCCCGAATT GCTGTCCCGC GCGATGTATT CCGCAGTGGT CTCAAACAAT
301 ATTGCCGGTA TCCGCGTTAT TTGCGCGATT TACCTACAAC AGGCGCAGCA
351 GGATAAGATG TTGGCACTTT ATGCACAAGG GATTTTGGCG CAGGCAGACG
401 GTAGGGTGAA GGAGGCGATT TCCCATTACC GGAATTGAT TGTCGCCCAA
451 CCCGACGCGC CGCCGCTCCG TATGCGTTG GCGGCGGCAT TGTTTGAAAA
501 CAGGCAGAAC GAGGCGGCGG CAGACCAATT CGACCGCTG AAGGCGGAAA
551 ACCTGCCCGC GCAGCTGATG GAGCAGGTG AGCTGTACCG CAAGGCATTG
601 CGCGAACGCG ATGCGTGGAA GGTAAATGGC GGCTTCAGCG TTACCCGCGA
651 ACACAATATC AACCAAGCCC CGAAACGGCA GCAGTACGGC AAATGGACTT
701 TCCCGAAACA GGTGGACGGC ACGGCGGTCA ATTACCGGCT CGGCGCGGAG
751 AAAAATGGT CGCTGAAAAA CGGCTGGTAC ACGACGCGCG GCGGCGACGT
801 GTCCGGCAGG GTTTATCCGG GGAATAAGAA ATTCAACGAT ATGACGGCAG
851 GCGTTTCCGG CGGCATCGGT TTTGCCGACC GGCCAAAGA TGCCGGGCTG
901 GCAGTGTTC ACGAACGCGC CACCTACGGC AACGACGCTT ATTCTTACAC
951 CAACGGCGCA CGCCTTTATT TCAACCGTTG GCAAACCCCG AAATGGCAAA
1001 CGTTGTCTTC GCGGAGTGG GGGCGTTGA AGAATACGCG CCGGCGCGGT
1051 TCCGACAATA CCCATTGCA AATTTCGAAT TCGCTGGTGT TTTACCGGAA
1101 TGCGGCGCAA TATTGGATGG GCGGTTTGA TTTTACCGC GAGCGCAACC
1151 CCGCCGACCG GGGCGACAAT TTCAACCGTT ACGGCCTGCG CTTTGCCTGG
1201 GGGCAGGAAT GGGCGGCGAG CGGCCTGTCT TCGCTGTGTC GCCTCGGCGC
1251 GCGCAACCGG CATTATGAAA AACCCGGCTT TTTACGCGT TTTAAAGGGG
1301 AAAGGCGCAG GGATAAGAA TTGAACACAT CCTTGAGCCT TTGGCACCGG
1351 GCATTGCATT TCAAGGCAT CACGCCGCGC CTGACGTGT CGCACCGCGA
1401 AACGCGGAGT AACGATGTGT TCAACGAATA CGAGAAAAT CGGCGCGTTG
1451 TCGAGTTTAA TAAAACGTTT TGA

```

This corresponds to the amino acid sequence <SEQ ID 2644; ORF 769.a>:

```

a769.pep
1  LIMVIFYFCG KTFMPARNRW MLLPLLASA AYAETPREP DLSRPEFRL
51  HEAEVKPIDR EKVPQVREK GKVLQIDGET LLKNPELLSR AMYSAVVSNN
101 IAGIRVILPI YLQQAQDDKM LALYAQGILA QADGRVKEAI SHYRELIVAQ
151 PDAPAVRMRL AAALFENRQN EAAADQFDRL KAENLPPQLM EQVELYRKAL
201 RERDAWKVNG GFSVTREHNI NQAPKRQYQG KWTFFPKQVDG TAVNYRLGAE
251 KRWGLKNQWY TTAGDVSGR VYPGNKKEND MTAGVSGGIG FADRRKDAGL
301 AVFHERRTYG NDAYSYTNGA RLYFNRWQTP KWOTLSSAEW GRLKNTRRAR
351 SDNTHLQISN SLVFYRNARQ YWMGGLDFYR ERNPADRGDN FNRVGLRFAW
401 QQEWGSGSL SLLRLGAAKR HYEKPGFFSG FKGERRRDKE LNTSLSLWHR
451 ALHFKGITPR LTLHRETRS NDVFNEYEKN RAFVEFNKTF *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 769 shows 99.8% identity over a 490 aa overlap with a predicted ORF (ORF 769) from *N. meningitidis*:

```

m769/a769  99.8% identity in 490 aa overlap

          10      20      30      40      50      60
a769.pep  LIMVIFYFCGKTFMPARNRWMLLLPLLASAAYAETPREPDLSRPEFRLHEAEVKPIDR
          |||||
m769      LIMVIFYFCGKTFMPARNRWMLLLPLLASAAYAETPREPDLSRPEFRLHEAEVKPIDR
          10      20      30      40      50      60

          70      80      90     100     110     120
a769.pep  EKVPQVREK GKVLQIDGETLLKNPELLSFAMYSVVSNNIAGIRVILPIYLQQAQDDKM

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m769					
	EKVP	GGVREK	GKVLQID	GETLLKN	PELLSRAMYS
	70	80	90	100	110
	120				
a769.pep	130	140	150	160	170
	LALYA	OGILAQ	ADGRVKEA	ISHYRELI	VAQPDAPAV
m769	130	140	150	160	170
	LALYA	OGILAQ	ADGRVKEA	ISHYRELI	VAQPDAPAV
a769.pep	190	200	210	220	230
	KAENL	PPQLMEQ	VELYRKAL	RERCAWK	VNGGFSVT
m769	190	200	210	220	230
	KAENL	PPQLMEQ	VELYRKAL	RERDAWK	VNGGFSVT
a769.pep	250	260	270	280	290
	TAVNY	RLGA	EKKWSL	KNGWYT	TAGGDVSG
m769	250	260	270	280	290
	TAVNY	RLGA	EKKWSL	KNGWYT	TAGGDVSG
a769.pep	310	320	330	340	350
	AVFH	ERTYGN	DAYS	SYTNGAR	LYFNRWOT
m769	310	320	330	340	350
	AVFH	ERTYGN	DAYS	SYTNGAR	LYFNRWOT
a769.pep	370	380	390	400	410
	SLVF	YRNARQ	YWMGGL	DFYRERN	PADRGDN
m769	370	380	390	400	410
	SLVF	YRNARQ	YWMGGL	DFYRERN	PADRGDN
a769.pep	430	440	450	460	470
	HYEK	PGFFSG	FKGERRR	DKE	NTSLSL
m769	430	440	450	460	470
	HYEK	PGFFSG	FKGERRR	DKE	NTSLSL
a769.pep	490				
	RAFV	EFNKTF	X		
m769	490				
	RAFV	EFNKTF	X		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2645>:

g770.seq

1	ATGAACAGAC	TGCTACTGCT	STCTGCCGCC	GTCCTGCCGA	CTGCCTGCCG
51	CAGCGGGCAA	ACCGATAAAA	TCGGACGGGC	AAGTACCGTT	TTCAACATST
101	TGGGCAAAAA	CGACCGTATC	GAAGTGAAG	GATTCGACGA	TCCCGACGTT
151	CAAGGGGTTG	CCTGTTATAT	TTCGTATGCA	AAAAAAGCGC	GCTTGAAGSA
201	AATGGTCAAT	TTGGAAGAGG	ACCGGTCGCA	CGCATCGGTT	TCGTGCGTTC
251	AGACGGCATC	TTGATTCT	TTTGACGAAA	CCGCCGTGCG	CAAACCGAAA
301	GAAGTTTTC	AGCGCGGTAC	GGGCTTCGCG	TTCAAGAGCC	GGCAGATTGT
351	CCGTTATTAC	GACCCCAAAC	GCAAGCCCTT	CGCCTATTTC	GTTTACAGCG
401	ATAAAATCGT	CCAAGGATCG	CCGAAAAATT	CCTTAAGCGC	GGTTTCCTGT
451	TTCGGCAGCG	GCATACCGCA	AACCGACGGG	GTGCAAGCCG	ATACTTCCGG
501	CAAACTGCTT	GCCGGCGCCT	GCATTATTTC	CAACCCGATA	AAAAATCCCG
551	ACAAACGCTG	A			

This corresponds to the amino acid sequence <SEQ ID 2646; ORF 770.ng>:

g770.pep

1	MNRLLLSAA	VLPTACGS	GE	TDKIGRA	STV
51	QGVACY	SYA	KKGLKEM	VN	LEEDAS
101	EVFKRG	TGFA	FKSRQIV	RY	DPKRAFA
151	FGSGIP	QTDG	VQADTSG	KLL	AGACIIS

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2647>:

m770.seq

1	ATGAACAGAC	TGCTACTGCT	GTCTGCCGCC	GTCCTGCTGA	CTGCCTGCCG
51	CAGCGGGCAA	ACCGATAAAA	TCGGACGGGC	AAGTACCGTT	TTCAACATAC

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101 TGGGCAAAAA CGACCGTATC GAAGTGAAG GATTGACGA TCCCGACGTT
151 CAAGGGGTTG CCTGTTATAT TTCGTATGCA AAAAAAGCG GCTTGAAGGA
201 AATGGTCAAT TTGGAAGAGG ACGCGTCCGA CGCATCGGT TCGTGCCTTC
251 AGACGGCATC TTCGATTCT TTTGACGAAA CCGCCGTGCG CAAACCGAAA
301 GAAGTTTCA AACACGGTGC GAGCTTCGCG TTCAAGAGCC GGCAGATTGT
351 CCGTTATTAC GACCCCAAAC GCAAAACCTT CGCCTATTG GTGTACAGCG
401 ATAAATCAT CCAAGGCTCG CCGAAAAAT CTTAAGCGC GGTTCCTGT
451 TTCGGCGGCG GCATACCGCA AACCAGTGGG GTGCAAGCCG ATACTTCCGG
501 CAACCTGCTT GCCGGCGCCT GCATGATTTC CAACCCGATA GAAATATCIG
551 ACAAACGCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2648; ORF 770>:

```

m770.pep
1  MNRLLLLSAA VLLTACSGE TDKIGRASTV FNILGKNDR I EVEGFDDPDV
51  QGVACYISYA KKGGLKEMVN LEEDASDASV SCVQTASSIS FDETAVRKPK
101 EVFKHGASFA FKSRIQVRY DPKRRTFAYL VYSDKIIQGS PKNSLSAVSC
151 FGGGIPQTDG VQADTSGNLL AGACMISNPI ENLDRK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 770 shows 93.5% identity over a 186 aa overlap with a predicted ORF (ORF 770) from *N. gonorrhoeae*

m770/g770 93.5% identity in 186 aa overlap

	10	20	30	40	50	60
g770.pep	MNRLLLLSAAV	LPTACSGE	TDKIGRASTV	FNILGKNDR I	EVEGFDDPDV	QGVACYISYA
m770	MNRLLLLSAAV	LPTACSGE	TDKIGRASTV	FNILGKNDR I	EVEGFDDPDV	QGVACYISYA
	10	20	30	40	50	60
g770.pep	KKGGLKEMVN	LEEDASDASV	SCVQTASSIS	FDETAVRKPK	EVFKRGTF	FAFKSEQIVRY
m770	KKGGLKEMVN	LEEDASDASV	SCVQTASSIS	FDETAVRKPK	EVFKHGASFA	FKSRQIVRY
	70	80	90	100	110	120
g770.pep	DPKRRTFAYL	VYSDKIIQGS	PKNSLSAVSC	FGGGIPQTDG	VQADTSGNLL	AGACMISNPI
m770	DPKRRTFAYL	VYSDKIIQGS	PKNSLSAVSC	FGGGIPQTDG	VQADTSGNLL	AGACMISNPI
	130	140	150	160	170	180
g770.pep	KNPDKRX	:	:	:	:	:
m770	ENLDRKX	:	:	:	:	:

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2649>:

```

a770.seq
1  ATGAACAGAC TGCTACTGCT GTCTGCCGCC GTCCTGCTGA CTGCCGCGG
51  CAGCGCGCAA ACCGATAAAA TCGGACGGGC AAGTACCGTT TTCACATAC
101 TGGGCAAAAA CGACCGTATC GAAGTGAAG GATTGACGA TCCCGACGTT
151 CAAGGGGTTG CCTGTTATAT TTCGTATGCA AAAAAAGCG GCTTGAAGGA
201 AATGGTCAAT TTGGAAGAGG ACGCGTCCGA CGCATCGGT TCGTGCCTTC
251 AGACGGCATC TTCGATTCT TTTGACGAAA CCGCCGTGCG CAAACCGAAA
301 GAAGTTTCA AACACGGTGC GAGCTTCGCG TTCAAGAGCC GGCAGATTGT
351 CCGTTATTAC GACCCCAAAC GCAAAACCTT CGCCTATTG GTGTACAGCG
401 ATAAATCAT CCAAGGCTCG CCGAAAAAT CTTAAGCGC GGTTCCTGT
451 TTCGGCGGCG GCATACCGCA AACCAGTGGG GTGCAAGCCG ATACTTCCGG
501 CAACCTGCTT GCCGGCGCCT GCATGATTTC CAACCCGATA GAAATATCCG
551 ACAAACGCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2650; ORF 770.a>:

```

a770.pep
1  MNRLLLLSAA VLLTACSGE TDKIGRASTV FNILGKNDR I EVEGFDDPDV
51  QGVACYISYA KKGGLKEMVN LEEDASDASV SCVQTASSIS FDETAVRKPK
101 EVFKHGASFA FKSRIQVRY DPKRRTFAYL VYSDKIIQGS PKNSLSAVSC

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151 FGGGIPQTDG VQADTSGNLL AGACMISNPI ENPDKR*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*ORF 770 shows 99.5% identity over a 186 aa overlap with a predicted ORF (ORF 770) from *N. meningitidis*:

m770/a770 99.5% identity in 186 aa overlap

	10	20	30	40	50	60
a770.pep	MNRLLLLSAAVLLTACGSGETDKIGRASTVFNILGKNDRIEVEGFDDPDVQGVACYISYA					
m770	MNRLLLLSAAVLLTACGSGETDKIGRASTVFNILGKNDRIEVEGFDDPDVQGVACYISYA					
	10	20	30	40	50	60
	70	80	90	100	110	120
a770.pep	KKGGLKEMVNLEEDASDASVSCVQTASSISFDETAVRKPKFVKHGASFAFKSRQIVRYY					
m770	KKGGLKEMVNLEEDASDASVSCVQTASSISFDETAVRKPKFVKHGASFAFKSRQIVRYY					
	70	80	90	100	110	120
	130	140	150	160	170	180
a770.pep	DPKRRTFAYLVYSDKIIQGSPPKNSLSAVSCFSGGGIPQTDGVQADTSGNLLAGACMISNPI					
m770	DPKRRTFAYLVYSDKIIQGSPPKNSLSAVSCFSGGGIPQTDGVQADTSGNLLAGACMISNPI					
	130	140	150	160	170	180
a770.pep	ENPDKRX					
m770	ENLDRX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2651>:

g771.seq

```

1  ATGGATTAT  TATCGGTTTT  CCACAAATAC  CGTCTGAAAT  ATGCGGTGGC
51  GGTGCTGACG  ATGCTGCTTT  TGGCGGCAGT  CGGGCTGCAC  GCTTCCGTAT
101  ATCGCACCTT  CACGCCCGAA  AACATCCGCA  GCCGCCTCCA  ACAAGCATT
151  GCCCATACCC  ACCGAAAAAT  CTCGTTTGAT  GCGGATATAC  GCGCAGGCT
201  TCTGCCCCGC  CCGACCGTCA  TCCTGAAAAA  CCTGACCATT  ACCGAACCCG
251  ACGCGCGCCG  GGTGCGCGTT  TCCGTCAAAG  AAACAAAAT  CGGATTGAGC
301  TGGAAAAACC  TGTGGTCGGA  TCGGATACAG  GTTGAAAAAT  GGGTGGTTTC
351  GGGTGC GGAT  CTTGCCCTGA  CGCGCGACAG  AAACGGCGCT  TGAACATCC
401  AAGACCTGTT  CGACGGCGCG  AAACACTCCG  CCTCAGTCAA  CGGCATTATC
451  GTCGAAAAAC  GCACCGTCCG  CCTCAATTTT  CTGCAGCAAC  AGCTTATCCT
501  GAAGGAATC  AGCCTCAACC  TGCAATCCCC  CGATTCTGTC  GGGCAGCAGT
551  TTGAAAGTTC  GGGCATACTG  GTTTGAGAA  AGCTGTCCGT  CCCGTGAAA
601  AGCAGGGGGC  TGTTCCTTTC  AGACGGCATC  GGCACGCCCG  AAATCTCACC
651  GTTCCATTTT  GAAGCTTCCA  CTTGCTGGA  CGGACACGGC  ATCACCATT
701  CCACCACCGG  CAGCCCTTCT  GTCCGCTTCA  ACGCCGGCGG  AGCGGATGCC
751  GCCGGCCTCG  GCCTGCGTGC  AGACACTTCC  TTCCGCAACC  TCCACCTGAC
801  CGCGCAATC  CCCGCACTGG  CACTCAAAAA  CAACAGCATC  AAAACCGGCA
851  CGGTCAACGG  CACGTTTACC  GCCGGCGGCG  AATATGCCCG  ATGGGACGGT
901  TCGTTCAAAC  TCGACAAAGC  CAACCTGCAC  TCCGGCATCG  CCAACATCGG
951  CAACGCCGAA  ATCTCCGGCA  GTTTCAAAC  ACCGCGCCTT  CAAACCAATT
1001  TCTCCCTCGG  CTCGCCGTTG  GTTTGGAGTC  GGGACAACGG  GCTGGACGCC
1051  CCGCGCCTGC  ACATATCGAC  CTTTCAAGAT  ACCGTGACAC  GCCTGCCGCA
1101  ACCCGGTTTC  ATCAGCCGGC  TCGACGGTTC  GCTGTCCATA  CCGAATCTGC
1151  AAAATTGGAA  TGCCGAATTA  AACGGCACAT  TCGACCGCCA  ACCCGTTGCC
1201  GCAAAATTCA  AATATACGCG  GGAAGGCGCA  CCGCACCTGG  AAGCCGCCGC
1251  CGCGCTGCAA  AAATTAAACC  TCGCCCCCTA  TCTTGACGAA  TTTCCGCAAC
1301  AAAACGGCAA  AATATTTCCC  GACATCTCTG  GCAGGCTGTC  CGGCAACGTC
1351  GAGGCACACC  TCAAAATCGG  CAGCATCCAA  CTCCCCGGCT  TCGAATCGGA
1401  CGATATGGAA  ACCTACCTCC  ACGCCGACAA  AGACCATATC  GCGCTCAGCC
1451  GTTTCAGCTC  AGGGCTTTAC  GCGCGCCATA  CCGAAGGCGG  CATCAGCATC
1501  CCCAACACCG  GTCCCGCCAC  TTACCGCTCG  CAACAGAATG  CAAGCAACAT
1551  CCAAATCCAA  CCGCTGCTGC  AAGACCTGTT  CGGCTTCCAC  AGCTTCAGCG
1601  GCAACGGCGA  TCGGGTTCAT  GACCTGACCG  CAAGCGGCGA  AAACCGCAAA
1651  CAGCTTATCC  GCTCGTGC  AGGCAGCCTG  TCGCTGAATA  TTTCAACGG
1701  CCGCTGGCAC  GGCATCGATA  TGGACAGCAT  TTTAAAAAAC  GGCCTTTCCG

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1751  GGAAATCTC  GGGCAGCACA  CCCTTCTACC  GATTACAGCT  CAACAGCGAA
1801  ATTTTCAGAG  GCATCAGCCG  CCACATCGAT  ACCGAACTCT  TCTCCGACAG
1851  CCTCTATGTT  ACCAGCAACG  GCTATACCAA  TCTGGATACG  CAGGAATTGT
1901  CTGAAGATGT  CTTATCCGC  AACGCCGTCC  ATCCGAAAAA  CAAACCGATT
1951  CCCCTGAAAA  TCACCGGTAC  GGTGGACAAG  CCGTCCATTA  CCGTCGATTA
2001  CGGCAGGCTG  ACCGGCGGCA  TCAATTCCGC  CAAAGAGAAA  CAGAAAATCC
2051  TCGAAGACAC  CCTGCTGGAA  CAATGGCAGT  GGCTCAAACC  TAAAGAACCG
3051  TAA

```

This corresponds to the amino acid sequence <SEQ ID 2652; ORF 771.ng>:

```

g771.pep
1  MDLLSVFHKY  RLKYAVAVLT  MLLLAAVGLH  ASVYRTFTPE  NIRSRLQQSI
51  AHTRKISFD  ADIRRRLLPR  PTVILKNLTI  TEPDGGRVAV  SVKETKIGLS
101 WKNLWSDRIQ  VEKVVVSGAD  LALTFDRNGA  WNIQDLFDGA  KHSASVNRRI
151 VENSTVRNLF  LQQQLILKEI  SLNLQSPDSS  GQOFESSGIL  VWRKLSVPWK
201 SRGLEFLSDGI  GTPDISPFHF  EASTELDGHG  ITISTGSPS  VRFNAGGADA
251 AGLGLRADTS  FRNLHLTAQI  PALALKNNIS  KGTGVNGTFT  AGGEYARWDG
301 SEKLDKANLH  SGIANIGNAE  ISGSFKTPRL  QTNFSLGSPL  VWSRDNLDA
351 PRLHISTLQD  TVDRLPQPRF  ISRLDGSLSI  PNLQNWNAEL  NGTFDRQPVA
401 AKFKYTREGA  PHLEAAAAAQ  KLNLAAPYLOE  FRQQNGKIFP  DILGRLSGNV
451 EAHKIGISIQ  LPGLQLDDME  TYLHADKDHI  ALSRFKSGLY  GGHTEGGISI
501 ANTRPATYRL  QQNASNIQIQ  PLLQLLFGFH  SFSNGDAVI  DLTASGENRK
551 QLIRSLQGS  SLNISNGAWH  GIDMESILKN  GLSGKISGST  PFYFTLNSE
601 ISDGISRHID  TELFSDSLYV  TSNGYTNLDT  QELSEDVLIR  NAVHPKNKPI
651 PLKI*GTVDK  PSITVDYGR  L  TGGINSRKEK  QKILEDTLLE  QWQWLKPKPE
701

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2653>:

```

m771.seq
1  ATGGATTAT  TATCGGTTTT  CCACAAATAC  CGTCTGAAAT  ATGCGGTGGC
51  CGTGCTGACG  ATACTGCTTT  TGGCGGCAGT  CGGGCTGCAC  GCTTCCGTAT
101 ATCCGACCTT  CACGCCTGAA  AACATCCGCA  GCCGCCTACA  ACAAGCATT
151 GCACACACAC  ACCGAAAAAT  CTCGTTTGAT  GCGGACATTC  AGCGCAGGCT
201 CCTGCCCCGG  CCGACCGTCA  TCCTGAAAAA  CCTGACCATT  ACCGAACCCG
251 GCGGCGACCA  GACTGCCGTT  TCCGTCCAAG  AAACCAAAAT  CGGATTGAGC
301 TGGAAAAAAC  TGTGGTCGGA  TCAGATACAG  ATTGAAAAAT  GGGTGGTTTC
351 GAGTGGCGAA  CTTGCCCTGA  CGCGCGACGG  GAAAGGTGTT  TGGAACATCC
401 AAGACCTGAT  CGACAGCCAA  AAACGCCAAG  CCTCAGTCAA  CCGCATTATC
451 GTCGAAAAAC  GCACCGTCCG  CCTCAATTTC  CTCGAGGAAC  AGCTTATCCT
501 GAAGGAAATC  AACCTCAACC  TGCAATCCCC  CGATTCTGTC  GGGCAGCCGT
551 TTGAAAGTTC  GGGCATACTG  GTTTGGGGAA  AGCTGTCCGT  CCCGTGGAAA
601 AGCAGGGGCG  TGTTCCTTTC  AAACGGCATC  GGCCCGCCCG  AAATCTCACC
651 GTTCCATTTC  GAAGCTTCCA  CTTGCGTGG  CGGACACGGC  ATTACCATTT
701 CCACCACCGG  CAGCCCTTCT  GTCCGCTTCA  ACGCCGGCGG  AGCGGATGCC
751 GCCGGCCTCG  GCCTGCGTGC  AGACACTTCC  TTCCGCAACC  TCCACCTGAC
801 CGCCCAAAAT  CCGCGCTGG  CACTCAGGAA  CAACAGCATT  AAAATTGAAA
851 CCGTCAACGG  CGCATTATCC  GCCGCGGCG  AATATGCCCG  ATGGGACGGT
901 TCGTTCAAA  TCGACAAAGC  CAACCTGCAC  TCCGGCATCG  CCAACATCGG
951 CAACGCCGAA  ATCTCCGGCA  GCTTCAAAAC  ACCGCGCCAC  CAGACCAACT
1001 TCTCCCTCAA  TTCGCCGCTC  GTATGGACGG  AAAACAAAGG  GCTGGACGCG
1051 CCGCGCCTGT  ATGTATCGAC  CCTCAGGAT  ACCGTCAACC  GCCTGCCGCA
1101 ACCCCGTTTC  ATCAGCCGGC  TCGACGGTTC  GCTGTCCGTA  CCGAATCTGC
1151 AAAATTGGAA  TGCCGAATTA  AACGGACAT  TCGACCGCCA  AACCGTTGCC
1201 GCGAAATTCA  GATACACACA  TGAAGACGCA  CCGCATCTGG  AAGCCGCCGT
1251 CGCACTGCAA  AAATTGAACC  TGACCCCTTA  TCTTGACGAC  GTGCGGCAAC
1301 AAAACGGCAA  AATATTTCCC  GACCCCTCG  CCAAGCTGTC  CGGCGACATC
1351 GAGGCGCACC  TGAATTCG  AAAAGTCCAA  CTTCCCGGCC  TGCAACTGGA
1401 CGATATGGAA  ACCTACCTCC  ACGCCGACAA  AGGCCATATC  GCGCTCAGCC
1451 GTTTCAAGTC  AGGGCTTTAC  GCGGCGCATA  CCGAAGGCGG  CATCAGCATC
1501 GCCAACACCC  GTCCCGCCAC  TTACCGCCTG  CAACAGAAAT  CAAGCAACAT
1551 CCAATCCAA  CCGCTGCTGC  AAGACCTGTT  CGGCTTCCAC  AGCTTCAGCG
1601 GCAACGGCGA  CGCGGTATC  GACCTGACCG  CGGCGGCGGA  AACC CGAPAA
1651 GAGCTTATCC  GCTCGCTTCA  GGGCAGCCTG  TCGCTAAATA  TTTCACACGG
1701 TGCATGGCAC  GGTATCGACA  TGGACAATAT  CCGTGAATAAC  GGCATTTCCG
1751 GCAAACTGTC  CGACAATGCC  GCACCCAGCA  CACCCTTCCA  CCGATTACCG
1801 CTCACACGCG  AAATTTTACA  CGGCATCAGC  CGCCACATCG  ATACCGAACT
1851 CTCTCCGAG  AGCCTCTATG  TTACAGCAA  CGGCTATACC  AATCTGGATA
1901 CGCAGGAATT  GTCTGAAGAT  GTCCTTATCC  GCAACGCCGT  CCATCCGAAA
1951 AACAAACCGA  TTCCCTTGAA  AATCAACGGC  ACGGTGGACA  AACCGTCCAT
2001 TACCGTCGAT  TACGGCAGGC  TGACC3GCGG  CATCAATTCC  CGCAAAGAGA
2051 AACAGAAAA  CCTCGAAGAC  ACCCT3CTGG  AACAAATGGCA  GTGGCTCAAA
2101 CCTAAAGAAC  CGTA

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m771.pgp

1	MDLLSVFHXY	RLKYAVAVLT	ILLAAVGLH	ASVYRTFTPE	NIRSRLQQSI
51	AHTHRKTSFD	ADTQRRLEP	PTVLKNTLI	TEPQGDQTAV	SVQETKIGLS
101	WNKLNWSDQI	IEKVVVLSAR	LATLDRGKV	NIQQLDISQ	KRQASVNRII
151	VENSTVRLNF	LQEQLILKEI	NLNLQSPDSS	GQPFESSGIL	VWGKLSVPWK
201	SRGLFSLNGI	GPPFISPFHF	EASTSLDGHG	ITISTTSGPS	VRFNAGGADA
251	AGLGLRADTS	FRNLHLTAOI	PALALRNNSI	KIETVNGAFT	AGGEYARNWG
301	SFKLDKANLH	SGIANIGNAE	ISGSFKTPRH	QTNFSLNSPL	VWTENKGLDA
351	PRLYVSTLQD	TVNLAPQALF	ISRLDGLSV	PNLQNWNAEL	NGTFDRQTVL
401	AKFRTYHEDA	PHLEAQQVR	KLNLTPYLD	VRQNGKQIFP	DLFLAKSGDI
451	EAHLKIGEVQ	LPGLQLDDME	TYLHADKGHI	ALSRFKSGLY	GGHTEGGISI
501	ANTRPATYRL	QQNASNTQIQ	PLLDQLFHG	SFSNGDAVIA	DLTAGGETRK
551	ELIRSLQGLS	LNSNIGAWH	GIDMNNILKN	GISGKTADNA	APSTFHRET
601	LNSEISDGIS	RHIDTELFSD	SLYVTSNGYT	NLDTOELSED	VLIRNAVHPK
651	NKPIPLKITC	TVDPKPSITVD	YGRLTGGINS	RKEKQKILED	TLLEQOWWLK
701	PKPFI				

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 771 shows 90.3% identity over a 704 aa overlap with a predicted ORF (ORF 771) from *N. gonorrhoeae*

m771/g771	90.3% identity in 704 aa overlap					
	10	20	30	40	50	60
g771.pep	MDLLSVFHKYRLKYAVAVLTMLLLAAVGLHASVYRTFTPENIRSRLLQQSIAHTRKRISFD					
m771	MDLLSVFHKYRLKYAVAVLTMLLLAAVGLHASVYRTFTPENIRSRLLQQSIAHTRKRISFD					
	10	20	30	40	50	60
	70	80	90	100	110	120
g771.pep	ADIRRRLLPRPTVILKNLTITPEPGGRVAVSVKETKIGLSWKNLWSDRIQVEKWVVS					
m771	ADIQRRLLPRPTVILKNLTITPEGGDQTAVSVQETKIGLSWKNLWSDQIQIEKWVSSAE					
	70	80	90	100	110	120
	130	140	150	160	170	180
g771.pep	LALTRDRNGAWNIIQDLFDGAKHSASVNRIIVENSTVRLNFLQQQLIKEISLNLQSPDSS					
m771	LALTRDGKGVWNIQDLIDSQKRQASVNRIIVENSTVRLNFLQEQLIKEINLNLQSPDSS					
	130	140	150	160	170	180
	190	200	210	220	230	240
g771.pep	GQQFESSGILVWRKLSVPWKSRLFLSDGIGTPEISPFHFEASTSLDGHGITISTTGSPS					
m771	GQPFESSGILVWGKLSVPWKSRLFLSNGIGPPEISPFHFEASTSLDGHGITISTTGSPS					
	190	200	210	220	230	240
	250	260	270	280	290	300
g771.pep	VRFNAGGADAAGLGLRADTSFRNLHLTAQIPALALKNNISIKTGTVNGFTTAGGEYARWDG					
m771	VRFNAGGADAAGLGLRADTSFRNLHLTAQIPALALRNNSIKIETVNGAFTTAGGEYARWDG					
	250	260	270	280	290	300
	310	320	330	340	350	360
g771.pep	SFKLDKANLHSGIANIGNAEISGSFKTPRLQTNFSLGSPLVWSRDNGLEAPRLHISTLQD					
m771	SFKLDKANLHSGIANIGNAEISGSFKTPRHQTNFSLNSPLVWTENKGLCAPRLYVSTLQD					
	310	320	330	340	350	360
	370	380	390	400	410	420
g771.pep	TVDRLPQPRFISRLDGSLSIPNLQWNNAELNGTFDRQPVAAKFYTTREGAPHLEAAAAAQ					
m771	TVNRLPQPRFISRLDGSLSVNLQWNNAELNGTFDRQTVAAKFYTHEDAPHLEAAVAALQ					
	370	380	390	400	410	420
	430	440	450	460	470	480
g771.pep	KLNLAPYLDVFRQONGKIFPDILGRLSGNVEAHLKIGSIQLPGLQLDDMETYLHADKDH					
m771	KLNLTPYLDVVRQONGKIFPDITLAKLSGDI EAHLKIGKVLPGLOLDDMETYLHADKGH					

1258

	430	440	450	460	470	480
	490	500	510	520	530	540
g771.pep	ALSRFKSGLYGGHTEGGISIANTRPATYRLQQNASNIQIPLLQDLFGFHSFSGNGDAVI					
m771	ALSRFKSGLYGGHTEGGISIANTRPATYRLQQNASNIQIPLLQDLFGFHSFSGNGDAVI					
	490	500	510	520	530	540
	550	560	570	580	590	
g771.pep	DLTASGENRKQLIRSLQGSLSLNISNGAWHGIDMDSILKNLSGKISG---STPFYRFT					
m771	DLTAGGETRKELIRSLQGSLSLNISNGAWHGIDMDNILKNISGKTADNAPSTPFHRT					
	550	560	570	580	590	600
	600	610	620	630	640	650
g771.pep	LNSEISDGISRHIDTELFSDSLVYTSNGYTNLDTQELSEDVLIRNAVHPKNKPIPLKITG					
m771	LNSEISDGISRHIDTELFSDSLVYTSNGYTNLDTQELSEDVLIRNAVHPKNKPIPLKITG					
	610	620	630	640	650	660
	660	670	680	690	700	
g771.pep	TVDKPSITVDYGRLTGGINSRKEKQKILEDTLLEQWQWLKPKEPX					
m771	TVDKPSITVDYGRLTGGINSRKEKQKILEDTLLEQWQWLKPKEPX					
	670	680	690	700		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2655>:

a771.seq

```

1  ATGGATTAT  TATCGGTCTT  CCACAAATAC  CGTCTGAAAT  ATGCGGTAGC
51  CGTGCTGACG  ATACTGCTTT  TGGCGGCAAT  CGGGCTGCAC  GCTTCCGTAT
101  ATCGCATCTT  CACACCTGAA  AACATCCGAA  GCCGCCTCCA  ACAAAGCATT
151  GCCCATACGC  ACCGGAATAT  CTCGTTTGAT  GCGGATATAC  AGCGCAGGCT
201  TCTGCCCGCG  CCGACCGTCA  TCCTGAAAAA  CCTGACCATT  ACCGAACCCG
251  GCGGCGACCG  GACTGCCGTT  TCCGTCCAAG  AAACCAAAT  CGGATTGAGC
301  TGGAAAAACC  TGTGGTCGGA  TCAGATACAG  ATTGAAAAAT  GGGTGGTTTC
351  GAGTGGCGAA  CTTCGCCCTG  CGCGCGACCG  GAAAGGTGTT  TGAACATCC
401  AAGACCTGAT  CGACAGCCAA  AAACGCCAAG  CCTCAGTCAA  CCGCATTATC
451  GTCGAAACAA  GCACCGTCCG  CCTCAATTTC  CTGCAGGAAC  AGCTTATCCT
501  GAAGGAATTC  AACCTCAACC  TGCAATCCCC  CGATTCTGTC  GGGCAGCCGT
551  TTCGAAAGTC  GGCATACTG  GTTGGGGAA  AGCTGTCCGT  TCCGTGGAAA
601  AGCAGGGGGC  TGTTCCTTTC  AGACGGCATC  GGCACGCCCA  AAATCTCACC
651  GTTCCATTTT  GAAGCTTCCA  CTTGCTGGA  CGGACACGGC  ATTACCATTT
701  CCACCCACCG  CAGCCCTTCT  GTCGCTTCA  ACGCCGCGCG  AGCGGATGCC
751  GCCGGCCTCG  GCCTGCGTGC  AGACACTTCC  TTCGCAATCC  TCCACCTGAC
801  CGCCCAATAC  CCTACGCTGG  CACTCAGGAA  CAACAGCATT  AAAATTGAAA
851  CCGTCAACGG  CGCATTATAC  GCCGGCGCG  AATATGCCCA  ATGGGACGGT
901  TCGTTCAAAC  TCGACAAAGC  CAACCTGCAC  TCCGGCATCG  CCAACATCGG
951  CAACGCCGAA  ATCTCCGGCA  GCTTCAAAAC  ACCGCGCCAC  CAGACCAACT
1001  TCTCCCTCAA  TTCGCCGCTC  GTATGGACGG  AAAACAAAGG  GCTGGACGGC
1051  CCGCGCTGT  ATGTATCGAC  CCTCAGGAT  ACCGTCAACC  GCCTGCCGCA
1101  ACCCGCTTTC  ATCAGCCGGC  TCGACGGTTC  GCTGTCCGTA  CCGAATCTGC
1151  AAAATTGGAA  TGCCGAATTA  AACGGCACAT  TCGACCGCCA  AACCGTTGCC
1201  GCGAAATTC  GATACACACA  TGAAGACGCA  CCGCATCTGG  AAGCCGCCGT
1251  CGCACTGCAA  AATTTGAACC  TGACCCCTTA  TCTTGACGAC  GTGCGGCAAC
1301  AAAACGGCAA  AATATTTCCT  GACACCTCG  CCAAGCTGTC  CGGCGACATC
1351  GAGGCGCACC  TGAATACTCG  AAAAGTCCAA  CTTCCTCGCC  TGCAACTGGA
1401  CGATATGGAA  ACCTACCTCC  ACGCCGACAA  AGGCCATATC  GCGCTCAGCC
1451  GTTTCAGTTC  AGGCTTTTAC  GCGGGCCATA  CCGAAGGCGG  CATCAGCATC
1501  GCCAACACCC  GTCCCGCCAC  TTACCGCCTG  CAACAGAATG  CAAGCAACAT
1551  CCAAAATCAA  CCGCTGCTGC  AAGACCTGTT  CGGCTTCCAC  AGCTTCAGCG
1601  GCAACGGCGA  CGCGGTCAAT  GACCTGACCG  CGGCGGCGCA  AATCCGAAAA
1651  GAGCTTATCC  GCTCGCTTCA  GGGCAGCCTG  TCGCTAAATA  TTTCAAACCG
1701  TGCATGGCAC  GGTATCGACA  TGGACAATAT  CCTGAAAAAC  GGCATTTCGG
1751  GCAAACTGTC  CGACAATGCC  GCACCCAGCA  CACCCTTCCA  CGATTTCACG
1801  CTCAACAGCG  AAATTTTACA  CGGCATCAGC  CGCCACATCG  ATACCGAACT
1851  CTCTCTCGAC  AGCCTCTATG  TTACCAAGCA  CGGCTATACC  AATCTGGATA
1901  CGCAGGAATT  GTCTGAAGAT  GTCCTTATCC  GCAACGCCGT  CCATCCGAAA
1951  AACAAACCGA  TTCCCTGAA  AATCACCAGG  ACGGTGGACA  AATCCGTCAT
2001  TACCGTCGAT  TACGGCAGGC  TGACCGGCGG  CATCAATTTC  CGCAAAGAGA
2051  AACAGAAAT  CCTCGAAGAC  ACCCTGCTGG  AACAAATGCA  GTGGCTCAAA
2101  CCTAAAGAAC  CGTAA

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This corresponds to the amino acid sequence <SEQ ID 2656; ORF 771.a>:

1259

a771.pep
 1 MDLLSVFHKY RLKYAVAVLT ILLLAAGLH ASVYRIFTPE NIRSRLQQSI
 51 AHTHRKISFD ADIQRRLPR PTVILKNLTI TEPGGDRTAV SVQETKIGLS
 101 WKNLWSDQIQ IEKWWVSSAE LALTRDGKGV WNIQDLIDSQ KRQASVNRII
 151 VENSTVRLNF LQEQILILKEI NLNLQSPDSS GQPFESSGIL VWGKLSVPWK
 201 SRGLFLSDGI GTPKISPFHF EASTSLDGHG ITISTTGSFS VRFNAGGADA
 251 AGLGLRADTS FRNLHLTAQI PTLALRNNSI KIETVNGAFT AGGEYAQWDG
 301 SFKLDKANLH SGIANIGNAE ISGSFKTPRH OTNFSLSPL VWTENKGLDA
 351 PRLYVSTLQD TVNRLPQPRF ISRLDGSLSV PNLQNWNAEL NGTFDRQTV
 401 AKERYTHEDA PHLEAAVALQ KNLNTPYLDV VRQONGKIFP DTLAKLSGDI
 451 EAHLKIGKVQ LPGLQLDDME TYLHADKGGHI ALSRFKSGLY GGHTGGGSI
 501 ANTRPATYRL QQNASNIQIQ PLLQDLFGFH SFGNGDAVI DLTAGGETRK
 551 ELIRSLQGS LNLISNGAWH GIDMDNILKN GISGKTADNA APSTPFHRFT
 601 LNSEISDGIS RHIDTELFSD SLYVTSNGYT NLDTOELSED VLIRNAVHPK
 651 NKPIPLKITG TVDKPSITVD YGRLTGGINS RKEKQKILED TLLEQWQNLK
 701 PKEP*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 771 shows 98.9% identity over a 704 aa overlap with a predicted ORF (ORF 771) from *N. meningitidis*

m771/a771 98.9% identity in 704 aa overlap

	10	20	30	40	50	60
a771.pep	MDLLSVFHKYRLKYAVAVLTILLAAIGLHASVYRIFTPENIRSRLQQSI	AHTHRKISFD				
m771	MDLLSVFHKYRLKYAVAVLTILLAAVGLHASVYRTFTPENIRSRLQQSI	AHTHRKISFD				
	10	20	30	40	50	60
a771.pep	ADIQRRLPRPTVILKNLTI	TEPGGDR	TA	VS	VQ	ETKIGLSWKNLWSDQIQIEKWWVSSAE
m771	ADIQRRLPRPTVILKNLTI	TEPGGDR	TA	VS	VQ	ETKIGLSWKNLWSDQIQIEKWWVSSAE
	70	80	90	100	110	120
a771.pep	ADIQRRLPRPTVILKNLTI	TEPGGDR	TA	VS	VQ	ETKIGLSWKNLWSDQIQIEKWWVSSAE
m771	ADIQRRLPRPTVILKNLTI	TEPGGDR	TA	VS	VQ	ETKIGLSWKNLWSDQIQIEKWWVSSAE
	70	80	90	100	110	120
a771.pep	LALTRDGKGVWNIQDLIDSQ	KRQASVNRI	IVENSTVRLN	FLQEQILILKEI	NLNLQSPDSS	
m771	LALTRDGKGVWNIQDLIDSQ	KRQASVNRI	IVENSTVRLN	FLQEQILILKEI	NLNLQSPDSS	
	130	140	150	160	170	180
a771.pep	LALTRDGKGVWNIQDLIDSQ	KRQASVNRI	IVENSTVRLN	FLQEQILILKEI	NLNLQSPDSS	
m771	LALTRDGKGVWNIQDLIDSQ	KRQASVNRI	IVENSTVRLN	FLQEQILILKEI	NLNLQSPDSS	
	130	140	150	160	170	180
a771.pep	GQPFESSGILVWGKLSVPWKS	RGFLFLSDGIGTPKISPFHF	EASTSLDGHG	ITISTTGSFS		
m771	GQPFESSGILVWGKLSVPWKS	RGFLFLSDGIGTPKISPFHF	EASTSLDGHG	ITISTTGSFS		
	190	200	210	220	230	240
a771.pep	GQPFESSGILVWGKLSVPWKS	RGFLFLSDGIGTPKISPFHF	EASTSLDGHG	ITISTTGSFS		
m771	GQPFESSGILVWGKLSVPWKS	RGFLFLSDGIGTPKISPFHF	EASTSLDGHG	ITISTTGSFS		
	190	200	210	220	230	240
a771.pep	VRFNAGGADAAGLGLRADTS	FRNLHLTAQIPTLALRNNSI	KIETVNGAFT	AGGEYAQWDG		
m771	VRFNAGGADAAGLGLRADTS	FRNLHLTAQIPTLALRNNSI	KIETVNGAFT	AGGEYAQWDG		
	250	260	270	280	290	300
a771.pep	VRFNAGGADAAGLGLRADTS	FRNLHLTAQIPTLALRNNSI	KIETVNGAFT	AGGEYAQWDG		
m771	VRFNAGGADAAGLGLRADTS	FRNLHLTAQIPTLALRNNSI	KIETVNGAFT	AGGEYAQWDG		
	250	260	270	280	290	300
a771.pep	SFKLDKANLHSGIANIGNAE	ISGSFKTPRHQT	NFSLNSPLVW	TENKGLDAPRLYVSTLQD		
m771	SFKLDKANLHSGIANIGNAE	ISGSFKTPRHQT	NFSLNSPLVW	TENKGLDAPRLYVSTLQD		
	310	320	330	340	350	360
a771.pep	SFKLDKANLHSGIANIGNAE	ISGSFKTPRHQT	NFSLNSPLVW	TENKGLDAPRLYVSTLQD		
m771	SFKLDKANLHSGIANIGNAE	ISGSFKTPRHQT	NFSLNSPLVW	TENKGLDAPRLYVSTLQD		
	310	320	330	340	350	360
a771.pep	TVNRLPQPRFISRLDGSLSV	PNLQNWNAEL	NGTFDRQTV	AAKFRYTHEDAPHLEAAVALQ		
m771	TVNRLPQPRFISRLDGSLSV	PNLQNWNAEL	NGTFDRQTV	AAKFRYTHEDAPHLEAAVALQ		
	370	380	390	400	410	420
a771.pep	TVNRLPQPRFISRLDGSLSV	PNLQNWNAEL	NGTFDRQTV	AAKFRYTHEDAPHLEAAVALQ		
m771	TVNRLPQPRFISRLDGSLSV	PNLQNWNAEL	NGTFDRQTV	AAKFRYTHEDAPHLEAAVALQ		
	370	380	390	400	410	420
a771.pep	KNLNTPLYLDDVRQONGKIF	PDTLAKLSGDI	EAHLKIGKVQLPGLQLDDME	TYLHADKGGHI		
m771	KNLNTPLYLDDVRQONGKIF	PDTLAKLSGDI	EAHLKIGKVQLPGLQLDDME	TYLHADKGGHI		
	430	440	450	460	470	480
a771.pep	KNLNTPLYLDDVRQONGKIF	PDTLAKLSGDI	EAHLKIGKVQLPGLQLDDME	TYLHADKGGHI		
m771	KNLNTPLYLDDVRQONGKIF	PDTLAKLSGDI	EAHLKIGKVQLPGLQLDDME	TYLHADKGGHI		
	430	440	450	460	470	480

1260

	490	500	510	520	530	540
a771.pep	ALSRFKSGLYGGHTEGGISIANTRPATYRLQONASNIQIQPLLQDLFGFHSFSGNGDAVI					
m771	ALSRFKSGLYGGHTEGGISIANTRPATYRLQONASNIQIQPLLQDLFGFHSFSGNGDAVI					
	490	500	510	520	530	540
	550	560	570	580	590	600
a771.pep	DLTAGGETRKELIRSLQGSLSLNI SNGAWHGI DMDNILKNGI SGKTADNAAPSTPFHRET					
m771	DLTAGGETRKELIRSLQGSLSLNI SNGAWHGI DMDNILKNGI SGKTADNAAPSTPFHRET					
	550	560	570	580	590	600
	610	620	630	640	650	660
a771.pep	LNSEISDGISRHIDTELFSDSLYVTSNGYTNLDTQELSEDVLIRNAVHPKNKPIPLKITG					
m771	LNSEISDGISRHIDTELFSDSLYVTSNGYTNLDTQELSEDVLIRNAVHPKNKPIPLKITG					
	610	620	630	640	650	660
	670	680	690	700		
a771.pep	TVDKPSITVDYGRLTGGINSRKEKQKILEDTLLEQWQWLKPKEPX					
m771	TVDKPSITVDYGRLTGGINSRKEKQKILEDTLLEQWQWLKPKEPX					
	670	680	690	700		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2657>:

```

g772.seq
1  GTGTTCCGCA CGGTCTTGCG GACTGATGCC GACTGCCTGC AAATCATCGT
51  CGTCGCAAG TTCTTTCAGG TTGTGCGTA TGGTTTTCGG GCGTTGGCGG
101 AAGGCGAGTT TCACCAAGTTT GCGAAATGA TCGAAATCGT CCGCCTTGCC
151 GATACGGTGT TTCACCGGAA TCATGCGCAC CACTGCGGAA TCGATTTTCG
201 GCGCGGATC GAACGATTCG GCGGCACGT CAATCAGCAG CTCATATCG
251 AAAAAATATT GCAGCATCAC ACCCAAGCGA CCGTAGTCGT TGCTTTTCGG
301 CGCGGCAACC ATGCGCTCGA CCACTTCTTT TTGCAACATA AAGTGCATAT
351 CGCGGACATC GTCCGCCACC TCCGCCAGTT TGAACAAAAG CGGCGTGGAG
401 ATGTTATACG GCAGGTGTCG GACGATTTTC TTTTTCCTG AGATGCCGTT
451 GAAATCAAAC TGCAACACGT CGCCTTCGTG AATCACCAGT TTATCCGCAA
501 ACGGCAGCGT TTTCAGACGG CATACGATGT CGCGGTCGAT TTCGACAACG
551 TGCAGGCGGT TCAGCTTTTTC CGCCAAAGGT TCGGTAATTG CCGCCAAACC
601 CGGGCCGATT TCAATCACGA CATCATCCGC CTGCGGGCGC ACGGCGTTGA
651 CAATATCGCC GATAATCCGC GTGTCCTGCA AAAAATTCTG CCCGAAACGC
701 TTGCGGGCTT TGTGTTCTTT CATCGTGTTC CCTCTTCGGT TGAACCCCGT
751 CCGCTTAGGG CGGCAGGATC AGACTCTGTT TGGCGGGGCG GTAACCCCTT
801 CCAATCAGG ACGACACATA GGGCGGTGCT TTATGTGTCT TCCTGTGTGT
851 TGAACATAA ATGTGTTTAC AGTATCCGTT TGATGTCGGC ATTGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2658; ORF 772.ng>:

```

g772.pep
1  VEGTVLRDA DCLQIIVVGK FFOVVAYGFA ALAEGEFHOF GEMIEIVRLA
51  DTVFHRNHAH HCGIDFRGI ERFGRHVNQO LHIEKILQHH TOATVVVAFR
101 RGNHALDHFF LQHKVHIGDI VRHLRQFEQK RRGDVIRQVA DDFLFA*DAV
151 EIKLQHVAFV NHQFIRKROR FOTAYDVAVD FDNVQAVQLF RQREGNCRQT
201 RADFNHDIIR LRAHGVNDIA DNPRLVQKIL PETLAGFVFF HRVSSSVETP
251 PFRAAGSDSV WAGRNPFQIR TTHRAVLVVS SCVLEHKCVY SIRLMSAL*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2659>:

```

m772.seq
1  ATGTTCCGCG CGGTCTTGCG GATTGATGCC GACTGCCTGC AAATCATCGT
51  CGCCTGCAAG CTCTTTCAGA TTGTGCGTA TGGTTTTCGG GCGTTGGTGG
101 AAGGCGAGTT TCACCAAGTTT GCGAAATGC TCGAAATCGT CCGCCTTGCC
151 GATGCGGTGT TTCACCGGAA TCATACGGAC GACGGCGGAA TCCACTTTCG
201 GCGCAGGATC GAACGATTCG GCGGTACGT CAATCAGCAT TTCATATCG
251 AAAAAATATT GCAGCATCAC GCCCAAGCGG CCGTAGTCGT TGCTTTTCGG
301 CGCGGCAACC ATACGCTCGA CCACTTCTTT TTGCAGCATA AAGTGCATAT
351 CGACGACATC GTCCGCCACC TCCGCCAGCT TGAACAAAAG CGGTGTGGAA
401 ATGTTGTACG GGAGGTGTCG GACGATTTTC TTTTTCCTG CGATGCCGTT
451 GAAATCAAAC TGCAATACAT CGCCTTCGTG AATCACCAGT TTATCCGCAA
501 ACGGCAGCGT TTTCAGACGG CATACGATGT CGCGGTCGAT TTCGACAACG
551 TGCAGGCGGT TCAGCTTTTTC CGCCAAAGGT TCGGTAATCG CCGCCAAACC
601 CGGGCCGATT TCAATCACGA CATCATCCGC CTGCGGGCGC ACGGCGTTGA
651 CAATATCGCT GATAATCCGC GTGTCCTGCA AAAAATTCTG CCCGAAACGC

```

1261

```

701 TTGCGGGCTT TGTGTTCTTT CATCGTGTTT CCTTTTCGGT TGAACCCCG
751 CCCTTTAGGG CGGTAGAATC AGACTCTATT TGGGAGGGGC GTAACCTTTT
801 CCAAATCAGG ATGGCACATA GGGCGGTGCT TTATGTGTCG TCCTGTGTGT
851 TGAACATAA ATGTGTTTAC AGTATCCGTT TGATGTCGGC ATTGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2660; ORF 772>:

```

m772.pep
1  MFGAVLRIDA DCLQIIVACK LFOIVAYGFA ALVEGEFHEF GKMLEIVRLA
51  DAVFHRNHTD DGGIHFRRRV ERFGRYVNH FHIEKILQHH AQAQVVAER
101 RGNHTLDHFF LQHKVHIDDI VRHLRQLEOK RCGNVVREVA DDFLFACDAV
151 EIKLQYIAFV NHQFIRKRQR FQTAYDVAVD FDNVQAVQLF RQRFGNRRQT
201 RADENHDIIR LRAHGVNDIA DNPRVLQKIL PETLAGFVFF HRVSFSVETP
251 PFRAVESDSI WEGRNSFQIR MAHRAVLVVS SCVLKHKCVY SIRLMSAL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 772 shows 85.2% identity over a 298 aa overlap with a predicted ORF (ORF 772) from *N. gonorrhoeae*

```

m772/g772    85.2% identity in 298 aa overlap

          10      20      30      40      50      60
g772.pep    VFGTVLRTDADCLQIIVVGKFFQVYAGFAALAEGEFHQFGEMIEIVRLADTVFHRNHAH
              |||:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
m772         MFGAVLRIDADCLQIIVACKLFOIVAYGFAALVEGEFHEFGKMLEIVRLADAVFHRNHTD
              10      20      30      40      50      60

          70      80      90      100     110     120
g772.pep    HCGIDFRRGIERFGRHVNQQLHIEKILQH:TOATVVVAFRRGNHALDHFFLQHKVHIGDI
              || | | | | | | | | | | | | | | | | | | | | | | | | | |
m772         DGGIHFRRRVERFGRYVNOHFHIEKILQHHAAQAAVVVAFRRGNHTLDHFFLQHKVHIDDI
              70      80      90      100     110     120

          130     140     150     160     170     180
g772.pep    VRHLRQFEQKRRGDVIRQVADDFLFXDAVEIKLQHVAFVNHQFIRKRQRQTAYDVAVD
              |||:| | | | | | | | | | | | | | | | | | | | | | | | | |
m772         VRHLRQLEQKRCGNVVREVADDFLACDAVEIKLQYIAFVNHQFIRKRQRQTAYDVAVD
              130     140     150     160     170     180

          190     200     210     220     230     240
g772.pep    FDNVQAVQLFRQRFNGCRQTRADFNHDIIRLRAHGVNDIADNPRVLQKILPETLAGFVFF
              |||:| | | | | | | | | | | | | | | | | | | | | | | |
m772         FDNVQAVQLFRQRFGNRRQTRADFNHDIIRLRAHGVNDIADNPRVLQKILPETLAGFVFF
              190     200     210     220     230     240

          250     260     270     280     290     299
g772.pep    HRVSSSVETPPFRAAGSDSVWAGRNPFQIRTHRAVLVSSCVLEHKCVYSIRLMSALX
              ||| | | | | | | | | | | | | | | | | | | | | | | |
m772         HRVSFSVETPPFRAVESDSIWEGRNSFQIRMAHRAVLVSSCVLKHKCVYSIRLMSALX
              250     260     270     280     290

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2661>:

```

a772.seq
1  ATGTTTCGGCG CGGTCTTGCG GATTGATGCC GACTGCCTGC AAATCATCGT
51  CGCCTGCAAG CTCCTTCAGA TTGTTGCGTA TGGTTTTCGG GCGTTGGTGG
101 AAGGCGAGTT TCACGAGTTT GCGGAAATGC TCGAAATCGT CCGCCTTGCC
151 GATACGGTGT TTCACCGGAA TCATGCGGAC GACGGCCGAA TCCACTTTCG
201 GCGCGGGGTC GAACGATTCT GCGGCGACGT CAATCAGCAT TTCCATATCG
251 AAGAAATATT GCAGCATCAC GCCCAAGCGG CCGTAGTCGT TGCTTTTCGG
301 CGCGGCAACC ATACGATCGA CCACTTCTTT TTGCAGCATA AAGTGCAAT
351 CACGACATC GTCCGCCACC TCCGCCAGCT TGAACAAAAG CGGCGTGGAA
401 ATGTTGTAGG GCAGGTGCCC GACGATTTTC TTTTTCCTG CGATGCCGTT
451 GAAATCAAAC TGCAATACAT CGCCTTCGTG AATCACCAGT TTATCCGCAA
501 ACGGCAGCGT TTTCAGACGG CATAAGATGT CGCGGTCGAT TTCGACAACG
551 TGCAGGCGGT TCAGCTTTTTC CGCCAAAGGT TCGGTAATCG CCGCCAAACC
601 CCGACCGATT TCAATCACGA CATCATCCGC CTGCGGGCGC ACGGCGTTGA
651 CAATATCGCT GATAATCCGC GTGTCTTGCA AAAAATTCTG CCCGAACGC
701 TTGCGGGCTT TGTGTTCTTT CATCGTGTTT CCTTTTCGGT TGAACCCCG
751 CCCTTTAGGG CGGTAGAATC AGACTCTATT TGGGAGGGGC GTAACCTCTT
801 CCAAATCAGG ACGGCACATA GGGCGGTGCT TTATGTGTCG TCCTGTGTGT
851 TGAACATAA ATGTGTTTAC AGTATCCGTT TGATGTCGGC ATTGTAA

```

1262

This corresponds to the amino acid sequence <SEQ ID 2662; ORF 772.a>:

```
a772.pep
1  MFGAVLRIDA DCLQIIVACK LFOIVAYGFA ALVEGEFHEF GEMLEIVRLA
51  DTVFHRNHAD DGRHFRRGV ERFGRHVNQH FHIEEILQHH AQAQVAVAFR
101 RGNHTIDHFF LQHKVHIDDI VRHLRQLEOK RRGNVVGQVA DDFLFACDAV
151 EIKLQYIAFV NHQFIRKRQR FQTAYDVAVD FDNVQAVQLF RQRFGNRRQT
201 RTDFNHDII RLAHGVNDIA DNPRVLQKIL PETLAGFVFF HRVSFSVETP
251 PFRAVESDSI WEGRNSFQIR TAHRVLYVS SCVLKHKCVY SIRLMSAL*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 772 shows 95.6% identity over a 298 aa overlap with a predicted ORF (ORF 772) from *N. meningitidis*

```
m772/a772 95.6% identity in 298 aa overlap

a772.pep      10      20      30      40      50      60
MFGAVLRIDADCLQIIVACKLFOIVAYGFAALVEGEFHEFGEMLEIVRLADTVFHRNHAD
|||||
m772          10      20      30      40      50      60
MFGAVLRIDADCLQIIVACKLFOIVAYGFAALVEGEFHEFGKMLEIVRLADAVFHRNHTD
|||||

a772.pep      70      80      90      100     110     120
DGRHFRRGVVERFGRHVNQHFHIEEILQHHAAQAVVAFRRGNHTIDHFFLQHKVHIDDI
|||
m772          70      80      90      100     110     120
DGGIHFRRRVVERFGRYVNQHFHIEKILQHHAAQAVVAFRRGNHTLDHFFLQHKVHIDDI
|||||

a772.pep      130     140     150     160     170     180
VRHLRQLEQKRGRNVVGQVADDFLFACDAVEIKLQYIAFVNHQFIRKRQRFQTAYDVAVD
|||||
m772          130     140     150     160     170     180
VRHLRQLEQKRCGNVVREVADDFLFACDAVEIKLQYIAFVNHQFIRKRQRFQTAYDVAVD
|||||

a772.pep      190     200     210     220     230     240
FDNVQAVQLFRQRFGNRRQTRTDFNHDIIRLAHGVNDIADNPRVLQKILPETLAGFVFF
|||||
m772          190     200     210     220     230     240
FDNVQAVQLFRQRFGNRRQTRADFNHDIIRLAHGVNDIADNPRVLQKILPETLAGFVFF
|||||

a772.pep      250     260     270     280     290     299
HRVSFSVETPPFRAVESDSIWEGRNSFQIRTAHRVLYVSSCVLKHKCVYSIRLMSALX
|||||
m772          250     260     270     280     290
HRVSFSVETPPFRAVESDSIWEGRNSFQIRMAHRVLYVSSCVLKHKCVYSIRLMSALX
|||||
```

g773.seq not found yet

g773.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2663>:

```
m773.seq
1  ATGGGATTGG GTGCAACGAC TTTTGTGGT TCGGGTGCTA TAGGCGGAGG
51  TCTGTGCACT ACCGGGATTG GCTGTGCGGC CGGTGGACTT ATTGCAACGG
101 CAGGTATGAC CGGTGGTTAT ACACAGGCCT CAGAAGGAAG CCGGCAATGG
151 TTTGGCACTT ACCAGTCCGA TTTTGGTAAA AAAGTTGTCC TATCTTTGGG
201 TACACCAATA GAATACGAAT CGCCGTTAGT ATCTGATGCG AAAAATCTAG
251 CCGTATGGGG ATTGGAAACG CTGATTACGC GCAAATTGGG AAAC TTGGCA
301 ACGGGTGTGA AAAC TTCCCTT GACTCCGAAA ACTGCTGACG TACAGCGAAA
351 TATCTGTGCC CAATCCGAAG TCGGTATCAA CTGGGGCAAG GGGATTGAAG
401 GACAGGGAAT GCCTTGGGAG GATTATGTCG GTAAGGCGCT GTCTGCCAAT
451 GCAAGGTTAC CTAAAAATTT TAAAAACATT GATTATTTTG ATCGTGGTAC
501 AGGCACGGCA ATCAGTGCCA AACTCTGGA TACGCAAACT ACGGCACGCC
551 TGTCCAAACC CGAACAGCTT TACAGTACCA TGAAAGGGTA CATCGATAAG
601 ACGGCAAAAT TCAAAAGTTA TGAATTATCA GAAGTACCGT TAAGGGCAGA
651 CATGATCAAA CAGCGCGAAA TCCATCTGGC CATACCCGCA CAACTAATA
701 AGGAGCAAAG ATTGCAGTTG CAACGTGTGG TAGAGTATGG CAAAAGTCAA
751 AACATTACAG TCAAATTAC GGAGATCGAA TAA
```

1263

This corresponds to the amino acid sequence <SEQ ID 2664; ORF 773>:

```
m773.pep
  1  MGLGATTFVG  SGAIGGGLCS  TGIGCAAGGL  IATAGMTGGY  TQASEGSROL
 51  FGTYQSDFGK  KVVLSLGTPI  EYESPLVSDA  KNLAVWGLET  LITRKIGNIA
101  TGVKTSLTPK  TADVORNILS  OSEVGIKWGK  GIEGQGPWE  DYVGKGLSAN
151  ARLPKNFKTF  DYFDRGTGTA  ISAKTLDTQT  TARLSKPEQL  YSTMKYIDK
201  TANFKSYELS  EVPLRADMIK  QREIHLAIPA  QTNKEQRLQL  QRVVEYKGSQ
251  NITVKITEIE  *
```

a773.seq not found yet

a773.pep not found yet

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2665>:

```
g774.seq
  1  ATGAAGACCA  AATTACCGCT  TTTTATCATT  TGGCTGTCTG  TGTCTGCCTC
 51  CTGTGCTTCC  GTTTTACCCG  TTCCGGAGGG  CAGCCGAACC  GAAATGCCGA
101  CACAGGAAAA  TGCTTCAGAC  GGCATTCCCT  ATCCCGTTCC  CACTCTGCAA
151  GACCGTTTGG  ACTATCTGGA  AGGCAAAATC  GTCCGGCTGT  CGAACGAAAT
201  GGAATGTGTA  AACGGGAAAG  TCAAAGCATT  GGAGCATACG  AAAATACACC
251  CTTCGGCGAG  GACATACGTC  CAAAAACTCG  ACGACCGCAA  ATTGAAAGAG
301  CATTACCTCA  ATACCGAAGG  CGGCAGCGCA  TCCGCACATA  CCGTCGAAAC
351  CGCACAAAAC  CTCTACAATC  AGGCACTCAA  ACACTATCAA  AACGGCAGGT
401  TTTCTGCGCG  AGCCGCCCTG  TTGAAGGGGG  CGGACGGCGG  AGACGGCGGG
451  AGCATCGCGC  AACGCAGTAT  GTACCTGTTG  CTGCAAAGCA  GGGCGCGTAT
501  GGGGAACGTG  GAATCTGTCA  TCGAAATCGG  AGGGCGTTAC  GCCAACCGTT
551  TCAAAGACAG  CCCAACCGCG  CCCGAAGTCA  TATTCAAAAT  CGGCGAATGC
601  CAATACAGCG  TTCAGCAAAA  AGACATTGCA  AGGCGCACTT  GCGCGAGCCT
651  GATACAGACC  TATCCCGGCA  GCCCGGCGGC  AAAACGCGCC  GCCCGAGCGC
701  TACGCAACG  ATAG
```

This corresponds to the amino acid sequence <SEQ ID 2666; ORF 774.ng>:

```
g774.pep
  1  MKTKLPLFII  WLSVSASCAS  VLPVPEGSRT  EMPTQENASD  GIPYPVPTLQ
 51  DRLDYLEGKI  VRLSNEVEML  NGKVKALEHT  KIHPSGRITY  QKLDRLKLE
101  HYLNTEGGS  SAHTVETAQN  LYNQALKHYQ  NGRFSAAL  LKADGDCG
151  SIAQRSMYLL  LQSRARMGNC  ESVIEIGGRY  ANRFKDSPTA  PEVIFKIGEC
201  QYRLQKDIA  RATWRSLIQT  YPGSPAARKA  AAARVRKR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2667>:

```
m774.seq
  1  ATGAAGATCA  AATTACCGCT  TTTTATCATT  TGGCTGTCTG  TGTCCGCCTC
 51  CTGTGCTTCC  GTTTTACCCG  TTCCGGCAGG  CAGCCAAACC  GAAATGTGCA
101  CACGGGAAAA  TGCTTCAGAC  GGCATTCCCT  ATCCCGTTCC  GACCTTGCAA
151  GACCGTTTGG  ACTATCTGGA  AGGCAAAATC  GTCCGGCTGT  CGAACGAAAT
201  GGAACCTTAA  AACGGCAAAG  TCAAAGCACT  GGAACACGCA  AAAACACATT
251  CTTCGGCGAG  GGCATACGTC  CAAAAACTCG  ACGACCGCAA  GTTGAAGAG
301  CATTACCTCA  ATACCGAAGG  CGGCAGCGCA  TCCGCACATA  CTGTGCAAAC
351  CGCACAAAAC  CTCTACAATC  AGGCACTCAA  ACACTATAAA  AGCGGCAAGT
401  TTTCTGCGCG  TGCTCCCTG  TTGAAGGGCG  CGGACGGAGG  CGACGGCGGC
451  AGCATCGCGC  AACGCAGTAT  GTACCTGTTG  CTGCAAAGCA  GGGCGCGTAT
501  GGGCAACTGC  GAATCCGTCA  TCGAAATCGG  AGGGCGTTAC  GCCAACCGTT
551  TCAAAGACAG  CCCAACCGCG  CCTGAAGCCA  TGTTCAAAAT  CGGCGAATGC
601  CAATACAGCG  TTCAGCAAAA  AGACATTGCA  AGGCGCACTT  GCGCGAGCCT
651  GATACAGACC  TATCCCGGCA  GCCCGGCGGC  AAAACGCGCC  GCCCGAGCGC
701  TCGCAACG  ATAG
```

This corresponds to the amino acid sequence <SEQ ID 2668; ORF 774>:

```
m774.pep
  1  MKIKLPLFII  WLSVSASCAS  VSPVPAGSQT  EMSTRENASD  GIPYPVPTLQ
 51  DRLDYLEGKI  VRLSNEVETL  NGKVKALEHA  KTHSSGRAYV  QKLDRLKLE
101  HYLNTEGGS  SAHTVETAQN  LYNQALKHYK  SGKFSAAASL  LKADGDCG
151  SIAQRSMYLL  LQSRARMGNC  ESVIEIGGRY  ANRFKDSPTA  PEAMFKIGEC
201  QYRLQKDIA  RATWRSLIQT  YPGSPAARKA  AAARVRKR*
```

Computer analysis of this amino acid sequence gave the following results:

1264

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 774 shows 92.8% identity over a 237 aa overlap with a predicted ORF (ORF 774) from *N. gonorrhoeae*

m774/g774 92.8% identity in 237 aa overlap

	10	20	30	40	50	60
g774.pep	MKTKLPLFIIWLSVSASCASVLPVPEGSRT	EMPTQENASDGIPYPVPTLQDRLCYLEGKI				
m774	MKIKLPLFIIWLSVSASCASVSPV	PAGSQTEMSTRENASDGIPYPVPTLQDRLCYLEGKI				
	10	20	30	40	50	60
	70	80	90	100	110	120
g774.pep	VRLSNEVEMLNGKVKALEHTKIHPSGR	TYVQKLDRLKEHYLNTEGG	SAS	AHTVETAQN		
m774	VRLSNEVEMLNGKVKALEHAKTHSSGR	AYVQKLDRLKEHYLNTEGG	SAS	AHTVETAQN		
	70	80	90	100	110	120
	130	140	150	160	170	180
g774.pep	LYNQALKHYQNGRFSAAAALLKGADGG	DGGSIAQRSMYLLQSRARMGN	CESVIEIGGRY			
m774	LYNQALKHYKSGKFSAAASLLKGADGG	DGGSIAQRSMYLLQSRARMGN	CESVIEIGGRY			
	130	140	150	160	170	180
	190	200	210	220	230	
g774.pep	ANRFKDSPTAPEVIFKIGECQYRLQ	QKDIARATWRS	LIQTYPGSPA	KRAAAVRKR		
m774	ANRFKDSPTAPEAMFKIGECQYRLQ	QKDIARATWRS	LIQTYPGSPA	KRAAAVRKR		
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2669>:

a774.seq

```

1  ATGAAGACCA AATTACCGCT TTTTATCATT TGGCTGTCCG TATCCGCCGC
51  CTGTTCTTCC CCTGTTTCCC GCAATATTCA GGATATGCGG CTCGAACCGC
101 AGGCAGAGGC AGGTAGTTCG GACGCTATTC CCTATCCCGT TCCCACTCTG
151 CAAGACCGTT TGGATTATCT GGAAGGCACA CTCGTCCGCC TGTCGAACGA
201 AGTGGAAACC TTAACGGCA AAGTCAAAGC ACTGGAGCAT GCGAAACAC
251 ACCCTTCCAG CAGGGCATAC GTCCAAAAC TCGACGACCG CAAGTTGAAA
301 GAGCATTACC TCAATACCGA AGGCGGCAGC GCATCCGCAC ATACCGTCGA
351 AACCGCACAA AACCTCTACA ATCAGGCACT CAAACACTAT AAAAGCGGCA
401 GGTTTTCTGC CGCTGCCTCC CTGTTGAAAG GCGCGGACGG AGGCGACGGC
451 GGCAGCATCG CGCAACGCAG TATGTACCTG TTGCTGCAAA GCAGGGCGCG
501 TATGGGCAAC TGCGAATCCG TCATCGAAAT CGGAGGGCGT TACGCCAACC
551 GTTTCAAAGA CAGCCCAACC GCGCCTGAAG CCATGTTCAA AATCGGCGAA
601 TGCCAATACA GGCTTCAGCA AAAAGACATT GCAAGGGCGA CTTGGCGCAG
651 CCTGATACAG ACCTATCCCG GCAGCCCGGC GGCAAAACGC GCGGCCGCAG
701 CCGTGCACAA ACGATAG

```

This corresponds to the amino acid sequence <SEQ ID 2670; ORF 774.a>:

a774.pep

```

1  MKTKLPLFII WLSVSAACSS PVSRIQDMR LEPQAEAGSS DAIPYPVPTL
51  QDRLDYLEGT LVRLSNEVET LNGKVKALEH AKTHPSSRAY VQKLDRLK
101 EHYLNTEGGS ASHTVETAQ NLYNQALKHY KSGRFSAAAS LLKGADGGDG
151 GSIAQRSMYL LLQSRARMGN CESVIEIGGR YANRFKDSPT APEAMFKIGE
201 CQYRLQKDI ARATWRS LIQTYPGSPA KR AAAAVRKR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 774 shows 89.5% identity over a 238 aa overlap with a predicted ORF (ORF 774) from *N. meningitidis*

m774/a774 89.5% identity in 238 aa overlap

	10	20	30	40	50	60
a774.pep	MKTKLPLFIIWLSVSAACSSPVSRIQDMR	LEPQAEAGSSDAIPYPVPTLQDRLDYLEGT				
m774	MKIKLPLFIIWLSVSASCAS-VSPV	PAGSQTEMSTRENASDGIPYPVPTLQDRLDYLEGK				
	10	20	30	40	50	

1265

```

      70      80      90      100     110     120
a774.pep  LVRLSNEVETLNGKVKALEHAKTHPSSRAYVQKLDRLKEHYLNTGGSSASAHTVETAQ
          :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m774      IVRLSNEVETLNGKVKALEHAKTHSSGRAYVQKLDRLKEHYLNTGGSSASAHTVETAQ
          60      70      80      90      100     110

      130     140     150     160     170     180
a774.pep  NLYNQALKHYKSGRFSAAAALLKGADGGDGGSIQORSMYLLQSRARMGNCSVIEIGGR
          :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m774      NLYNQALKHYKSGRFSAAAALLKGADGGDGGSIQORSMYLLQSRARMGNCSVIEIGGR
          120     130     140     150     160     170

      190     200     210     220     230     239
a774.pep  YANRFKDSPTAPEAMFKIGECQYRLQOKDIARATWRSLIQTYPGSPAARAAAARVRKRX
          :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m774      YANRFKDSPTAPEAMFKIGECQYRLQOKDIARATWRSLIQTYPGSPAARAAAARVRKRX
          180     190     200     210     220     230

```

g790.seq not found yet

g790.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2671>:

```

m790.seq
1  ATGGCAAGAA  GGTCAAAAAC  ATTTGAAGAA  GCTGCTGCTG  AGGTTGAGGA
51  ACGTTTCGGT  CATCGTGGCA  TTAAGTTGGT  CGAGTTTGAG  GGTACAGCCA
101 AGCCGTGTGT  AATCAACTGC  CCTAAACATG  GAAACCAAAC  CTGTTGAGG
151 TACTCCAATA  TGTTCATAGG  AAGTAGCTGG  GGTGCCCCCT  CTTGTGGTAA
201 TGAGCAAGCT  GCAAAGCCG  GTATAGCGAC  CCTAGGAAG  AATCACATAG
251 CGTTAGAAAT  GCTGAAACAG  GCTGTAACAG  GTATGACCAA  GCAAGAGCGC
301 ATCAGCAGCG  AAGCCTACAA  TGAGATGACC  AATCCGTGG  CAGGTTCAAA
351 CAGCATAGTC  CTTAACGATG  TCCAAGGCGA  TACGACCATC  AACAACCATC
401 ATACGCATAC  GCACAACCAC  AGCGATGCCG  ATGGCAAAGC  ACTGTCGATG
451 AGGCTCACAC  CCCGTCCTTT  GTTGTACAG  CGTCAGGCGG  CGGCTTTCGC
501 CCGTACAGGC  AAACCTACGG  GCAGTTTCGA  CCTGTTTGCT  TCGGTGGTCG
551 CCCCTTCGCA  GTACACGTTT  GCCGTTGCCA  TGCCCGACAC  GTCCATGTCG
601 CCGGTTATCG  AAAAGGGAGA  CTTGCTGGTG  GTCGAGCCGC  GTATGTGCCC
651 TCGCGACGAA  GACATCGCGC  TGATTGAACT  GTCCGACAAG  CGGCTGGTCG
701 TCGCGACCT  TGTATCGAT  ATTGCGGGCA  GGATGCTGAT  TTATCAGACG
751 AGGAGGCGGT  CTGAAGCCTT  TGACCTGCC  GAAGGCAGCA  CGATTTTAGG
801 TGTGGTGTG  GAGTCAAAA  ACGGTTTATG  TCCGCCGCAC  AGGCAAGAAG
851 GCGTGTGAT  TCGGATTACC  GCCCTGATG  TGTGGACGGT  TGGTATGATT
901 TCCGCTTCCA  AAACGTCGTG  TACGCGCCG  ACCGAGCCG  GGAATCAGC
951 CGTATGCTT  CTTGATTTT  GGCAGGCTAC  GCGTGGGATA  CCGAAAACCC
1001 GTTCGTGGCG  AAATCCGAAC  AACGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2672; ORF 790>:

```

m790.pep
1  MARRSKTFEE  AAEEVEERFG  HRGIKLVEFE  GTAKPCVINC  PKHGNQTCSS
51  YSNMFIGSSW  GPCSCGNEQA  AKAGIATLRK  NHIALEMLKQ  AVTGMTKQER
101 ITTQAYNEMT  KSVAGSNSIV  LNDVQGDFTI  NNHHTHTHNH  SDADGKALSM
151 RLIPRPLSLD  RQAAAFARTG  KLTGSFDLFA  SVVAPSQYTF  AVAMPDTSMS
201 EVIEKGDLLV  VEPRMCPADE  DIALIELSDK  RLVAHLVID  IAGRMILYQT
251 GRFSEAFDLP  EGSTILGVVL  ESKNGLCPPH  RQEGVLIRIT  APDVWTVGMI
301 SASKTSCTRP  TAARKSAVCF  LRFQATRGI  PKTRSWRNP  NA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2673>:

```

a790.seq
1  ATGGCAAGAA  GGTCAAAAAC  ATTTGAAGAA  GCTGCTGCTG  AGGTTGAGGA
51  ACGTTTCGGT  CATCGTGGCA  TTAAGTTGGT  CGAGTTTGAG  GGTACAGCCA
101 AGCCGTGTGT  AATCAACTGC  CCTAAACATG  GAAACCAAAC  CTGTTGAGG
151 TACTCCAATA  TGTTCATAGG  AAGTAGCTGG  GGTGCCCCCT  CTTGTGGTAA
201 TGAGCAAGCT  GCAAAGCCG  GTATAGCGAC  CCTAGGAAG  AATCACATAG
251 CGTTAGAAAT  GCTGAAACAG  GCTGTAACAG  GTATGACCAA  GCAAGAGCGC
301 ATCAGCAGCG  AAGCCTACAA  TGAGATGACC  AATCCGTGG  CAGGTTCAAA
351 CAGCATAATC  CTTAACGATG  TCCAAGGCGA  TACGACCATC  AACAACCATC
401 ATACGCATAC  GCACAACCAC  AGCGATGCCG  ATGGCAAAGC  ACTGTCGATG
451 AGGCTCACAC  CCCGTCCTTT  GTTGTACAG  CGTCAGGCGG  CGGCTTTCGC
501 CCGTACAGGC  AAACCTACGG  GCAGTTTCGA  CCTGTTTGCT  TCGGTGGTCG
551 CCCCTTCACA  ATATACGTTT  GCCGTTGCCA  TGCCCGACAC  GTCCATGTCG
601 CCGGTTATCG  AAAAGGGAGA  TTTGCTGGTG  GTCGAGCCGC  GTATGCGCCC
651 TCGCGACGAA  GACATCGTAC  TGATTGAACT  GTCCGACAAG  CGGCTGGTCG
701 TCGCGACCT  TGTATCGAT  ATTGCGGGCA  GGATGCTGAT  TTATCAGACG

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751 GGCAGGCCGT CTGAAGCCCT CGACCTGCCC GAAGGCAGCG TGATTTTAGG
801 TGTGGTGCTG GAGTCAAAA ACGGTTTATG TCCGCCGCAC AGGCAAGAAG
851 GCGTGTTGAT TCGGATTACC GCCCCTGATG TGTGGACGGT TGGTACGATT
901 TCCGCTTCCA AAACGTCGTG TACGCGCCCG ACCGCAGCCC GGAAATCAGC
951 CGTATGCTTT CTTGATTTT GGCAGGCTAC GCGTGGGATA CCGAAAACCC
1001 GTTCGTGGCG AAATCCGAAC AACGCCTGT

```

This corresponds to the amino acid sequence <SEQ ID 2674; ORF 790.a>:

```

a790.pep
1  MARRSKTFEE AAEEVEERFG HRGIKLVEFE GTAKPCVINC PKHGNQTCRS
51  YSNMFIGSSW GCPSCGNEQA AKAGIATLRK NHIALEMLKQ AVTGMTKQER
101 ITTQAYNEMT KSVAGSNSII LNDVQGDTTI NHHHTHTNH SDADGKALSM
151 RLTPRPLLSD RQAAAFARTG KLTGSFDLFA SVVAPSQYTF AVAMPDTSMS
201 PVIEKGDLLV VEPRMRPADE DIVLIELSDK RLVVAHLVID IAGRMLIYOT
251 GRPSEALDLP EGSVILGVVL ESKNGLCPPH RQEGVLIRIT APDVNTVGTI
301 SASKTSCTRP TAARKSAVCF LRFWQATRGI PKTRSWRNPN NAC

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 790 shows 98.2% identity over a 342 aa overlap with a predicted ORF (ORF 790) from *N. meningitidis*

a790/m790 98.2% identity in 342 aa overlap

	10	20	30	40	50	60
a790.pep	MARRSKTFEEAAAEVEERFGHRGIKLVEFE GTAKPCVINC PKHGNQTCRSRYSNMFIGSSW					
m790	MARRSKTFEEAAAEVEERFGHRGIKLVEFE GTAKPCVINC PKHGNQTCRSRYSNMFIGSSW					
	10	20	30	40	50	60
	70	80	90	100	110	120
a790.pep	GCPSCGNEQA AKAGIATLRKNHIALEMLKQAVTGMTKQERITTQAYNEMTKSVAGSNSII					
m790	GCPSCGNEQA AKAGIATLRKNHIALEMLKQAVTGMTKQERITTQAYNEMTKSVAGSNSIV					
	70	80	90	100	110	120
	130	140	150	160	170	180
a790.pep	LNDVQGDTTINHHHTHTNHS DADGKALSMRLTPRPLLSDRQAAAFARTGKLTGSFDLFA					
m790	LNDVQGDTTINHHHTHTNHS DADGKALSMRLTPRPLLSDRQAAAFARTGKLTGSFDLFA					
	130	140	150	160	170	180
	190	200	210	220	230	240
a790.pep	SVVAPSQYTF AVAMPDTSMS PVIEKGDLLVVEPRMRPADE DIVLIELSDKRLVVAHLVID					
m790	SVVAPSQYTF AVAMPDTSMS PVIEKGDLLVVEPRMCPAEDIALIELSDKRLVVAHLVID					
	190	200	210	220	230	240
	250	260	270	280	290	300
a790.pep	IAGRMLIYOTGRPSEALDLPESVILGVVLESKNGLCPPHRQEGVLIRITAPDVNTVGTI					
m790	IAGRMLIYOTGRPSEAFDLPEGSTILGVVLESKNGLCPPHRQEGVLIRITAPDVNTVGM					
	250	260	270	280	290	300
	310	320	330	340		
a790.pep	SASKTSCTRP TAARKSAVCF LRFWQATRGI PKTRSWRNPN NAC					
m790	SASKTSCTRP TAARKSAVCF LRFWQATRGI PKTRSWRNPN NAX					
	310	320	330	340		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2675>:

```

g791.seq
1  ATGGTAAATT ATTATTCAGC TATCATTTAA AAGATTTTAA CTACTTGTTT
51  TGGTTTGTTC TTTGGTTTTC GTGTATTTGG AGTGGGTCTG GTTGCCATTG
101 CTATTTTGGT AACGTATCCG AAAGTCCCGT CTTTGGATTC TTTGCAGCAT
151 TACCAGCCIA AAATGCCGTT GACTATTTAT TCGGCGGATG GAGAAGTCAT
201 CCGTATGTAT GGGGAGCAGC GCGCGAATT TACAATAATC GGCATTTC
251 CCGAGGTGTT GCGGAATCGG GTTATTGCCG CCGAGGATAA ACGCTTTTAC
301 CCGCATGGG GGGTGGATGT TTGGGGTGT CCGCGGCTG CCGTCGCCAA
351 TGTCGTGTCC GGCAGCGTGC AGTCGGGTGC GAGTACGATT ACACAGCAGG

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```

401 TGGCGAAAAA TTTTATTG AGCAGTGAAA AACGTTTAC ACGCAAATTC
451 AATGAGGTGT TGCTTGCCCTA TAAAATCGAG CAGTCTTTAA GCAAAGACAA
501 AATCCTTGAG TTGTATTTCA ATCAGATTTA CCTCGGTGAG CGCGCCTATG
551 GTTTTGCATC TGCCGCGCAA ATCTATTTCA ATAAGAAATG CCGAGATTG
601 ACTTTGGCGG AAGCCGCCAT GCTTGCGGGA CTGCCAAGG CTCGCTCTGC
651 CTATAATCCG ATTGTTAAAT CGAGCGGTGC CAAGTTGCGC CAGAAGTATA
701 TTTTGAACAA TATGCTCGAG GAGAAGATGA TTACCGTGCA ACAGCCGAT
751 CAGGCATTGA ATGAGGAACT GCATTATGAG CGGTTTGTTC GGAATAATCGA
801 TCAGAGTGCT TTATATGTGG CGGAAATGGT GCGTCGGGAA CTGTATGAGA
851 AATATGGTGA AGATGCCTAT ACGCAGGGTT TTAAGGTTTA TACCACGGTC
901 CGCACCGATC ATCAGAAAGC GGCACCCGAG GCATTGCGCA AGGCTCTACG
951 GAATTTCCAT CGCGGCAGCA GCTACCGCGG TGCGGAAAAC TATATCGATT
1001 TGAGTAAGAG TGAAGATGTC GAGGAGACTG TCAGCCAGTA TCTGTCCGGA
1051 CTCTATACCG TCGATAAAAT GGTTCGCCGC GTTGTGTTGG ATGTTACTAA
1101 AAAGAAAAAT GTCGTCATAC AGCTGCCCGG CGGCAGGCGG GTTGCCTTG
1151 ACAGCGCGCG CTGCGGTTTT GCGGCCCGAG CGGTCGATAA TGAGAAAAATG
1201 GGGGAGGACC GTATCCGAG GGGCGCGGTC ATCCGTGTCA AAAACAACGG
1251 CGGGCGTTGG GCGGTGGTTC AAGAGCCGTT GCTGCAGGGG GCTTGTGTTT
1301 CGCTGGATGC AAAAACCGGA GCTGTGCGCG CGCTGGTCGG CGGTTATGAT
1351 TTTCACAGCA AAACATTCAA TCGTGCCGTT CAGGCAATGC GGCAGCCGGG
1401 TTCGACCTTT AAGCCGTTTG TCTATTCGGC GGCATTATCT AAGGGATGA
1451 CCGCGTCCAC AGTGGTTAAT GATGCGCCGA TTTCCCTGCC GGGGAAAGGG
1501 CCGAACGGTT CGGTTTGAC ACCTAAAAAT TCAGACGGCA GATATTCCGG
1551 CTACATTACT TTGAGACAGG CTCTGACGGC TTCCAAGAAT ATGCTTTCCA
1601 TCCGTATTTT GATGTCATC GGTGTCGGTT ACGCGCAACA GTATATCCGG
1651 CGTTTCGGCT TCAGGCGGTC CGAGCTGCGG GCAAGCCTGT CTATGGCTTT
1701 AGGTACGGGC GAGACGACGC CGTTGAAAGT GCGGAGGCA TATAGTGTAT
1751 TTGCGAACGG CGGATATAGG GTTCTTCGCG ACGTGATCGA TAAGATTAT
1801 CACAGACAGC GCAGCTTCCG CCGCCAAATG CAACCTTTGG TGGCAGGGCA
1851 AAATGCGCCT CAGGCAATCG ATCCGCGCAA TGCCATATAT ATGTATAAGA
1901 TTAATGCAGA TGTGGTCCGT GTCGGTACGG CAAGGGGGGC AGTGCCTTG
1951 GAGAGAACGG ATATTGCCGG TAAACCGGTT ACGACCAACG ACAATAAGA
2001 TGCGTGGTTT GTCGGTTTTA ACCCTGATGT GGTACTGACC GTATATATCG
2051 GCTTCGACAA ACCTAAGAGT ATGGGCGGTG CCGGCTACGG CGGTACGATT
2101 CCGGTGCCGG TTTGGGTGGA CTATAIGCGT TTTGCGTGA AAGGAAAGCA
2151 GGGCAAAGGG ATGAAATGTC CTGAAGGTGT GGTGAGCAGC AATGGCGAAT
2201 ACTATATGAA GGAACGTATG GTAACCGATC CGGGCTTGAT GCTGGACAAC
2251 AGCGGTATTG CGCCGCAACC TTCCGACGG GCAAAAGAAG ATGATGAAGC
2301 GGCAGTAGAA AACGAACAGC AGGGAAGGTC TGACGAAACG CGTCAGGACG
2351 TACAGGAAAC GCCGGTGCTT CCGAGCAATA CGGATTCCAA ACAGCAGCAG
2401 TTGATTCCCC TGTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2676; ORF 791.ng>:

```

g791.pep
1 MVNYSAMIK KILTTCEGLF FGFCVFGVGL VAIAILVTYP KLPSLDSLQH
51 YQPMPLTIY SADGEVIGMY GEQRREFTKI GDFPEVLRNA VIAAEDKRFY
101 RHWGVVWGV ARAAVGNVVS GSVQSGASTI TQVAKNFYL SSEKTETRRF
151 NEVLLAYKIE QSLSKDKILE LYFNQIYLQ RAYGFASAAQ IYFNKNVRDL
201 TLAEAAMLAG LKAPSAYNP IVNPERAKLR OKYILNMLE EKMITVQORD
251 QALNEELHYE RFVRKIDQSA LYVAEMVRRE LYEKYGEDAY TQGFVYTTV
301 RTDHQKAATE ALRKALRNF D RGSSYRGAEN YIDLKSESDV EETVSQYLSG
351 LYTVDKMVA VVLDVTKKN VVIQLPGGRR VALDRRALGF AARAVDNEKM
401 GEDRIRRGAV IRVKNNGRW AVVQEPLLQG ALVSLDAKTC AVRALVGGYD
451 FHSKTFNRAV QAMRQPGSTF KPFVYSAALS KGMTASTVVN DAPISLPGKG
501 PNGSVWTFPN SDGRYSYIT LRQALTASKN MVSIRILMSI GVGYAQQYIR
551 RFGFRPSELP ASLSMALGTG ETPLKVAEA YSVFANGGYR VSSHVIDKIY
601 DRDRLRAQM QPLVAGQNAQ QAIDPRNAYI MYKIMQDVVR VGTARGAAAL
651 GRIDIAKGTG TTNDNKDAWF VGFPDVTVA VYIGFDKPKS MGRAGYGGTI
701 AVPVVVDYMR FALKGKQKKG MKMPEGVVSS NGEYYMKERM VTDPLMLDN
751 SGIAPOPSRR AKEDDEAAVE NEQQGRSDET RQDVQETPVL PSNTDSKQQQ
801 LDSL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2677>:

```

m791.seq
1 ATGGTAAATT ATTATTCAGC TATGATTAAA AAGATTTTAA CGACTTGTTT
51 TGGTTTGGTT TTTGGGTTTT GTGTATTTGG AGTGGGTTTG GTTGCCATTG
101 CTATTTTGGT AACGTATCCG AAAGTCCGCT CTTTGGATTC TTGTCAGCAT
151 TACCAGCTTA AATGCCGTT GACTATTAT TCGCGGATG GGAAGTCAT
201 CGGTATGTAT GGGGAGCAGC GCGCGGAATT TACAAAAATC GCGGATTTC
251 CAGAGGTGTT GCGGAATGCG GTTATCGCCG CCGAGGATAA ACGCTTTTAC
301 CGGCAATTGG GGTGGATGT TTTGGGTGTT GCCCGCGCTG CCGTCGGCAA
351 TGTCGTGTCC GGCAGCGTGC AGTCGGGTGC GAGTACGATT ACGCAGCAGG
401 TGGCGAAAAA TTTTATTG AGCAGTGAAA AACGTTTAC ACGCAAATTC

```

m791.pcp

g791/m791 97.3% identity in 805 aa overlap

	10	20	30	40	50	60
g791.pep	MVNYYSAMIKKILTTCTCFLGFFGFCVFGVGLVAIAILVTYPKLP	SLD	SLD	SLD	SLD	SLD
m791	MVNYYSAMIKKILTTCTCFLGFFGFCVFGVGLVAIAILVTYPKLP	SLD	SLD	SLD	SLD	SLD
	10	20	30	40	50	60
	70	80	90	100	110	120
g791.pep	SADGEVIGMYGEQRREFTKIGDFPEVLRNAVIAAEDKRFYRH	WG	VDV	WG	VARAAV	GNVVVS
m791	SADGEVIGMYGEQRREFTKIGDFPEVLRNAVIAAEDKRFYRH	WG	VDV	WG	VARAAV	GNVVVS
	70	80	90	100	110	120

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	130	140	150	160	170	180
g791.pep	GSVQSGASTITQQVAKNFYLSSEKTFTRKFNEVLLAYKIEQSLSKDKILELYFNQIYLGQ					
m791	GSVQSGASTITQQVAKNFYLSSEKTFTRKFNEVLLAYKIEQSLSKDKILELYFNQIYLGQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
g791.pep	RAYGFASAAQIYFNKNVRDLTLAEAAAGLGPAPSAYNPIVNERAKLRQKYILNNMLE					
m791	RAYGFASAAQIYFNKNVRDLTLAEAAAGLGPAPSAYNPIVNERAKLRQKYILNNMLE					
	190	200	210	220	230	240
	250	260	270	280	290	300
g791.pep	EKMITVQQRDQALNEELHYERFVRKIDQSALYVAEMVRRELYEKYGEDAYTQGFVYTTV					
m791	EKMITVQQRDQALNEELHYERFVRKIDQSALYVAEMVRRELYEKYGEDAYTQGFVYTTV					
	250	260	270	280	290	300
	310	320	330	340	350	360
g791.pep	RTDHQKAATEALRKALRNFDGSSSYRGAENYIDLKSEDEETVSQYLSGLYTVDKMVP					
m791	RTDHQKAATEALRKALRNFDGSSSYRGAENYIDLKSEDEETVSQYLSGLYTVDKMVP					
	310	320	330	340	350	360
	370	380	390	400	410	420
g791.pep	VVLDTVTKKKNVVIQLPGGRRVALDRRALGFAARAVDNEKMGEDRIIRGAVIRVKNNGGRW					
m791	VVLDTVTKKKNVVIQLPGGRRVALDRRALGFAARAVDNEKMGEDRIIRGAVIRVKNNGGRW					
	370	380	390	400	410	420
	430	440	450	460	470	480
g791.pep	AVVQEPQLQGALVSLDAKTGAVRALVGGYDFHSKTFNRAVQAMRQPGSTFKPFVYSAALS					
m791	AVVQEPQLQGALVSLDAKTGAVRALVGGYDFHSKTFNRAVQAMRQPGSTFKPFVYSAALS					
	430	440	450	460	470	480
	490	500	510	520	530	540
g791.pep	KGMTASTVVNDAPISLPKGPNGSVWTPKNSDGRYSGYITLRQALTASKNMVSIRILMSI					
m791	KGMTASTVVNDAPISLPKGPNGSVWTPKNSDGRYSGYITLRQALTASKNMVSIRILMSI					
	490	500	510	520	530	540
	550	560	570	580	590	600
g791.pep	GVGYAQQYIRRFGRFSELPAFLSMALGTGETTPLKVAEAYSVFANGGYRVSSHVIDKIY					
m791	GVGYAQQYIRRFGRFSELPAFLSMALGTGETTPLKVAEAYSVFANGGYRVSSHVIDKIY					
	550	560	570	580	590	600
	610	620	630	640	650	660
g791.pep	DRDGRRLRAQMPLVAGQNAPOAIDERNAYIMYKIMQDVVRVGTARGAAALGRDIAKGTG					
m791	DRDGRRLRAQMPLVAGQNAPOAIDERNAYIMYKIMQDVVRVGTARGAAALGRDIAKGTG					
	610	620	630	640	650	660
	670	680	690	700	710	720
g791.pep	TTNDNKDAWVGFNPDPVTVAVYIGFDKPKSMGRAGYGGTIAVPVWVDYMRFALKGKGK					
m791	TTNDNKDAWVGFNPDPVTVAVYIGFDKPKSMGRAGYGGTIAVPVWVDYMRFALKGKGK					
	670	680	690	700	710	720
	730	740	750	760	770	780
g791.pep	MKMPEGVSSNGEYMKERMVTDPLGLDNGSIAPOPSRRRAKEDDGAEEGGRQAADDEV					
m791	MKMPEGVSSNGEYMKERMVTDPLGLDNGSIAPOPSRRRAKEDDGAEEGGRQAADDEV					
	730	740	750	760	770	780
	790	800				
g791.pep	RQDVQETPVLPSNTGSKQQQLDSLFX					
m791	RQDMQETPVLPSNTGSKQQQLDSLFX					
	790	800				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2679>:

1270

a791.seq

```
1 ATGGTAAATT ATTATTCAGC TATGATTAAA AAGATTTTAA CGACTTGTTC
51 TGGTTTGGTT TTTGGGTTTT GTGTATTTGG AGTGGGTTTG GTTGCCATTG
101 CTATTTTGGT AACGTATCCG AAACGCGCGT CTTTGGATTC TTTGCAGCAT
151 TACCAGCCTA AAATGCCGTT GACTATTTAT TCGGCGGATG GGAAGTCAT
201 CGGTATGTAT GGGGAGCAGC GCGCGCAATT TACAAAAATC GGCATTTC
251 CAGAGGTGTT GCGGAATGCG GTTATCGCCG CCGAGGATAA ACGCTTTTAC
301 CCGCATTTGG GGGTGGATGT TTGGGGTGTG GCGCGCGCTG CCGTCGGCAA
351 TGTCTGTGCC GGCAGCGTGC AGTCGGGTGC GAGTACGATT ACGCAGCAGG
401 TGGCGAAAAA TTTTATTG AGCAGTGA AAACGTTTAC ACGCAAATTC
451 AATGAGGTGT TGCTTGCCCTA TAAAATCGAG CAGTCTTTAA GCAAAGACAA
501 AATCCTCGAG TTGTATTTCA ATCAGATTTA CCTCGGTGAG GCGCCTATG
551 GTTTTGCATC TGCCGCGCAA ATCTATTTCA ATAAGAATGT CCGAGATTTC
601 ACTTTGGCCG AAGCCGCCAT GCTTGCAGGA CTGCCCAAGG CTCCGCTGTC
651 CTATATATCCG ATTGTTAATC CAGAACGTGC CAAGTTGCGC CAGAGGTATA
701 TTTTGAACAA TATGCTCGAG GAGAAATGA TTACCGTGCA ACAGCGCGAT
751 CAGCGGTTGA ATGAGGAACT GCATTACGAG CGGTTTGTTC GGAAATCGA
801 TCAGAGTGCT TTATATGTGG CCGAAATGGT GCGTCAGGAA CTGTATGAGA
851 AATACGGTGA AGATGCCAT ATCAGAGGTT TTAAGGTTTA TACCACGGTC
901 CCGCGCCGAT ATCAGAAAGT GGCACCGAG GCATTGCGCA AGGCTCTACG
951 GAATTTCCGAT CGCGGCAGCA GCTACCGCGG TCGGGAAC TATATCGATT
1001 TGAGTAAGAG TGAAGATGTC GAGGAGACTG TCAGCCAGTA TCTGTCGCGA
1051 CTCTATACCG TCGATAAAAT GGTTCGCCGC GTTGTGTGG ATGTGACTAA
1101 AAAGAAAAAT GTCGTCATAC AGCTGCCCGG CCGCAGCGCG GTTACGCTTG
1151 ACAGGCGCGC CTGGGGTTTT GCGGCCCGCG CGGTCAATAA TGA AAAAATG
1201 GGGGAGGACC GTATCCGAG GGGCGCGGTC ATCCGTGTCA AAAACAACGG
1251 CCGGCGTTGG GCGGTGCTTC AAGAGCCGTT GCTGCAGGGG GCTTTGGTTT
1301 CGCTGGATGC AAAAACCGGA GCTGTGCGCG CGCTGGTCGG CGGTTATGAT
1351 TTTACACAGA AAACATTCAA TCGTGCCGTT CAGGCAATG GGCAGCCGGG
1401 TTCGACCTTT AAGCCGTTTG TCTATTCGCG GGCATTATCT AAGGGGATGA
1451 CCGCGTCCAC AGTGGTTAAT GATGCGCCGA TTTCCCTGCC GGGGAAAGGG
1501 CCGAACGGTT CGGTTTGGAC ACCTAAAAAT TCAGACGGCA GATATTCGGG
1551 CTACATTACT TTGAGACAGG CTCGTACGCG TTCCAAGAAT ATGGTTTCCA
1601 TCCGTATTTT GATGTCTATC GGTGTCGGTT ACGCGCAACA GTATATCCGG
1651 CGITTCGGCT TCAGGTGCTC CGAGCTGCCG GCAAGCCTGT CTATGGCTTT
1701 AGETACGGGC GAGACAACGC CGTTGAAGT GCGGAGGCA TATAGCGTAT
1751 TTGCGAACGG CGGATATAGG GTTCTTCGCG ACGTAATCGA TAAGATTAT
1801 GACAGAGAGC GCAGGTTGCG CGCCCAATG CAACCTTGG TGGCGGGCA
1851 AAATGCGCCT CAGGCAATCG ATCCGCGCAA TGCTATATT ATGTATAAGA
1901 TTATGCAGGA TGTGGTCCGT GTTGGTACGG CAAGGGGGGC AGCTGCGTTG
1951 GGAAGAACGG ATATTGCCGG TAAACGGGT ACGACCAATG ACAATAAGGA
2001 TGCGTGGTTT GTCGGTTTTA ACCCTGATGT GGTACTGCC GTATATATCG
2051 GCTTCGACAA ACCTAAGAGT ATGGGGCGTG TCGGCTACGG CCGTACGATT
2101 GCGGTGCCGG TTTGGGTGGA CTATATGCGT TTTGCGTTGA AAGGAAAGCA
2151 GGGCAAGGGG ATGAAAAATG CTGAAGGTGT GGTACAGCAG AATGGCGAAT
2201 ACTATATGAA GGAACGTATG GTAACCGATC CCGGCTTGAC GCTGGACAAC
2251 AGCGGTATTG CGCCGCAACC TTCCCGACGG GCAAAAGAAG ATGACGGGGG
2301 CGCGGCAGAA GCGGACGGC AGCGGCGGGA TGACGAGTGC CGCCAAGATA
2351 TGCAAGAAAC GCCGGTGCTT CCGAGTAATA CTGGTTCCAA ACAGCAGCAG
2401 TTGATTCTC TGTTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 2680; ORF 791.a>:

a791.pep

```
1 MVNYSAMIK KILTTFCGLV FGFCVFGVGL VAIALVITYP KLPSLDSLQH
51 YQPKMPLTIY SADGEVIGMY GEORREFTKI GDFFEVLRNA VIAAEDKRFY
101 RHWGVDVWGV ARAAVGNVVS GSVQSGASTI TQQVAKNFYL SSEKTFTRKF
151 NEVLLAYKIE QSLSKDKILE LYFNQIYLGQ RAYGFASAAQ IYFNKNVRDL
201 TLAEAAMLAG LKAPSAYNP IVNPERAKLR QKYILNNMLE EKMITVQQRD
251 QALNEELHYE RFVRKIDQSA LYVAEMVRQE LYEKYGEDAY TQGFVKYTTV
301 RADHQKVATE ALRKALRNFD RGSSYRGAEN YIDLKSESDV EETVSQYLSG
351 LYTVDKMPVA VVLDVTKKN VVIQLPGGRR VILDRRALGF ARAAVNNEKM
401 GEDRIRRAV IRVKNNGRW AVVQEPLLOQ ALVSLDAKTG AVRALVGGYD
451 FHSKTFNRAV QAMRQPGSTF KPFVYSAAALS KGMTASTVVN DAPISLPGKG
501 PNGSVWTFKN SDGRYSYIT LRQALTASKN MVSIRILMSI GVGYAQYIR
551 RFGRSSELP ASLSMALGTG ETTPLKVAEA YSVFANGGYR VSSHVIDKIY
601 DRDGLRAQM QPLVAGQNAQ QAIDPRNAYI MYKIMQDVVR VGTARGAAAL
651 GRTDIAGKTG TTNDNKDAWF VGFPDVTVA VYIGFDKPKS MGRVGYGGTI
701 AVPVWVDYMR FALKGQKQKG MKMPEGVVSS NGEYYMKERM VTDPLGLTDN
751 SGIAPQPSRR AKEDDGGAAE GGRQAADDEV RQDMQETPVL PSNTGSKQQQ
801 LDSLIF*
```

a791/m791 99.9% identity in 805 aa overlap

10 20 30 40 50 60

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a791.pep	MVNYYSAMIKKILTTTCFGLVFGFCVFGVGLVAIAILVTPKLPSLDSLQHYQPKMPLTIY
m791	MVNYYSAMIKKILTTTCFGLVFGFCVFGVGLVAIAILVTPKLPSLDSLQHYQPKMPLTIY
	10 20 30 40 50 60
a791.pep	70 80 90 100 110 120
m791	70 80 90 100 110 120
a791.pep	130 140 150 160 170 180
m791	130 140 150 160 170 180
a791.pep	190 200 210 220 230 240
m791	190 200 210 220 230 240
a791.pep	250 260 270 280 290 300
m791	250 260 270 280 290 300
a791.pep	310 320 330 340 350 360
m791	310 320 330 340 350 360
a791.pep	370 380 390 400 410 420
m791	370 380 390 400 410 420
a791.pep	430 440 450 460 470 480
m791	430 440 450 460 470 480
a791.pep	490 500 510 520 530 540
m791	490 500 510 520 530 540
a791.pep	550 560 570 580 590 600
m791	550 560 570 580 590 600
a791.pep	610 620 630 640 650 660
m791	610 620 630 640 650 660
a791.pep	670 680 690 700 710 720
m791	670 680 690 700 710 720
a791.pep	730 740 750 760 770 780
m791	730 740 750 760 770 780

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```

              730      740      750      760      770      780
              790      800
a791.pep      RQDMQETPVLPSNTGSKQQQLDSLFX
              |||||
m791          RQDMQETPVLPSNTGSKQQQLDSLFX
              790      800
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2681>:

```
g792.seq
1  ATGTTCCGCA TCGTCAAATG GCTGATTGCC CTGCCCGTCG GCATCTTTAT
51  CTTTTTCAAT GCCTATGTGT ACGGCAACAT CATCACCTAC CGCGCCGTCG
101 CGCCCCATCG GACTGCCTTT ATGTCGATGC GGATGAAGCA GTTTGAACAA
151 GAAGGTCGCG ATGTCGCACT GGATTACCGC TGGGTGCCCT ACAACCGCAT
201 TTCCACCAAC CTGAAAAAAG CCCTGATTGC TTCCGAAGAT GTCGTTTGT
251 CCggacacgg gggcttcGat GGGGACGGCa tTCAAAACGC CATCAGCGCG
301 AACCGGAACA GCGGCGAAGT GAAGGCGGGC GGATCGACCA TCAGCCAGCA
351 GCTTGCCAAA AACCTCTTCC TCAACGAAAG CCGCAACTAT CTGCGCAAAG
401 GGAAGAGAGC GCCATTACG GCAATGATGG AAGCTGTTAC CGACAAAAC
451 AGGATTTTICG AACTGTATTT AAACCTCAATC GAATGGCACT ACGGCgtTTT
501 CGGCGCGGAA GCTGCGTCCC GgtatTttTA TAAAAAACCG GCcgcaGACC
551 TGACCAACA GCAggcgggcG aaactgacgg tactcgtccc cgccccgttt
601 tactactctg accatccaaa aagcaaacgg ctgcgcaaca aaaccaatal
651 cgtgctcaga cgcattgggtt cggcaaatTA ccccaagcg aaacggactg
701 attgttcag atatggaaat gccgcctgaa ctgggggttcg aacggcatat
751 gttttctggg acttataa
```

This corresponds to the amino acid sequence <SEQ ID 2682; ORF 792.ng>:

```
g792.pep
1  MFRIVKWLIA LPVGIFIFFN AYVYGNIIITY RAVAPHRTAF MSMRMKQFEQ
51  EGRDVALDYR WVPYNRISTN LKKALIASD VRFAGHGGFD GDGIQNAIRR
101 NRNSGEVKAG GSTISQQLAK NLFLNESRNY LKKGEEAAIT AMMEAVTDKN
151 RIFELYLNSI EWHYGVFGAE AASRYFYKKP AADLTQQA KLTVLVPAPF
201 YYSDFPKSKR LRNKTNIVLR RMGSANYPKA KRTDCSRYGN AA*TGVRTAY
251 VFWDL*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2683>:

```
m792.seq
1  ATGTTCCGCA TCATCAAATG GCTGATTGCC CTGCCCGTCG GCATCTTTAT
51  CTTTTTCAAT GCCTATGTGT ACGGCAACAT CATTACCTAC CGCGCCGTCG
101 CGCCCCATCG GACTGCCTTT ATGTCGATGC GGATGAAGCA GTTTGAACAG
151 GAAGGTCGCG ATGTCGCACT GGATTACCGC TGGATGCCCT ACAACGCAAT
201 TTCCACCAAC CTGAAAAAAG CCCTGATTGC TTCCGAAGAT GCCGTTTCG
251 CGGGGCACGG CGGCTTCGAT TGGGGCGGCA TTCAAAACGC CATCAGGCGC
301 AACCGGAACA GCGGCGAAGT GAAGGCGGGC GGCTCGACCA TCAGCCAGCA
351 GCTTGCCAAA AACCTGTTTT TAAACGAAAG CCGCAGCTAT ATCCGCAAAG
401 GCGAAGAAGC GCGGATTACC GCGATGATGG AAGCCGTTAC CGACAAGAC
451 AGGATTTTTCG AACTGTATTT AAACCTCAATC GAATGGCACT ACGGCgTTTT
501 CGGCGCGGAA GCCGCGTCCC GGTATTTTTA TCAAAATACCC GCCGCCAAGC
551 TGACCAACA GCAAGCGGCA AAACCTGACGG CGCGCGTCCC CGCCCCGCTC
601 TACTACGCCG ACCATCCGAA AAGCAAAACGG CTCCGCAACA AAACCAATAT
651 CGTGCTCAAA CGCATGGGTT CGGCAGAGTT GCCTGAAAGC GACACGGACT
701 GA
```

This corresponds to the amino acid sequence <SEQ ID 2684; ORF 792>:

```
m792.pep
1  MFRIVKWLIA LPVGIFIFFN AYVYGNIIITY RAVAPHRTAF MSMRMKQFEQ
51  EGRDVALDYR WNPYKRISTN LKKALIASD ARFAGHGGFD WGGIQNAIRR
101 NRNSGKVKAG GSTISQQLAK NLFLNESRSY IRKGEEAAIT AMMEAVTDKD
151 RIFELYLNSI EWHYGVFGAE AASRYFYQIP AAKLTQQA KLTARVPAPL
201 YYADHPKSKR LRNKTNIVLK RMGSAELPES DTD*
```

g792 / m792 90.4% identity in 230 aa overlap

```

              10      20      30      40      50      60
g792.pep      MFRIVKWLIALPVGIFIFFNAYVYGNIIITYRAVAPHRTAFMSMRMKQFEQEGRDVALDYR
              |||||
m792          MFRIVKWLIALPVGIFIFFNAYVYGNIIITYRAVAPHRTAFMSMRMKQFEQEGRDVALDYR
              10      20      30      40      50      60
              70      80      90      100     110     120
g792.pep      WVPYNRISTNLKKALIASDVRFAGHGGFDGDGIQNAIRRNNSGEVKAGGSTISQQLAK
```

1273

[illegible]

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2685>:

```
a792.seq
1  ATGTTCCGCA TCAATCAATG GCTGATTGCC CTGCCCGTCG GCATCTTTAT
51  CTTTTTCAAT GCCTATGTGT ACGGCAACAT CATTACCTAC CGCGCCGTCG
101 CGAGGCTACG GACTGCCTTT ATGTGCGATG GATGAAGCA GTTTGAACAG
151 GAAGGTCGCG ATGTCGCATC GGATTACCGC TGGATGCCCT ACAAAAGCAT
201 TTCCACCAAC CTGAAAAAAG CCGTATTATG TCCGAAGAT TCCCGGTTTCG
251 CGGGGACGCG CGGCTTCGAT TGGGGCGGCA TTCAAAAAGC CATACGGCGC
301 AACCGBAACA CGCGCAAAAT GAAGGCGGGC GGCTGCAGCA TCAGCCAGCA
351 GCTTGCCAAA AACCTGTTTT TAAACGAAAG CCGCAGCTAT ATCCGCAAAG
401 GCGAAGAAGC AGCGATATACC GCGATGATGG AAGCCGTTAC CGCAAAAGAC
451 AGGATTTTTG AACTGTATTT AAACCTCAAT GAATGGCATC AC CGCGGTTTT
501 CGGCGCGGAA GCGCGGTCCC GGTATTTTTA TCAAATACCC GCGCCGAAGC
551 TGACCAAAAC CAGGGCGGCA AAACCTGACG CGCGCGTCCC CGCCCCCGTC
601 TACTACGCGC ACCATCCGAA AAGCAAAACG CTCGCAACAA AAACCAATAT
651 CGTGCTCAGA CGCATGGGTT CGGCAGAGTT GCCTGAAAGC GATACGGACT
701 GA
```

This corresponds to the amino acid sequence <SEQ ID 2686; ORF 792.a>:

```
a792.pep
1  MFRIIKWLIA LPVGIFIFNN AYVYGNIIITY RAVAPHRTAF MSMRMKQFEQ
51  EGRDVALDYR WMPYKRISTN LKKALIASED ARFAGHGDFD WGGIQNAIRR
101 NRNSGKVKAG GSTISQQLAK NLFNLNRSY IRKGEAAIT AMMEAVTDKD
151 RIFELYLNSI EWHYGVFGAE AASRYFYQIP AAKLTQQAA KLTARVPAPL
201 YYADHPKSRK LRHNKTYVLR RMSSFAELPS DTD*
```

m792/a792 99.6% identity in 233 aa overlap

	10	20	30	40	50	60
a792.pep	MFRIIKWLLALPVGIFIFNAYVYGNII	TYRAVAPHRTAFMSMRMKQFEQGRDVALDYR				
m792	MFRIIKWLLALPVGIFIFNAYVYGNII	TYRAVAPHRTAFMSMRMKQFEQGRDVALDYR				
	10	20	30	40	50	60
	70	80	90	100	110	120
a792.pep	WMPYKRISTNLKKALIASEDARFAGHG	GGFDWGGIQNAIRNRNRSKGVKAGGSTISQQLAK				
m792	WMPYKRISTNLKKALIASEDARFAGHG	GGFDWGGIQNAIRNRNRSKGVKAGGSTISQQLAK				
	70	80	90	100	110	120
	130	140	150	160	170	180
a792.pep	NLFLNESRSYIRKGEEAAITAMMEAVTDKDRIFEL	YLSNIEWHYGVFGAEAAASRYFYQIP				
m792	NLFLNESRSYIRKGEEAAITAMMEAVTDKDRIFEL	YLSNIEWHYGVFGAEAAASRYFYQIP				
	130	140	150	160	170	180
	190	200	210	220	230	
a792.pep	AAKLTQQAAKLTARVPAPLYADHPKSKRLRNKTNIVLRRMGS	AELPESD	TDX			
m792	AAKLTQQAAKLTARVPAPLYADHPKSKRLRNKTNIVLRRMGS	AELPESD	TDX			
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEO ID 2687>:

q793.seq

1274

```

1  ATGTTGATTA AAAGCGAATA TAAGCCCCGG ATGCTGCCCA AAGAAGAGCA
51  GGTCAAAAAG CCGATGACCA GTAACGGACG GATTAGCTTC GTCCTGATGG
101 CAATGGCGGT CTTGTTTGCC TGTCTGATTG CCCGCGGGCT GTATCTGCAG
151 ACGGTAACGT ATAACCTTTT GAAAGAACAG GCGGACAACC GGATTGTGCG
201 GACTCAAGCA TTGCCGGCTA CACGCGGTAC GGTTCGGAC CGGAACGGTG
251 CGGTTTTGGC GTTGAGCGCG CCGACGGAGT CCCTGTTTGC CGTGCCTAAA
301 GATATGAAGG AAATGCCGTC TGCCGCCCAA TTGGAACGCC TGTCCGAGCT
351 TGTGATGTG CCGGTGATG TTTTGAGGAA CAAACTCGAA CAGAAAGGCA
401 AGTCGTTTAT TTGGATCAAG CCGCAGCTCG ATCCCAAGGT TGCCGAAGAG
451 GTCAAAAGCCT TGGGTTTGA AACTTTGTA TTTGAAAAAG AATTAAAAAG
501 CCATTACCCG ATGGGCAACC TGTTGCACA CGTCATCGGA TTTACCGATA
551 TTGACGGCAA AGGTCAGGAA GGTTTGGAAC TTTGCTTGA AGACAGCCTG
601 TATGGCGAAG ACGGCGCGGA AGTTGTTTGG CCGGACCGGC AGGGCAATAT
651 TGTGGACAGC TTGGACTCCC CGCGCAATAA AGCACCGCAA AACGGCAAG
701 ACATCATCCT TTCCTCGAT CAGAGGATTC AGACCTTGGC CTATGAAGAG
751 TTGAACAAGG CGGTCGAATA CCATCAGGCA AAAGCCGGAA CGGTGGTGGT
801 TTTGGATGCC CGCACGGGGG AATCCTCGC CTTGGCCAAT ACGCCCGCCT
851 ACGATCCCAA CAGACCGGCG CGGGCAGACA GCGAACAGCG GCGCAACCGT
901 GCCGTAACCG ATATGATCGA ACCTGGTTCG GCAATCAAAC CGTTCGTGAT
951 TGCGAAGGCA TTGGATGCGG GCAAAACCGA TTTGAACGAA CGGCTGAATA
1001 CGCAGCCTTA TAAATCGGA CCGTCTCCCG TCGCGATGA TACCCATGTT
1051 TACCCCTCTT TGGATGTGCG CGGCATTATG CAGAAATCGT CCAACGTCGG
1101 CACAAGCAAA CTGCTGCGC GTTTCGGCGC CGAAGAAATG TATGACTTCT
1151 ATCATGAATT GGCATCGGT GTGCGIATGC ACTCGGCTT TCCGGGGGAA
1201 ACTGCAGGTT TGTGAGAAA TTGGCGCAGG TGGCGGCCCA TCGAACAGGC
1251 GACGATGTCT TTCGGTTACG GTCTGCAATT GAGCCTGCTG CAATTGGCGC
1301 CGCCTATAC CGCACTGACG CACGACGGCG TTTTGCTGCC GCTCAGCTTT
1351 GAGAAGCAGG CGGTTGCGCC GCAAGSCAAA CGCATATCA AAGAATCGAC
1401 CGCGCGCGAG GTACGCAATC TGATGGTTTC CGTAACCGAG CCGGGCGGCA
1451 CCGGTACGCG GGGTGCAGTG GACGGTTTCG ATGTCGCGCG TAAACCGGCG
1501 ACGGCGCGCA AGTTCGTCAA CGGCGTTAT GCGGACAACA AACACGTCGC
1551 TACCTTTATC GGTTTTGCCC CGGCCAAAAA CCCCCGTGTG ATTGTGGCGG
1601 TAACCATCGA CGAACCGACT GCCACGGCT ATTACGCGCG CGTAGTGCCA
1651 GGGCCGCCCT TCAAAAAAAT TATGGGCGGC AGCCTGAACA TCTTGGGCAT
1701 TTCCCGGACC AAGCCACTGA CCGCGCAGC CGTCAAAACA CCGTCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2688; ORF 793.ng>:

g793.pep

```

1  MLIKSEYKPR MLPKEEQVKK PMTSNGRISF VLMAMAVLFA CLIARGLYLQ
51  TVTYNFKLEQ GDNRIVRTQA LPATRGTVSD RRGAVLALSA PTESLFAVPK
101 DMKEMPAAQ LERLSELVDV PVDVLRNKLE QKGSFIWIK RQLDPKVAEE
151 VKALGLENFV FEKELKRHYD MGNLFHIVIG FTDIDGKGQE GLELSLEDSL
201 YGEDGAEVFL RDRQGNIVDS LDSPRNKAPQ NGKDIILSLD QRIOTLAYEE
251 LNKAVEYHQA KAGTVVVLDA RTGEILALAN TPAYDPNRPD RADSEQRNR
301 AVTDMIEPGS AIKPFVIAKA LDAGKTDLNE RLNTQPYKIG PSPVRDDTHV
351 YPSLDVRGIM QKSSNVGTSK LSARFGAEM YDFYHELIGV VRNHSGFPE
401 TAGLLRNWRR WRPIEQATMS FGYGLQLSLL QLARAYTALT HDGVLLPLSF
451 EKQAVAPQK RIFKESTARE VRNLMVSVTE PGGTGTAGAV DGFVDVGAKE
501 TARKFVNGRY ADNKHVATFI GFAPAKNPRV IVAVTIDEPT AHGYGGVVA
551 GPFFKIMGG SLNILGISPT KPLTAAAVKT PS*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2689>:

m793.seq

```

1  ATGTTGATTA AGAGCGAATA TAAGCCTCGG ATGCTGCCCA AAGAAGAGCA
51  GGTCAAAAAG CCGATGACCA GTAACGGACG GATCAGCTTC GTCCTGATGG
101 CAATAGCGGT CTTGTTTGCC GGTCTGATTG CTCGCGGACT GTATCTGCAG
151 ACGGTAACGT ATAACCTTTT GAAAGAACAG GCGGACAACC GGATTGTGCG
201 GACTCAAAACA TTGCCGGCTA CACGCGGTAC GGTTCGGAC CGGAACGGTG
251 CGGTTTTGGC GTTGAGTGGC CCGACGGAGT CCCTGTTTGC CGTGCCTAAA
301 GAGATGAAGG AAATGCCGTC TGCCGCACAA TTGGAACGCC TGTCCGAGCT
351 TGTGATGTG CCGGTTGATG TTTTGAGGAA CAAGCTCGAA CAGAAAGGCA
401 AGTCGTTTAT CTGGATTAAG CCGCAGCTCG ATCCCAAGGT TGCCGAAGAG
451 GTCAAAAGCCT TGGGTTTGA AACTTTGTA TTTGAAAAAG AATTAAAAAG
501 CCATTACCCG ATGGGCAACC TGTTGCACA CGTCATCGGA TTTACCGATA
551 TTGACGGCAA AGGTCAGGAA GGTTTGGAAC TTTGCTTGA AGACAGCCTG
601 CATGGCGAAG ACGGCGCGGA AGTCGTTTGG CCGGACCGGC AGGGCAATAT
651 TGTGACAGC TTGGACTCCC CGCGCAATAA AGCCCCGAAA AACGGCAAAG
701 ACATCATCCT TTCCTCGAT CAGAGGATTC AGACCTTGGC CTATGAAGAG
751 TTGAACAAGG CGGTCGAATA CCATCAGGCA AAAGCCGGAA CGGTGGTGGT
801 TTTGGATGCC CGCACGGGGG AATCCTCGC CTTGGCCAAT ACGCCCGCCT
851 ACGATCCCAA CAGGCCCGGC CGGGCAGACA GCGAACAGCG GCGCAACCGT
901 GCCGTAACCG ATATGATCGA ACCCGGTTTC GCAATCAAAC CGTTTGTGAT
951 TGCGAAGGCA TTGGATGCGG GCAAAACCGA TTTGAACGAA CGGCTGAATA

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1275

```

1001 CGCAGCCTTA TAAATCGGA CCGTCTCCCG TGC GCGATAC CCATGTTTAC
1051 CCCTCTTTGG ATGTGCGCGG CATCATGCAG AAATCGTCCA ACGTCGGCAC
1101 AAGCAAACCTG TCTGCGCGTT TCGGTGCCGA AGAAATGTAT GACTTCTATC
1151 ATGAGTTGGG CATCGGTGTG CGTATGCACT CGGGCTTTCC GGGCGAAACT
1201 GCAGGTTTGT TGAGAAATTG GCGCAGGTGG CGGCTATCG AACAGCGGAC
1251 GATGTCCTTC GGTACGGCC TGCAATTGAG CCTGCTGCAA TTGGCGCGCG
1301 CCTATACCGC ACTGACGCAC GACGGCGTTT TACTGCCGGT CAGCTTTGAA
1351 AAACAGGCGG TTGCGCCGCA AGGCAAACGC ATATTCAAAG AATCGACCGC
1401 GCGCGAGGTA CGCAATCTGA TGGTTTCCGT AACCGAGCCG GCGCGCACCG
1451 GTACGGCGGG TCGGTGGAC GGTTCGATG TCGGCGCGAA AACCGGCACG
1501 GCGCGCAAGT TCGTCAACGG GCGTTATGCC GACAACAAAC ACATCGCTAC
1551 CTTTATCGGT TTTGCCCCCG CCAAAATCC CCGTGTGATT GTGGCGGTAA
1601 CCATTGACGA ACCGACTGCC CACGTTATT ACGGCGCGGT AGTGGCAGGG
1651 CGGCCCTTCA AAAAAATTAT GGGCGGCAGC CTGAACATCT TGGCATTTC
1701 CCCGACCAAG CCACTGACCG CCGCAGCCGT CAAAACACCG TCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2690; ORF 793>:

m793.pep

```

1  MLIKSEYKPR MLPKEEQVK PMTSNGRISF VLMAIAVLFA GLIARGLYLO
51  TVTYNFKLEQ GDNRIVRTQT LPATRGTVSD RINGAVLALSA PTESLFAVPK
101 EMKEMPSSAQ LERLSELVDV PVDVLRNKLE QKGKSFIVIK RQLDPKVAEE
151 VKALGLENFV FEKELKRHPY MGNLFAHVIG FTDIDGKGQE GLELSLEDSL
201 HGEDGAEEVL RDRQGNIVDS LDSPRNKAPK NGKDIILSLD QRIQTLAYEE
251 LNKAVEYHQA KAGTVVVLDA RTGEILALAN TPAYDPNRPGRADSEQRNR
301 AVTDMIEPGS AIKPFVIAKA LDAGKTDLNE RLNTQPKYIG PSPVRDTHVY
351 PSLDVRGIMQ KSSNVGTSKL SARFGAEMY DFLYHGLGIV RMHSGFPGET
401 AGLLRNWRWR RPIEQATMSF GYGLQLSLQ LARAYTALH DGVLLPVSF
451 KQAVAPQGRK IFKESTAREV RNLMSVTEP GGTGTAGAVD GFDVGAKTGT
501 ARKFNVRGVA DNKHIATFIG FAPAKNPRVI VAVTIDEPTA HGYGGVVVAG
551 PPFKKIMGGS LNILGISPTK PLTAAAVKTP S*

```

g793/m793 98.5% identity in 582 aa overlap

	10	20	30	40	50	60
g793.pep	MLIKSEYKPRMLPKEEQVKPMTSNGRISFVLMAIAVLFAGLIARGLYLQTVTYNFKLEQ					
m793	MLIKSEYKPRMLPKEEQVKPMTSNGRISFVLMAIAVLFAGLIARGLYLQTVTYNFKLEQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
g793.pep	GDNRIVRTQALPATRGTVSDRNGAVLALSAPTESLFAVPKDMKEMPSSAQRLERLSELVDV					
m793	GDNRIVRTQTLPATRGTVSDRNGAVLALSAPTESLFAVPKEMPSSAQRLERLSELVDV					
	70	80	90	100	110	120
	130	140	150	160	170	180
g793.pep	PVDVLRNKLEQKGKSFIVIKRQLDPKVAEEVKALGLENFVFEKELKRHPYPMGNLFAHVIG					
m793	PVDVLRNKLEQKGKSFIVIKRQLDPKVAEEVKALGLENFVFEKELKRHPYPMGNLFAHVIG					
	130	140	150	160	170	180
	190	200	210	220	230	240
g793.pep	FTDIDGKGQEGLELSLEDSLYGEDGAEEVLDRQGNIVDSLDSPRNKAPQNGKDIILSLD					
m793	FTDIDGKGQEGLELSLEDSLHGEDGAEEVLDRQGNIVDSLDSPRNKAFKNGKDIILSLD					
	190	200	210	220	230	240
	250	260	270	280	290	300
g793.pep	QRIQTLAYEELNKAVEYHQA KAGTVVVLDA RTGEILALAN TPAYDPNRPGRADSEQRNR					
m793	QRIQTLAYEELNKAVEYHQA KAGTVVVLDA RTGEILALAN TPAYDPNRPGRADSEQRNR					
	250	260	270	280	290	300
	310	320	330	340	350	360
g793.pep	AVTDMIEPGSAIKPFVIAKALDAGKTDLNERLNTQPKYIGPSPVRDTHVYPSLDVRGIM					
m793	AVTDMIEPGSAIKPFVIAKALDAGKTDLNERLNTQPKYIGPSPVRD-THVYPSLDVRGIM					
	310	320	330	340	350	
	370	380	390	400	410	420
g793.pep	QKSSNVGTSKLSARFGAEMYDFYHGLGIVRMHSGFPGETAGLLRNWRWRPIEQATMS					
m793	QKSSNVGTSKLSARFGAEMYDFYHGLGIVRMHSGFPGETAGLLRNWRWRPIEQATMS					
	360	370	380	390	400	410

1276

```

          430      440      450      460      470      480
g793.pep  FGYGLQLSLLQLARAYTALTHDGVLLPLSFERQAVAPQGKRIFKESTAREVRNLMVSVTE
          |||||
m793      FGYGLQLSLLQLARAYTALTHDGVLLPVSEKQAVAPQGKRIFKESTAREVRNLMVSVTE
          420      430      440      450      460      470

          490      500      510      520      530      540
g793.pep  PGGTGTAGAVDGFVGAKTGTARKFVNGRYADNKHVATFIGFAPAKNPRVIVAVTIDEPT
          |||||
m793      PGGTGTAGAVDGFVGAKTGTARKFVNGRYADNKHVATFIGFAPAKNPRVIVAVTIDEPT
          480      490      500      510      520      530

          550      560      570      580
g793.pep  AHGYGGVVAGPPFKKIMGGSNLILGISPTKPLTAAAVKTPSX
          |||||
m793      AHGYGGVVAGPPFKKIMGGSNLILGISPTKPLTAAAVKTPSX
          540      550      560      570      580

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2691>:

```

a793.seq
1  ATGTTGATTA AGAGCGAATA TAAGCCTCGG ATGCTGCCCA AAGAAGAGCA
51  GGTCAAAAAG CCGATGACCA GTAACGGACG GATCAGCTTC GTCCIGATCG
101 CAATAGCGGT CTTGTTTGCC GGTCTGATTG CTCGCGGACT GTATCTGCAG
151 ACGGTAACGT ATAACTTTTT GAAAGAACAG GCGCACAACC GGATTGTGCG
201 GACTCAACA TTGCCGCTA CACCGGTAC GGTTCGGAC CGGAACGGTG
251 CGGTTTGGC GTTGAGTGGC CCGACGGAGT CCCTGTTGC CGTGCTAAA
301 GAGATGAAGG AAATGCCGTC TGCCGCACAA TTGGAACGCC TGTCCGAGCT
351 TGTCGATGTG CCGGTTGATG TTTGAGGAA CAAGCTCGAA CAGAAAGGCA
401 AGTCGTTTAT CTGGATTAA GCGCAGCTCG ATCCCAAGGT TGCCGAAGAG
451 GTCAAAAGCCT TGGGTTTGA AACTTTGTA TTGAAAAAG AATTAAACG
501 CCATTACCCG ATGGGCAACC TGTTCGACA CGTCATCGGA TTTACCGATA
551 TTGACGGCAA AGGTCAGGAA GGTTCGAAC TTTCGTTGA AGACAGCCTG
601 CATGGCGAAG ACGGCGCGGA AGTCGTTTG CGGGACCGGC AGGGCAATAT
651 TGTGGACAGC TTGGACTCCC CGCGCAATAA AGCCCCGAAA AACGGCAAAG
701 ACATCATCCT TTCCCTCGAT CAGAGGATTC AGACCTTGGC CTATGAAGAG
751 TTGAACAAGG CGGTGGAATA CCATCAGGCA AAAGCCGGA CGGTGGTGTG
801 TTTGGATGCC CGCACGGGGG AAATCCTCGC CTTGGCCAAT ACGCCCGCCT
851 ACATGCCCAA CAGGCCCGGC CGGCGAGACA GCGAACAGCG GCGCAACCGT
901 GCGGTAACCG ATATGATCGA ACCCGGTTCC GCAATCAACG CTTTGTGAT
951 TGCGAAGGCA TTGGATGCGG GCAAAACCGA TTGAACGAA CGGCTGAATA
1001 CGCAGCCTTA TAAATCGGA CCGTCTCCCG TCGCGGATAC CCATGTTTAC
1051 CCCTCTTTG ATGTGCGCGG CATCATGCAG AAATCGTCCA ACGTCGGCAC
1101 AAGCAAACTG TCTGCGCGTT TCGGTGCCGA AGAAATGTAT GACTTCTATC
1151 ATGAGTTGGG CATCGGTGTG CGTATGCACT CGGGCTTTCC GGGCGAAACT
1201 GCASGTTTGT TGAGAAATTG GCGCAGGTGG CGGCTATCG AACAGGCGAC
1251 GATGTCTTTC GGTACGGGCC TGCAATTGAG CCGTGTGCAA TTGGCGCGCG
1301 CCTATACCGC ACTGACGCAC GACGGCGTTT TACTGCCGGT CAGCTTTGAA
1351 AAACAGGCGG TTGCGCCGCA AGGCAACGCG ATATTCAAAG AATCGACCGC
1401 CGCGGAGGTA CGCAATCTGA TGGTTCCCGT AACCGAGCCG GCGCGCACCG
1451 GTACGGCGGG TCGGTTGGAC GGTTCGATG TCGGCGCGAA AACCGGCACG
1501 GCGCGCAAGT TCGTCAACGG GCGTTATGCC GACAACAAAC ACATCGCTAC
1551 CTTTATCGGT TTTGCCCCCG CCAAAAATCC CCGTGTGATT GTGGCGGTAA
1601 CCATTGACGA ACGGACTGCC CACGGTTATT ACGGCGCGGT AGTGGCAGGG
1651 CCGCCCTTCA AAAAAATTAT GGGCGGCAGC CTGAACATCT TGGGCATTTC
1701 CCGGACCAAG CCACTGACCG CCGCAGCCGT CAAAACACCG TCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2692; ORF 793.a>:

```

a793.pep
1  MLIKSEYKPR MLFKEEQVKK PMTSNERISF VLMAIAVLFA GLIARGLYLQ
51  TVTYNFKLEQ GDNRIVRTQT LPATRCTVSD RRGAVLALSA PTESLFAVPK
101 EMKEMPSAAQ LERLSELVDV PVDVLRNKLK QKGSFIWIK RQLDPKVAEE
151 VKALGLENFV FEKELKRHYF MGNLFHVIG FTDIDGKQGE GLELSLEDSL
201 HGEDGAEVVL RDRQGNIVDS LDSPRNKAPK NGKDIIILSLD QRIQTLAYEE
251 LNKAVEYHQA KAGTVVVLDA RTGEILALAN TPAYDPNRPD RADSEQRNRN
301 AVTDMLEPGS AIKPFVIAKA LDAGKTDLNE RLNTOPYKIG PSPVRDTHVY
351 PSLDVRGIMQ KSSNVGTSKL SARFGAEMY DFXHELIGIV RMHSGFPGET
401 AGLLRNWRW RPIEQATMSF GYGLQLSLLQ LARAYTALTII DGVLLPVSE
451 KQAVAPQGKR IFKESTAREV RNLMSVTEP GGTGTAGAVD GFDVGAKTGT
501 ARKFVNGRYA DNKHIATFIG FAPAKNPRVI VAVTIDEPTA HGYGGVVAG
551 PPFKKIMGGS LNILGISPTK PLTAAAVKTP S*

```

a793/m793 100.0% identity in 581 aa overlap

1277

	10	20	30	40	50	60
a793.pep	MLIKSEYKPRMLPKEEQVKKPMTSNGRISFVLMAIAVLFAGLIARGLYLQTVTYNFLKEQ					
m793	MLIKSEYKPRMLPKEEQVKKPMTSNGRISFVLMAIAVLFAGLIARGLYLQTVTYNFLKEQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
a793.pep	GDNRIVRTQTLPATRGTVSDRNGAVLALSAPTESLFAVPKEMKEMPSAAQLERLSELVDV					
m793	GDNRIVRTQTLPATRGTVSDRNGAVLALSAPTESLFAVPKEMKEMPSAAQLERLSELVDV					
	70	80	90	100	110	120
	130	140	150	160	170	180
a793.pep	PVDVLRNKLEQKGKFSFIWIKRQLDPKVAEEVKALGLENFVFEKELKRHYPMGNLFAHVIG					
m793	PVDVLRNKLEQKGKFSFIWIKRQLDPKVAEEVKALGLENFVFEKELKRHYPMGNLFAHVIG					
	130	140	150	160	170	180
	190	200	210	220	230	240
a793.pep	FTDIDGKGQEGLELSLEDSLHGEGDAEVVLRDRQGNIVDSLDSFRNKAPKNGKDIILSLD					
m793	FTDIDGKGQEGLELSLEDSLHGEGDAEVVLRDRQGNIVDSLDSFRNKAPKNGKDIILSLD					
	190	200	210	220	230	240
	250	260	270	280	290	300
a793.pep	QRIQTLAYEELNKAVEYHQAKAGTVVVLARTGEILALANTPAYDPNRPGRADSEQRNR					
m793	QRIQTLAYEELNKAVEYHQAKAGTVVVLARTGEILALANTPAYDPNRPGRADSEQRNR					
	250	260	270	280	290	300
	310	320	330	340	350	360
a793.pep	AVTDMIEPGSAIKPFVIAKALDAGKTDLNERLNTQPYKIGSPVVRDTHVYPSLDVRGIMQ					
m793	AVTDMIEPGSAIKPFVIAKALDAGKTDLNERLNTQPYKIGSPVVRDTHVYPSLDVRGIMQ					
	310	320	330	340	350	360
	370	380	390	400	410	420
a793.pep	KSSNVGTSKLSARFGAEMYDFYHELIGIVRMHSGFPGETAGLLRNWRRWRPIEQATMSF					
m793	KSSNVGTSKLSARFGAEMYDFYHELIGIVRMHSGFPGETAGLLRNWRRWRPIEQATMSF					
	370	380	390	400	410	420
	430	440	450	460	470	480
a793.pep	GYGLQLSLLQLARAYTALHDGVLLPVSEKQAVAPQKRI FKESTAREVRNLMVSVTEP					
m793	GYGLQLSLLQLARAYTALHDGVLLPVSEKQAVAPQKRI FKESTAREVRNLMVSVTEP					
	430	440	450	460	470	480
	490	500	510	520	530	540
a793.pep	GGTGTAGAVDGFVGAKTGTARKFVNGRYADNKHIATFIGFAPAKNPRVIVAVTIDEPTA					
m793	GGTGTAGAVDGFVGAKTGTARKFVNGRYADNKHIATFIGFAPAKNPRVIVAVTIDEPTA					
	490	500	510	520	530	540
	550	560	570	580		
a793.pep	HGYYGUVVAGPPFKKIMGSSLNILGISPTKPLTAAAVKTPSX					
m793	HGYYGUVVAGPPFKKIMGSSLNILGISPTKPLTAAAVKTPSX					
	550	560	570	580		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2693>:

g794.seq
1 gtgcgtttca ATCATTTCAT AATGGTAACG ATTATTATAT ATGTGATTC
51 CCCTGCAAAC AAGCCGGTCC GCCGCCCGG CGTCCCACT TATCCGGCTT
101 TGCCCTTATAA TTGCTTTTTT TATGTAACAG ATTCACCTAT GAATTTCCCC
151 AAAACAGCGG CCTCCCTGCT GCTGCTTCTC GCCTCCCTCG CGCACACGC
201 GCTCGATACC GGC CGCATT CCGAAAACGA AATCGCTGTA TATGTCCAAG
251 AGCTTGACAG CGGAAAAGTC ATCATTGACC ACCGTGCCGG CATACCCGTC
301 AATCCCGCGT CCACGATGAA GCTCGTTACC GCGTTGCCG CCTTCAAAC
351 CTTCGGCAGC AATTACCGCT GGGCGACCGA GTTTAAAGC AACGGTACCG
401 TAAACGACGG CACGCTTGAC GGAAACCTGT ATGGGCGGG CAGCGCGCAC
451 CCCGTTTCA ATCAGGAAAA CCTGCTTGCC GTCCAACGCC AGTTGCGCGA
501 CAAAGGCATC CGCAATATCA CGGGGCGCCT SATGCTCGAC CACAGCCTGT

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551 GGGGCGAAGT CGGCAGTCCC GACCATTITG AAGCCGACAG CGGTTGCGCG
601 TTTATGACGC CCCCAATCC GACTATGCTG TCTGCCGTA TGGTTATGGT
651 GCAGCGCGAA CGCAATGCCG CCGGCAGTAC CGACATCCTC ACCGATCCGC
701 CTTTCCCGCA TATTTTGGC CAAAACAAC TGAAAATTAC CGCCTCCCA
751 GCTGCTGCGC CTTGCGTCAA AAAACTGATG CGCGCATCTT TTTGCGGCAA
801 TACGCTGAAA TTGCGCGGCA ATATTCCCGA AAGCTGTTTG GGCAGGCTG
851 TCGGTGTCCG GATGTTGCGG CTTGACGAAC TGATCCGCCA AAGTTTACC
901 AACCGCTGSC TGCTCGGCGG CGGACGGATT TCAGACGGCA TCGGCATAGC
951 CGACACACCG GAAGGCGCGC AGACGCTTGC CGTTGCACAC TCCAAACCGA
1001 TGAAGGAAAT TTTGACGGAC ATGAACAAGC GTTCGGACAA TCTGATTGCG
1051 CGTTCCTGCT TCCTCAAAC CCGCGCGGAC GGCAAACTGC CCGCGTTTC
1101 CGAACAGGCG GCGTCTGCCG TCCGGCGAGA ACTTGCCGTA TCGGGCATCG
1151 ATGTTGCGGA TTTGGTTTTG GAAAACGGTT CGGGTCTGTC CAGAAAAGAA
1201 AGGGTAACGG CGAGAATGAT GCGCAAAATG TTGGAACCGG CTTATTTTCA
1251 CCGTTTGCA CAAGATTCA TCGACACGCT GCCATCGCC GGCACAGACG
1301 GGACTTTACG CAACCGCTTC AAACAAAGCG CGGGCTGTT GCGCTTAAAA
1351 ACCGGCACGC TCAACAATGT CCGCGCCCTT GCAGGTTATT GGCTGGGCGA
1401 CAAACCGATG GCGGTGGTCG TCATCATCAA CAGCGGCCGC GCCGTTTCCC
1451 TGCTGCCCGA CTTGGACAAC TTCGTTGCCA AAAACATCAT CTCGGCGCGC
1501 GACGGCTGGC TGGATGCGAA ACTGATGTGC AAAGAACGCC GCGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2694; ORF 794.ng>:

g794.pep

```

1 VRFNHFIMVT ILYVISPAN KPVRRPGVPT YPALPYNCFF YVTDSPMNEP
51 KTAASLLLLL ASLAHALDT GRIPQNEIAV YVQELDSGKV IIDHRAGIPV
101 NPASTMKLVT AFAAFKTFGS NYRWATEFKS NGTVNDGTLN GNLYWAGSGD
151 PVFNQENLLA VQRQLRDKGI RNITGRLMLD HSLWGEVSGP DHFEADSGSP
201 FMTPPNPMTL SAGMVMVRAE RNAAGSTDIL TDPPLPHIFA QNNLKITASQ
251 AACPSVKKLM RASFSGNLTK LRGNIPESCL GKPVGVMFMA LDELIRQSFT
301 NRWLLGGGRI SDGIGIADTP EGAQTLAVAH SKPMKEILT MNKRSNLLIA
351 RSVFLKLGSD GKLPVSEQA ASAVRRELAV SGIDVADLVL ENGSGLSRKE
401 RVFARMMAQM LETAYFSPFA QDFIDTLPIA GTDGLTRNRF KQSGLLRLK
451 TGTLLNVRAL AGYWLGDKPM AVVVIINSR AVSLLPDLN FVAKNIISG
501 DGWLDKLMC KERRA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2695>:

m794.seq

```

1 GTGCGTCTCA ATCATTTCAT AATGATAGCG ATTATTATAT ATGTGATTTC
51 CCTGTCAAAC AAGCCGCGCC GCCGCCACAG CGTTCCTACT TATCCGGCTT
101 TGCCCTTATAA TTGCTTTTTT TATGTAACAG ATTTACCTAT GAATTTCCCC
151 AAAACAGCGG CCTCCCTGCT GCTGCTTCTC GCCTCCCTCG CCGCACACGC
201 GCTCGATACC GGCCGCATTC CGCAAAACGA AATCGCCGTA TATGTCGAAG
251 AGCTTGACAG CGGAAAAGTC ATCATTGACC ACCGCTCGGA TGTCCCGTTC
301 AACCCCGCCT CCACAATGAA ACTCGTTACC GCGTTGCGCG CTTCAAAC
351 CTTGCGCAGC AATTACCGCT GGGCGACCGA GTTTAAAGC AACGTTACGG
401 TAAACGACGG CACGCTTGAC GGAACCTAT ATTGGCGGG CAGCGCGCAG
451 CCGGTTTTCA ATCAGGAAAA CCTGCTTGAT GCTCAAAAAC AGTTGCGCGA
501 ACAAGGCATA CTCAATATCA CGGACACCT GATGCTCGAC CACAGCCTGT
551 GGGGCGAAGT CGGCAGCCCC GACGATTTCG AAGCCGACAG CGGTTGCGCG
601 TTTATGACGC CCCCCAATCC AACTATGCTG TCTGCCGTA TGGTTATGGT
651 GCGCGCGGAA CGCAATGCCG CCGGCAGTAC CGACATCCTC ACCGATCCGC
701 CTTTCCCGCA TATTTTCGCC CAAAACAAC TGAAAATTAC CGCCTCCCA
751 GCTGCCTGCC CTTGATCAA AAAACTGATG CGTGATCTT TTTGCGGCAA
801 TACGCTGAAA TTGCGCGGCA ATATTCCCGA GAGCTGTTTG GGCAGGCTG
851 TCGGTGTCCG GATGTTCCGC CTTACGAAC TGATCCGGCA AAGTTTACC
901 AACCACTGGC TGCTCGGCGG CGGACGGATT TCAGACGGTA TCGGCATAGC
951 CGACACGCGG GAAGGCGCGC AGACACTTGC CGTTGCACAC GCCAAACCGA
1001 TGAAGAAAT TTTGACGGAC ATGAACAAGC GTTCGGACAA TCTAATTGCG
1051 CGTTCCTGCT TCCTCAAAC CCGCGCGGAC GGCAAACTGC CCGCGTTTC
1101 CGAACAGGCG GCGTCTGCCG TCCGGCGCGA ACTTGCCGTA TCGGGCATCG
1151 ATGTTGCGGA TTTGGTTTTG GAAAACGGTT CGGGCTGTC CAGAAAAGAA
1201 AGGGTAACGG CGAGAATGAT GCGCAAAATG TTGGAACCGG CTTATTTTCA
1251 CCGTTTGCA CAAGATTCA TCGACACGCT ACCCATCGCC GGCACAGACG
1301 GAACCTTACG CAACCGCTTC AAACAAAGCG CGGGCTGTT GCGCTTAAAA
1351 ACCGGCACGC TCAACAATGT CCGCGCCCTT SCAGGTTATT GGCTGGGCGA
1401 CAAACCGATG GCGGTGGTCG TCATCATCAA CAGCGGCCGC GCCGTTTCCC
1451 TGCTGCCAGA CTTGGACAAC TTCGTTGCCA ACAACATCAT CTCGGCGCGC
1501 GATGGCTGGC TGGATGCGAA ACTGATGTGC AAAGAACGCC GAGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2696; ORF 794>:

m794.pep

```

1 VRLNHFIMIA ILYVISPAN KPARRHSVPT YPALPYNCFF YVTDLPMNEP
51 KTAASLLLLL ASLAHALDT GRIPQNEIAV YVQELDSGKV IIDHRSVPMV

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101 NPASTMKLVT AFAAFKTFGS NYRWATEFKS NGTVNDGTLD GNLWAGSGD
151 PVFNQENLLD AQKQLREQGI LNITGHLMLD HSLWGEVGSF DFEADSGSP
201 FMTPPNPTML SAGMVMVRAE RNAAGSTDIL TDPPLPHIFA QNNLKITASQ
251 AACPSIKKLM RASFSDNTLK LRGNIPESCL GKPVGVRMFA LDELIRQSFT
301 NHWLLGGGRI SDGIGIADTP EGAQTLAVAH AKPMKEILTD MNKRSNLI
351 RSVFLKLGSD GKLPVSEQA ASAVRRELAV SGIDVADLVL ENGSGLSRKE
401 RVTARMAQM LETAYFSPFA QDFIDTLPIA GTDGLNRNF KQSGGLRLK
451 TGTNNVRAL AGYWLGDKPM AVVVIINSGR AVSLLPDLDN FVANNIISGG
501 DGWLDKLMC KERRA*

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g794/m794 95.5% identity in 515 aa overlap

	10	20	30	40	50	60
g794.pep	VRFNHFIMVTIIIVIS	PANKPVR	RGVPTYP	ALPYNCFY	VTDSPMNF	PKTAASLLLL
m794	VRLNHFIMIAIIIVIS	PANKPARRH	SVPTYP	ALPYNCFY	VTDLPMNF	PKTAASLLLL
	10	20	30	40	50	60
g794.pep	ASLAHAHALDTGRIPQNEI	AVYVQEL	DSGKVIID	HRRAGIPVN	PASTMKLVT	AFAAFKTFGS
m794	ASLAHAHALDTGRIPQNEI	AVYVQEL	DSGKVIID	HRRSDVPVN	PASTMKLVT	AFAAFKTFGS
	70	80	90	100	110	120
g794.pep	NYRWATEFKSNGTVNDGTLD	GNLYWAGSGDPVFNQENLL	AVQRQLRDKGIRNITGR	LMLD		
m794	NYRWATEFKSNGTVNDGTLD	GNLYWAGSGDPVFNQENLL	DAQQLREQGILNITGH	LMLD		
	130	140	150	160	170	180
g794.pep	HSLWGEVGSFDPHFEADSGSP	FMTPPNPTMLSAGMVMVRAE	RNAAGSTDILTDPPLPHIFA			
m794	HSLWGEVGSFDPHFEADSGSP	FMTPPNPTMLSAGMVMVRAE	RNAAGSTDILTDPPLPHIFA			
	190	200	210	220	230	240
g794.pep	QNNLKITASQAACPSVKKLM	RASFSGNTLKL	LRGNIPESCLGKPV	GVRMFALDELIRQSFT		
m794	QNNLKITASQAACPSVKKLM	RASFSDNTLKL	LRGNIPESCLGKPV	GVRMFALDELIRQSFT		
	250	260	270	280	290	300
g794.pep	NRWLLGGGRISDGIGIADTP	EGAQTLAVAH	SKPMKEILTD	MNKRSDNLI	ARSVFLKLGSD	
m794	NHWLLGGGRISDGIGIADTP	EGAQTLAVAH	AKPMKEILTD	MNKRSDNLI	ARSVFLKLGSD	
	310	320	330	340	350	360
g794.pep	GKLPVSEQAASAVRRELAV	SGIDVADLVL	ENGSGLSR	KERV	TARMAQMLETAYFSPFA	
m794	GKLPVSEQAASAVRRELAV	SGIDVADLVL	ENGSGLSR	KERV	TARMAQMLETAYFSPFA	
	370	380	390	400	410	420
g794.pep	QDFIDTLPIAGTDGTLNRNF	KQSGGLRLK	GTGLNNVRAL	AGYWLGDKPM	AVVVIINSGR	
m794	QDFIDTLPIAGTDGTLNRNF	KQSGGLRLK	GTGLNNVRAL	AGYWLGDKPM	AVVVIINSGR	
	430	440	450	460	470	480
g794.pep	AVSLLPDLDN	FVAKNIISGGDGWLD	AKLMCKERRAX			
m794	AVSLLPDLDN	FVANNIISGGDGWLD	AKLMCKERRAX			
	490	500	510			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2697>:

```

a794.seq
1 GTGCGTCTCA ATCATTTCAT AATGATAGCG ATTATTATAT ATGTGATTTC
51 CCCTGCAAAC AAGCCGGCCC GCCGCCACAG CGTTCCTTAT TATCCGGCTT
101 TGCCCTATAA TTGCTTTTTT TATGTAACAG ATTTACCTAT GAATTCCTCC
151 AAAACAGCGG CCTCCCTGCT GCTGCTTCTC GCCTCCCTCG CCGCACACGC
201 GCTCGATACA GGTCCGATTC CGCAAAACGA AATCGCCGTA TATGTCCAAAG
251 AGCTTGACAG CGGAAAAGTC ATCATTGACC ACCGCTCGGA TGTCCCGTCT

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301 AACCCCGCCT CCACAATGAA ACTCGTTACC GCGTTTGCCG CTTTCAAAC
351 CTTCCGGCAGC AATTACCGCT GGGCGACCGA GTTTAAAAGC AACGGTACGG
401 TAAACGACGG CACGCTTGAC GGAAACCTGT ATTGGGCGGG CAGCGGCGAC
451 CCCGTTTTCA ATCAGGAAAA CTTGCTTGCC GTCCAACGCC AGTTGCGCGA
501 ACAAGGCATA CGCAATATCA CGGGACACCT GATGCTCGAC CACAGCCTGT
551 GGGCGGAAGT CGGCAGCCCC GACGATTTCG AAGCCGACAG CGGTTCCCGG
601 TTTATGACGC CCCCCAATCC AACTATGCTG TCTGCCGTA TGGTTATGGT
651 GCGCGCCGAA CGCAATGCCG CCGACAGTAC CGACATCCTC ACCGATCCGC
701 CTTTGCCGCA TATTTTCGCC CAAAACAAC TGAATAATAC CGCCTCCCAA
751 GCTGCCTGCC CTTGCATCAA AAAACTGATG CGTGCATCTT TTTCGGACAA
801 TACGCTGAAA TTGCGCGGCA ATATTCCCGA GAGCTGTTTG GGCAAGCCTG
851 TCGGTGTCCG GATGTTCCGG CTTGACGAAC TGATCCGSCA AAGTTTACC
901 AACCACTGGC TGCTCGGCGG CCGACGGATT TCAGACGGCA TCGGCATATC
951 CGACACGCGC GAAGGCGCGC AGACGCTTGC CGTTGCACAC TCAAAGCCGA
1001 TGAAGGAAAT TTTGACGGAC ATGAACAAGC GTTCGGACAA TCTAATGCG
1051 CGTTCCGTCT TCCTCAAACT CGGCGCGCAC GGCAAACTGC CCGCGTTTC
1101 CGAACAGGCA GCGTCTGCCG TCCGGCGTGA ACTTGCCGTG TCGGGCATCG
1151 ATGTTGCGGA TTTGGTTTTG GAAAACGGTT CAGGCTGTGC CAGAAAAGAA
1201 AGGGTAACGG CGAGAATGAT GCGGCAAAATG TTGGAACCGG CTTATTTCAG
1251 CCGGTTTGCA CAAGATTTC TCGATACGCT GCCCATCGCC GGCACAGACG
1301 GGACTTTACG CAACCGCTTC AAACAAGCG GCGGGCTGTT GCGCTTAAAA
1351 ACCGGCAGCG TCAACAATGT CCGCGCCCTT GCAGGTATT GGCTGGGCGA
1401 CAAACCGATG GCGGTGGTGC TCATCATCAA CAGCGGCGCG GCCGTTTCCC
1451 TGCTGCCCGA CTTGGACAAC TTCGTTGCCA ACAACATCAT CTCGCGCGGC
1501 GATGGCTGGC TGGATGCGAA ACTGATGTGC AAAGAACGCC CAGCCTGA

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This corresponds to the amino acid sequence <SEQ ID 2698; ORF 794.a>:

a794.pep

```

1  VRLNHFIMIA IIIYVISPA KPARHSVPT YPALPYNCF YVTDLPNMF
51  KTAASLLLLL ASLAHALDT GRIPQNEIAV YVQELDSGXV IIDHRSDVPV
101 NPASTMKLVT AFAAFKTFGS NYRWATEFKS NGTVNDGTLG GNLVWAGSGD
151 PVFNOENLLA VOROLREOGI RNITGHLMLD HSLWGEVGSF DDFEADSGSP
201 FMTPPNPTML SAGVMVRAE RNAADSTDIL TDPPLPHIFA QNNLKITASQ
251 AACPSIKKLM RASFSDNTLK LRGNIPESCL GKPVGVRMFA LDELIRQSFT
301 NHWLLGGGRI SDGIGISDTP EGAQTLAVAH SKPMKEILD MNKRSDNLIA
351 RSVFLKGGD GKLPAVSEQA ASAVRRELAV SGIDVADLVI ENGSGLSRKE
401 RVTARMMQM LETAYFSPFA QDFIDTLPIA GTDGLRNRN KQSGGLRLK
451 TGTLNNVRAL AGYWLGDKPM AVVVIINSGR AVSLLPDLN FVANNIISGG
501 DGWLDAKLMC KERRA*

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a794/m794 98.6% identity in 515 aa overlap

	10	20	30	40	50	60
a794.pep	VRLNHFIMIA	IIIIYVISPA	KPARHSVPT	YPALPYNCF	YVTDLPNMF	KTAASLLLLL
m794	VRLNHFIMIA	IIIIYVISPA	KPARHSVPT	YPALPYNCF	YVTDLPNMF	KTAASLLLLL
	10	20	30	40	50	60
a794.pep	ASLAHALDT	GRIPQNEIAV	YVQELDSGXV	IIDHRSDVP	NPASTMKLVT	AFAAFKTFGS
m794	ASLAHALDT	GRIPQNEIAV	YVQELDSGXV	IIDHRSDVP	NPASTMKLVT	AFAAFKTFGS
	70	80	90	100	110	120
a794.pep	ASLAHALDT	GRIPQNEIAV	YVQELDSGXV	IIDHRSDVP	NPASTMKLVT	AFAAFKTFGS
m794	ASLAHALDT	GRIPQNEIAV	YVQELDSGXV	IIDHRSDVP	NPASTMKLVT	AFAAFKTFGS
	70	80	90	100	110	120
a794.pep	NYRWATEFKS	NGTVNDGTLG	GNLVWAGSGD	PVFNOENLLA	VQRQLREQG	RNITGHLMLD
m794	NYRWATEFKS	NGTVNDGTLG	GNLVWAGSGD	PVFNOENLLA	VQRQLREQG	RNITGHLMLD
	130	140	150	160	170	180
a794.pep	NYRWATEFKS	NGTVNDGTLG	GNLVWAGSGD	PVFNOENLLA	VQRQLREQG	RNITGHLMLD
m794	NYRWATEFKS	NGTVNDGTLG	GNLVWAGSGD	PVFNOENLLA	VQRQLREQG	RNITGHLMLD
	130	140	150	160	170	180
a794.pep	HSLWGEVGS	PDDFEADSGS	PFMTPPNPT	MLSAGVMVRAE	RNAADSTDIL	TDPPLPHIFA
m794	HSLWGEVGS	PDDFEADSGS	PFMTPPNPT	MLSAGVMVRAE	RNAAGSTDIL	TDPPLPHIFA
	190	200	210	220	230	240
a794.pep	HSLWGEVGS	PDDFEADSGS	PFMTPPNPT	MLSAGVMVRAE	RNAADSTDIL	TDPPLPHIFA
m794	HSLWGEVGS	PDDFEADSGS	PFMTPPNPT	MLSAGVMVRAE	RNAAGSTDIL	TDPPLPHIFA
	190	200	210	220	230	240
a794.pep	QNNLKITASQ	AACPSIKKLM	RASFSDNTLK	LRGNIPESCL	GKPVGVRMFA	LDELIRQSFT
m794	QNNLKITASQ	AACPSIKKLM	RASFSDNTLK	LRGNIPESCL	GKPVGVRMFA	LDELIRQSFT
	250	260	270	280	290	300
a794.pep	QNNLKITASQ	AACPSIKKLM	RASFSDNTLK	LRGNIPESCL	GKPVGVRMFA	LDELIRQSFT
m794	QNNLKITASQ	AACPSIKKLM	RASFSDNTLK	LRGNIPESCL	GKPVGVRMFA	LDELIRQSFT
	250	260	270	280	290	300
a794.pep	NHWLLGGGRI	SDGIGISDTP	EGAQTLAVAH	SKPMKEILD	MNKRSDNLIA	RSVFLKGGD
m794	NHWLLGGGRI	SDGIGISDTP	EGAQTLAVAH	SKPMKEILD	MNKRSDNLIA	RSVFLKGGD
	310	320	330	340	350	360
a794.pep	NHWLLGGGRI	SDGIGISDTP	EGAQTLAVAH	SKPMKEILD	MNKRSDNLIA	RSVFLKGGD
m794	NHWLLGGGRI	SDGIGISDTP	EGAQTLAVAH	SKPMKEILD	MNKRSDNLIA	RSVFLKGGD

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|||||
m794 NHWLLGGGRISDGIADTPEGACTLAVAHAKPMKEILTDNKRSDNLARSVFLKLGGD
      310      320      330      340      350      360
a794.ppep GKLPVSEQAASAVRRELAVSGIDVADLVLENGSGLSRKERV TARMMAOMLETAYFSPFA
      370      380      390      400      410      420
m794 GKLPVSEQAASAVRRELAVSGIDVADLVLENGSGLSRKERV TARMMAOMLETAYFSPFA
      370      380      390      400      410      420
a794.ppep QDFIDTLPIAGTDGTLNRNRFKQSGGLRLKLTGT LNNVRALAGYWLGDKPMV VVIINSGR
      430      440      450      460      470      480
m794 QDFIDTLPIAGTDGTLNRNRFKQSGGLRLKLTGT LNNVRALAGYWLGDKPMV VVIINSGR
      430      440      450      460      470      480
a794.ppep AVSLLPDLDNFVANNIISGGDGWLD AKLMCKERRAX
      490      500      510
m794 AVSLLPDLDNFVANNIISGGDGWLD AKLMCKERRAX
      490      500      510

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The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2699>:

```

g900.seq
1   ATGccgTCTG AAATGCCGTC TGAACCGTGG CAGGCGGAGG TTCGGACGGC
51  ATTGGGTTTA TTTCAACGGG CGGATGCCGA CCGCATCGCG TACTTTATCC
101 AACAAATTCGC GCGCTTCTTT GCGCGCTTTT TGCGGcctg cctGCAAAAT
151 CTCTTCGATT TGCGAAGGAT TAGAGGTCAA TGCGTTGTAG CGTTCGCGCA
201 GTTCTGCCAA TTCGGCGTTG ATTTTCGCCG CCGAAAGTTT TTTCGCCTCG
251 CCCCAAGCCA AGCCGTCGGC AAGCATTTGC GTAAATTCCG CCGTTTCAGA
301 CGGCGTGGAG AAGGCTTTAT AGATTTCAAA CAAAGGGCTT TCGTCGGGCT
351 GTTTCGGCTC GCCCGGCTCT TTCATGTTGG TAATGATTTT GTTGACCGAT
401 TTTTGGGTTT TTTTGTGCTT TTCCCAAAGC GGAATGGTAT TGCCGTAGGA
451 TTTGGACATT TTGCGTCCGT CCAAACCGAC CAAGAGTTCC ACGTTTTCGT
501 CGATTTTCAC TTCGGGCagg GTGaagagtt cTTGGAaacc gtgggtgaag
551 cggccggcAa tgtcgcgcg cATTTCgacg tgttgGATTT GGTGCGGCC
601 GACGGGGACT TCGTTGGCGT TGAACATCAA AATGTCGCGA GTCATCAGAA
651 TCGGATAACT GAACAAACCC ATTTCCACAC CGAAATCGGG GTCTTCCTGC
701 CCGTTTTCG CATTGGCTTG AACGGCGGCT TTGTAGGCGT GGGCGCGGTT
751 CATCAAACCC TTGGCGGTGA TGCAGGTCAG AATCCAGTTC AACTCCATCA
801 CTTCGGGAAT GTCGCTTTGG CGGTAGAAGG TGGTGCCTC GGGGTGAGT
851 CCGCAGGCAA GCCAAGTGGC GGCAACGGCt tggGTGGATT GGTGAATCAT
901 CTCCTGCTCG TGGCATTGTA TGATGCCGTG GTAATCGCG AGGAAGAGGA
951 AGGATTCGGT ATCGGGGTTT TGCGCGCGC GGACGGCGGG GCGGATGGCG
1001 CCGACGTAGT TGCCAGATG CGGGGTGCC GTGGTGGTTA CGCCGTCAG
1051 AACTCGTTTT TTGCTCATAA AAATGTCCTT ACGGCAGCAA TGCCGTCTGA
1101 AAGGAAAa. gatgcgCCGA TTATACCCGA TTTGCCACAT ACATCCAGCC
1151 GacaACagaC TTTTCCATAT TAA

```

This corresponds to the amino acid sequence <SEQ ID 2700; ORF 900.ng>:

```

g900.ppep
1   MPSEMPSETW QAEVRTALGL FQRADADRIA YFIQQFARFF ARFLRACLQN
51  LFDLRRIRGQ CVVAFQFCQ FGVDFFFFKF FRLAPSQAVG KHLRKFRFRF
101 RRGEFIDFK QRAFVGLFRL ARLFHVGNDF VDRFLGFFV FPKRNGIAGV
151 FGHFASVQTD QEFVVFVDFH FGQGEFLET VGEAAGNVAR HFDVLDLVAP
201 DGDFVGVHEQ NVGSHQNRIT EQTHFTEIG VFPLPVFRIGL NGGFVGVGAV
251 QHTLGGDAGQ NPVQLHHFGN VALAVEGGAL GVESAGKPSG GNLGGLVNH
301 LLLVAFDDAV VIGEEEGFG IGVLRRADG ADGADVVAQM RGAGGGYAGQ
351 NSFFAHKNVL TAAMPSEKREK DAPIIPDLPH TSSRQOTFPY *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2701>:

```

m900.seq
1   ATGCCGTCTG AAACGCGGCA GCGGAGGTT CCGACGGCAT CCGGTTCATT
51  TCAACGGCGG GATGcCGACC GCATCgG.TA CTTTGTCCAA TAATTCGCGT
101 GCTTCTTTAC GCGCTTTCGC CGCGCCTGCC TGCAAAATCT CTTGATTTG

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1282

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151 CGAAGGGTCG GCGGTCAGCT CGTTGTAGCG TTCGCGCGGT TCGGCGAGTT
201 CCGCGTTGAT TTTCGCGGCC AAAAGTTTTT TGGCTTCACC CCACGCCAAG
251 CCGTCGGCAA GCATTTTCGT AAATTCCACC GTTTCAGACG GCGTGGAGAA
301 GGCTTTGTAG ATTTCAAACA ATGGGCTTTC GTCGGGCTGT TTCGGCTCGC
351 CCGGCTCTTT CATATTGGTG ATGATTTTGT TGACCGATTT TTGGGTTTTT
401 CTGTCTGTTT CCCAAAGCGG AATGGTGTG CCGTAGGATT TGGACATTTT
451 GCGTCCGTCC AAACCGACCA AGAGTTCGAC GTTTTCATCG ATTTTCACTT
501 CCGGCAGGGT GAAGAGTTCC CGGAAGCGGT GGTGGAAGCG GCCGGCGATG
551 TCGCGCGCCA TTTCGACGTG TTGGATTGTG TCGCGCCCGA CgGGCaCTTC
601 GTTGGCGTTG AACATCAGAA TATCGGCGAGT CATCAGAATC GGATAACTGA
651 ACAAACCCAT TTCCACACCG AAATCAGGGT CTTCTGCCC GTTTTCTGCA
701 TTTGCCTGCA CGGCGGCTTT GTAGGCATGG GCGCGGTTCA TCAAACCTT
751 GGCAGTGATG CAGGTGAGAA TCCAGTCAA TTCCATCACT TCgGGAGTGT
801 CGCTTTGGCG GTAGAAGGTG GTGCGCTCGG GGTGAGTCC GCAGCAAGC
851 CAAGTGGCGG CAACGGCTTG GGTGGATTGG TGAATCATCT CCGGCTCGTG
901 GCATTTGATG ATACCGTGGT AATCGGCGAG GAAGAGGAAG GATTGCGTAT
951 CGAGGTTTTG CGCCGCGCGG ACGGCGGGGC GGATGGCGCC GACGTAGTTG
1001 CCCAGATGCG GGATGCCGCT GGTGGTTACG CCGGTCAGAA CTCGTTTTTT
1051 GCTCATAAAA ATGTCCTTGC GGCATCAATG CCGTCTGAAA GGGAAAAAGA
1101 TGTGCCGATT ATACCGGATT TGCCACCTAC ATCCAGCCGA CAACAGACTT
1151 TTCCATATTA A

```

This corresponds to the amino acid sequence <SEQ ID 2702; ORF 900>:

m900.pep

```

1 MPSETRQAEV RTASGSFQRA DADRIXFVQ *FACFFTRFR RACLQNLFDL
51 RRVGGQLVVA FARFGEFGVD FRRQKFFGFT PRQAVGKHFR KFHRRRRRGE
101 GFVDFKQWAF VGLFRLARLF HIGDDFVDRF LGFFVVFPRK NGVAVGFGHF
151 ASVQTDQEPD VFIDFHFGQG EEFPEAVVEA AGDVARHFDV LDLVAPDGHF
201 VGVEHQNIGS HQNRITEQTH FHTEIRVFLP VFCICLHGGF VGMGAHVQTL
251 GSDAGQNPVQ FHHFGSVALA VEGGALGVES AGKPSGGNGL GGLVNHLRLV
301 AFDDTVVIGE EEEFGFIEVL RRDAGGADGA DVVAQMRDAG GGYAGQNSFF
351 AHKNVLAASM PSEREKDVPI IPDLPTSSR QQTFPY*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 900 shows 87.0% identity over a 386 aa overlap with a predicted ORF (ORF 900.ng) from *N. gonorrhoeae*:

m900/g900

```

              10      20      30      40      50
m900.pep      MPSETRQAEVRTASGSFQRADADRIGYFVQXFACFFTRFRRAACLQNLFDLRRVGGQ
              ||||| ||||| | |||||:|:| || ||:| ||||| |||||: ||
g900          MPSEMPSETWQAEVRTALGLFQRADADRIAYFIQQFARFFARFLRACLQNLFDLRRIRGQ
              10      20      30      40      50      60

              60      70      80      90      100     110
m900.pep      LVVAFARFGEFGVDFRRQKFFGFTPRQAVGKHFRKFHRRRRRGEFGVDFKQWAFVGLFRL
              |||||:| :|||:|:| || :| |||||:|:|:| |||||:| |||||
g900          CVVAFAPQFCQFGVDFRRRKFFRLAPSOAVGKHLRKFRFRRRRGEFGFIDFKQRAVGLFRL
              70      80      90      100     110     120

              120     130     140     150     160     170
m900.pep      ARLFHIGDDFVDRFLGFFVVFPRKNGVAVGFGHFASVQTDQEFVDFIDFHFGQGEFPEA
              |||||:|:| |||||:| |||||:| |||||:| |||||:| |||||
g900          ARLFHVGNDFVDRFLGFFVVFPRKNGIAVGFGHFASVQTDQEFVDFVDFHFGQGEFLET
              130     140     150     160     170     180

              180     190     200     210     220     230
m900.pep      VVEAAGDVARHFDVLDLVAPDGHFVGVEHQNIGSHQNRITEQTHFHTEIRVFLPVFCICL
              |||||:| |||||:| |||||:| |||||:| |||||:| |||||
g900          VGEAAGNVARHFDVLDLVAPDGDFVGVEHQNVGSHQNRITEQTHFTEIGVFLPVFRIGL
              190     200     210     220     230     240

```

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	240	250	260	270	280	290
m900.pep	HGGFVGMGAVHQTGSDAGQNPVQFHHFGSVALAVEGGALGVESAGKPSGGNGLGGLVNH					
	: : : : : : :					
g900	NGGFVGVGAVHQTGSDAGQNPVQLHHFGNVALAVEGGALGVESAGKPSGGNGLGGLVNH					
	250	260	270	280	290	300
	300	310	320	330	340	350
m900.pep	LRLVAFDDTVVIGEEEEFGFIEVLRRADGGADGVVAQMRDAGGGYAGQNSFFAHKNVL					
	: : : : : : :					
g900	LLLVAFDDAVVIGEEEEFGFIEVLRRADGGADGVVAQMRGAGGGYAGQNSFFAHKNVL					
	310	320	330	340	350	360
	360	370	380			
m900.pep	AASMPSEREKDVPIIPDLPTSSRQOTFPYX					
	: : : : : :					
g900	TAAMPSEEREKDAPIIPDLPTSSRQOTFPYX					
	370	380	390			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2703>:

a900.seq (partial)

```

1   GAGGTTCCGA CGGCATTGGG TTTATTTCAA CGGGCGGATA CCGACCGCAT
51  CACGTACTTT GCCAATAAT TCGCGTGTCT CTTTACGCGC TTTTTCGCGC
101 CCTGCCTGCA AAATCTCTTC GATTTCGCAA GGGTCGGCGG TCAGCTCGTT
151 GTAGCGTTTCG CGCGGTTTCGG CGAGTTCGGC GTTGATTTCG GCCGCCAAAA
201 GTTTTTTTGTC CTGCCCCCAA GCCAAGCCGT CGGCAAGCAT TTTCGTAAAT
251 TCTGCCGTTT CAGACGGCGT GGAGAAAGCT TTGTAGATT CAAACAGAGG
301 GCTTTCGTCG GGTCTCTTCG GCTCGCCCGG CTCTTTCATA TTGGTGATGA
351 TTTTGTTGAC CGATTTTGGT GTTTTTTGT CGTTTTCCCA AAGCGGAATG
401 GTGTTGCCGT AGGATTTGGA CATTTTGCCT CCGTCCAAAC CAACCAAGAG
451 TTCGACGTTT TCGTCGATTT TCACTTCGGG CAGTGTGAAG AGTTCGCCGA
501 AGCGGTGGTT GAAGCGGCCG GCAATATCGC GTGCCATTTC AACGTGTTGG
551 ATTTGGTCGC GACCGACTGG AACTTCATGG GCATTGAACA TGAGAATGTC
601 GGCACTCATG AGGATAGGGT AGCTGTACAA ACCCATTTC ACGCCGAAAT
651 CGGGGTCTTC CTGCCCGTTT TCCGCATTG CCTGCACGGC GGCTTTGTAG
701 GCGTGGGCGC GGTTCATCAA ACCCTTGCGC GTGATGCAGG TCAGAATCCA
751 GTTCAATTC ATCACTTCGG GAATGTCGCT TTGACGGTAG AAGGTGGTGC
801 GTTCGGGGTC GAGTCCGCG GCAAGCCAAG TGGCGGCAAC GGCTTGGGTG
851 GATTGGTGAA TCATCTCCGG CTCGTGGCAT TTGATGATAC CGTGGTAATC
901 GCGGAGGAAG AGGAAGGATT CGGTATCAGG GTTTTGGCCC GCGCGGACGG
951 CGGGGCGGAT AGCACCAGC TAGTTGCCCA GATGCGGGAT GCCGGTGGTG
1001 GTTACGCCGG TCAGAACTCG TTTTGTGCTC ATAAAAATGT CCTTGC GGCA
1051 TCAATGCCGT CTGAAAGGGA AAAAGATGCG CCGATTATAC CCGATTGGCC
1101 ACCTACATCC AGCCGACAAC AGACTTTTCC ATATTAA

```

This corresponds to the amino acid sequence <SEQ ID 2704; ORF 900.a>:

a900.pep (partial)

```

1   EVRTALGLFQ RADTDRITYF AQ*FACFFTR FLRAQLQNLF DLRRVGGQLV
51  VAFARFGEFG VDFRRQKEFC LAPSQAVGKH FRKFCRFRFR GESFVDFKQR
101 AFVGLLRLAR LFHIGDDFVD RFLGFFVVFV KRNGVAVGFG HFASVQTNQE
151 FDFVDFHFG QCEEFPEAVV EAAGNIACHF NVLDLVATDW NFMGIEHENV
201 GSHEDRVAVQ THEHAEIGVF LPVFRICLHG GFVGVGAVHQ TLGGDAGQNP
251 VQFHHFGNVA LTVEGGALGV ESAGKPSGGN GLGGLVNHRL LVAFDDTVVI
301 GEEEEFGIR VLRRADGGAD STDVVAQMRD AGGGYAGQNS FFAHKNVLAA
351 SMPSEREKDA PIIPDLPTS SRQOTFPY*

```

m900/a900 88.4% identity in 378 aa overlap

	10	20	30	40	50	60
m900.pep	MPSETRQAEVRTASGSFQRADADRIXFYVQXFACFFTRFRRAQLQNLFDLRRVGGQLVVA					
	: : : : : :					
a900	EVRTALGLFQRADTDRITYFAQXFACFFTRFLRAQLQNLFDLRRVGGQLVVA					
	10	20	30	40	50	
	70	80	90	100	110	120

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```

m900.pep    FARFGEFGVDFRRQKFFGFTPRQAVGKHFRKFHRRRGEFVDFKQWAFVGLFRLARLF
             |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a900        FARFGEFGVDFRRQKFFCLAPSAQVAGKHFRKFHRRRGEFVDFKQRAFVGLLRLARLF
             60      70      80      90      100     110

             130     140     150     160     170     180
m900.pep    HIGDDFVDRFLGFFVFPKRNGVAVGFGHFASVQTDQEFDFIDFHFQGEFFPEAVVEA
             |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a900        HIGDDFVDRFLGFFVFPKRNGVAVGFGHFASVQTNQEFDFVDFHFQCEEFPEAVVEA
             120     130     140     150     160     170

             190     200     210     220     230     240
m900.pep    AGDVARHFDVLDLVAPDGHFVGVGHQNGSHQNRITEQTHFHTAIRVFLPVFCICLHGGF
             ||::| ||:||||| |::|:||||:||||:||||:||||:||||:|||||
a900        AGNIACHFNVLVLVATDWNFMGIEHENVGSHEDRVAVQTHFAEIGVFLPVFRICLHGGF
             180     190     200     210     220     230

             250     260     270     280     290     300
m900.pep    VGMGAHVQTLGSDAGQNPVQFHHFGSVALAVEGGALGVESAGKPSGGNGLGGLVNHRLRV
             ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a900        VGVGAHVQTLGSDAGQNPVQFHHFGNVALTVEGGALGVESAGKPSGGNGLGGLVNHRLRV
             240     250     260     270     280     290

             310     320     330     340     350     360
m900.pep    AFDDTVVIGEEEEGFIEVLRADGGADGADVVAQMRDAGGGYAGQNSFFAHKNVLAASM
             |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a900        AFDDTVVIGEEEEGFIRVLRADGGADSTDVVAQMRDAGGGYAGQNSFFAHKNVLAASM
             300     310     320     330     340     350

             370     380
m900.pep    PSEREKDVPIIPDLPTSSRQQTFFPYX
             |||||:|||||:|||||:|||||:|||||
a900        PSEREKDAPIIPDLPTSSRQQTFFPYX
             360     370

```

g901.seq not found yet

g901.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2705>:

m901.seq

```

1  ATGCCCGATT TTTCGATGTC CAATTTGGCC GTTGCCTTTT CCATCACATT
51  GGCTGCCGGT TTGTTTACCG TATTAGyAG TGGCTTGGTG ATGTTTTCCT
101 AAACGCCCAA TCCGCGTGTG TTGTCGTTG GTTGGCGTT TCCCGCGCGT
151 GCGATGGTAT ATGTTTCCCT GACGGAGATT TTCAGTAAGT CCAGCGAGGC
201 GTTCGCTGAA ATTATGATA AAGACCACGC GTTGGCGCG GCGACCATGG
251 CATTTTTGGC CGGGATGGGC GGCATTGCGC TGATTGACCG TCTGGTGCCG
301 AACCCGCATG AAACCTTTAGA CCGCAAGAC CCGTCGTTT AAGAAAGCAA
351 ACGCCGCCAT ATCGCGCGAG TCGGCATGAT GCGCGCGTT GCGATTACTG
401 CGCACAAATT CCCCGAAGGC TTGGCGACGT TTTTGGCCAC ATTGGAAAAT
451 CCAGCAGTCG GGATGCCTTT GGCCTTGGCG ATTGCCATCC ATAATATTC
501 GGAGGGCATT TCCATCGCCG CGCCGTTTA TTTTGCCACC CGCAGCCGTA
551 AGAAAACGGT GTGGGCGTGT CTGCTATCCG GCTTGGCCGA GCCGTGGGG
601 GCGGCTTTGG GCTATTGTTG TTGCAGCCG TTTTGTGCG CTGCCGTGTT
651 TGSTTCGGTA TTCGGCGTGA TAGCCGTTG GATGGTGTG TTGGCGTTGG
701 ACGAGCTGnt GCCGGCTGCC AAACGCTATT CAGACGCCA TGAAACCGTT
751 TACGGCTCGA CAACGGGTAT GCGGTGATT GCCGTCAGCC TGGTATTGTT
801 CCATTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2706; ORF 901>:

m901.pep

```

1  MPDFSMNL A VAFSITLAAG LFTVLXSLV MFSKTPNPRV LSFGLAFAGG
51  AMVYVSLTEI FSKSSEAF AE IYDKDHAF AA ATMAFLAGMG GIALIDRLVP

```

1285

101 NPHETLDAQD PSFQESKRRH IARVGMMAAF AITAHNFPEG LATFFATLEN
 151 PAVGMPLALA IAIHNIPEGI SIAAPVYFAT RSRKKTWAC LLSGLAEPLG
 201 AALGYLVLP FLSPAVFGSV FGVAGVMVF LALDELXPAA KRYSDGHETV
 251 YGLTTGMAVI AVSLVLFHF*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2707>:

a901.seq

1 ATGCCCCGATT TTTGATGTC CAATTGCGC GTTGCCCTTT CCATTACGTT
 51 GGCTGCCGGT TTGTTTACCG TATTAGGCAG CGGCTTGGTG ATGTTTTCCT
 101 AAACCGCCAA TCCGCGCGTG TTGTCGTTTG GTTGCCATT TGCCGGCGGT
 151 GCGATGGTGT ATGTTTCCCT GACGGAGATT TTCAGTAAGT CCAGCGAGGC
 201 GTTCGCTGAA ATTTATGATA AAGACCACGC GTTGCGGCG GCGACCATGG
 251 CATTTTTGGC AGGGATGGGC GGCATTGCGC TGATTGACCG TCTGGTGCCG
 301 AACC CGCATG AACTTTAGA CGCGAAGAC CCGTCGTTT AAGAAAGCAA
 351 ACGCCGCCAT ATCGCGCGAG TCGGCATGAT GCGGCGGTTT GCGATTACTG
 401 CGACAATTT CCCGAAGGC TTGGCGACGT TTTTGCCAC ATGGAATAAT
 451 CCAGCAGTCG GGATGCCTTT GGCCTTGGCG ATTGCCATCC ATAATATPCC
 501 GGAGGGCATT TCCATCGCCG CGCGGTTTA TTTGCCACC CGCAGCCGTA
 551 AGAAACCGGT GTGGGCGTGT CTGCTATCCG GCTTGGCCGA GCCGTTGGGG
 601 GCGGCTTTGG GCTATTTGGT TTGCGAGCG TTTTGTGCG CTGCCGTGTT
 651 TGGTTCGGTA TTCGGCGTGA TAGCCGGTGT GATGGTGTG TTGGCGTTGG
 701 ACGAGCTGCT GCCGCTGCC AAACGCTATT CAGACGCCA TGAAACCGTT
 751 TACGGCCTGA CAATGGGCAT GCGGCTGATT GCCGTCAGCC TGGTATTGTT
 801 CCATTTTAA

This corresponds to the amino acid sequence <SEQ ID 2708; ORF 901.a>:

a901.pep

1 MPDFSMNLAVAFSITLAAG LETVLGSGLV MFSKTPNPRV LSFGLAFAGG
 51 AMVYVSLTEI FSKSSEAF AE IYDKDHAF AA ATMAFLAGMG GIALIDRLVP
 101 NPHETLDAQD PSFQESKRRH IARVGMMAAF AITAHNFPEG LATFFATLEN
 151 PAVGMPLALA IAIHNIPEGI SIAAPVYFAT RSRKKTWAC LLSGLAEPLG
 201 AALGYLVLP FLSPAVFGSV FGVAGVMVF LALDELLPAA KRYSDGHETV
 251 YGLTMGMAVI AVSLVLFHF*

m901/a901 98.9% identity in 269 aa overlap

m901.pep	10	20	30	40	50	60
	MPDFSMNLAVAFSITLAAGLETVLXSGLVMSKTPNPRVLSFGLAFAGGAMVYVSLTEI					
a901	10	20	30	40	50	60
	MPDFSMNLAVAFSITLAAGLETVLXSGLVMSKTPNPRVLSFGLAFAGGAMVYVSLTEI					
m901.pep	70	80	90	100	110	120
	FSKSSEAF AE IYDKDHAF AA ATMAFLAGMG GIALIDRLVP NPHETLCAQDPSFQESKRRH					
a901	70	80	90	100	110	120
	FSKSSEAF AE IYDKDHAF AA ATMAFLAGMG GIALIDRLVP NPHETLCAQDPSFQESKRRH					
m901.pep	130	140	150	160	170	180
	IARVGMMAFAITAHNFPEGLATFFATLENPAVGMPLALAIHNIPEGISIAAPVYFAT					
a901	130	140	150	160	170	180
	IARVGMMAFAITAHNFPEGLATFFATLENPAVGMPLALAIHNIPEGISIAAPVYFAT					
m901.pep	190	200	210	220	230	240
	RSRKKTWACLLSGLAEPLGAALGYLVLPFLSPAVFGSVFGVAGVMVFLALDELXPAA					
a901	190	200	210	220	230	240
	RSRKKTWACLLSGLAEPLGAALGYLVLPFLSPAVFGSVFGVAGVMVFLALDELLPAA					
m901.pep	250	260	270			
	KRYSDGHETVYGLTTGMAVIAVSLVLFHF					
a901	250	260	270			
	KRYSDGHETVYGLTMGMAVIAVSLVLFHF					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2709>:

g902.seq

```

1  ATGCCGTCCG AACCCGAACG GCGGCATGGC AATACTGCCC TACCCTTCCC
51  GATAGCCGCA CGCCCAACGG TCGTTTTTTC CGGCAAGCCT TTCAAGATAA
101 CCGGCAAGTG TGTCGTATTG CGCCGCCGCA TTGTCCAAGC GGTTGATTTT
151 ACGCCGCGCG TGTTGCGCGT CGGGCATTTC GCCGATGTAC CAGCCTATGT
201 GTTTGCGTGC GATGCGCACA CCGACGGTCT CACCATAAAA CGCGTGCATG
251 GCGCGGATGT GGTTCAAAAT GGCGGCTCTG CATTCTGCCA AACTCAAGGC
301 AGGCGGTAAA ACGCCGTGTT CGGCATAATG CTTCAAATCG CGGAAAAACC
351 ACGGCCTGCC TTGCGCGCCG CGCCCTATCA TGATGCCGTC GGCGGCGGTT
401 TGTTTGAGGA cggCGGCGGC TTTTgcggc GAagtGATGT CGCCGTTGac
451 cCaggCCGGG ATGTTCAgAc ggCTTTTGGT CTCGcgatg agttCGTAAC
501 gcGCCTCGCC TTTGTACATT TGCGTGcgCG CGcgccgtg aacgcaagGg
551 gcggaatgc cgcaatcttc ggcgatttg gcgacggcgG gcaggttttg
601 atcgctcgtc tgccaaccca AacggGTTTT GaggGTAAAG GGTAcgcCCG
651 CCGCCTTgac caccgcctcc aAAatggcGg caaccagcgg CTCGTCTGc
701 ATCagcGGC TACCGGCTTG GACGTTGCAC ACTTTcttgg cgggGCAGCC
751 CATattgATG TCGATGACCT GCGCCCGAG TCCGACGTTg taacgcgCG
801 catCCGCCAT CtgctcggGG TCGTGCcGG CAATCTGCAC GGCAACGATG
851 CCGccttcac cggcaAAAtc actgcggtgc aGGGTTTTTC CGGTATTCCT
901 GAGCGTCGGA TCGCTGGCCA GCATTTCGCA CACCGCCAA CCTGCGCCAA
951 ACGCCCGACA GAGGCGCGG AAGGGTTGT CGGCAATGCC CGCCATCGGC
1001 GCAAGTGCga TGGGTTGTC GATAAAATAA CCGCCGATGT GCATAATGGG
1051 CCCGCGTTTC AAAAAAGTGC GCCATTGTAC ATTTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2710; ORF 902.ng>:

g902.pep

```

1  MPSEPERRHG NTALPFPIAA RPTVGFSGKP FKITGKCVVL RRRIVQAVDF
51  TPRLFAVGHF ADVPAYVFAC DAHTDGLTIK RVHGADVQN GGSAPCQTQG
101 RR*NAVFIM LQIAEKPRPA LRAAPYHDAV GGGLFEDGG FLRRSDVAVD
151 PGRDVQTAFG LGDEFVTRLA FVHLRARAPV NGKGGNAIF GDFDGGQVL
201 IVVVPTQTGF EGNGYARRLD HRLQNGGNQR LVLHORATGL DVAHFLGGAA
251 HIDVDLRLPE SDVVTRRIRH LFGVAAGNLH GNDAAFIGKI TAVQFSGIP
301 ERRIAGQHFA HRPTCAKRPT EAAEGFVGNA RHRRKCDGVV DKITADVHNG
351 PAFQKSAPLY IF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2711>:

m902.seq

```

1  TTGCACITTC AAAGGATAAT CAAGTGTTCA GAAGGCATT TGGCGGTAGG
51  CGCACGCCCA ACTGTCGGTT TTTTCGGCAA GTCTTTCAAG ATAACCTGCA
101 AGCATGTCGT ATTGCGCCGC CGCACTGTCC AAGCGGTTGA TTTCACGACG
151 TgTCTgTTTC CCGTcGGGCA TTTCTGCGAT GTACCAGCCT ATGTGTTTGC
201 GTGCGATGCG CACACCGCGG GTGTGCGCGT AAAACGCGTG TATGGCGCGG
251 ATGTGTTTCA AAATAGCGGC GCGCATTCT GCCAACTCA AGGCAGGCGG
301 CAAAACACCG TGTTCGGCAT AATGTTTCAA ATCGCGGAAG AACCACGGCC
351 TGCCTTGCGC GCGCGCCCT ATCATAATGC CGTCGGCGGC GGTGTGTTTG
401 AGGACGGCTT GGGCTTTTTC CGGCGAAGTA ATGTCGCCGT TGACCCAGAC
451 CGGGATGTTT AGACGGCATT TGGTTTCGGC GATGAGTTTC TAACGCGCTT
501 CGCCTTTGTA CATTTGCGTA CGCGTGCGTC CGTGGACGGC AAGGGCGCGG
551 ATGCCGCAAT CTTCGCGCAT TTTGGCGATG ACGGGCAGGT TTTGATGTC
601 GTCGTGCCAA CCCAAACGGG TTTTGAGGGT AACGGGTACG CCTGCCGCAC
651 GGACGACGGC TTCCAAAATG GCGGCAACCA GCGGCTCGTT CTGCATCAGC
701 GCGCTACCGG CTTGGACAT TGCAGACTTT TTAGCGGGAC AGCCCATGTT
751 GATGTCGATA AGCTGCGCCC CAAGGCTGAC GTTGTAAACG GCGGCATCCG
801 CCATCTGCTG CGGATCGCTT CCGGCAATCT GCACGGCAAC AATGCCGCCT
851 TCATCGGCAA AATCGCTGCG GTGCAAGGTT TTTCTAGTAT TTTGAGCGT
901 CGGGTCGCTG GTCAGCATT GCGACACCG CCAACCTGCG CCAAAATCTC
951 GGGCAAAGTC GCGGAACGGT TTGTGCGTAA TGCCCGCAT CGGcGCaAGT
1001 GCGATGGGGT TGTCGATAAA ATAGCCGCG ATGTGCATAA TGGATCCGCG
1051 TTTCAAAAAA GTACGCCATT GTACATTTT TAA

```

This corresponds to the amino acid sequence <SEQ ID 2712; ORF 902>:

m902/q902

		10	20	30	40	50
m902.pep	LHFQRIIKCSEGIWAVGARPTVGFFGKSPKITCKHVVLLRRRTVQAVDFTTCLFAVGHF					
	:	:	:	:	:	:
g902	MPSEPERRHGNTALPFPPIAARPTVGFSGKPFKITGKCVVLLRRRIVQAVDFTPRLFAVGHF					
		10	20	30	40	50
						60
m902.pep	60	70	80	90	100	110
	VDVPAYVFACDAHTGGVAVKRVYGADVQNSGGAFQCTQGRRQNTVFGIMFQIAEEPRPA					
	:	:	:	:	:	:
g902	ADVPAVVFACDAHTDGLTIKRVHGADVQNSGGSAFCQCTQGRRXNAVFGIMLQIAEKPRPA					
		70	80	90	100	110
						120
m902.pep	120	130	140	150	160	170
	LRAAPYHNNAVGGGLFEDGLGLRRSNVAVDPDRDVQTAFFGFGDEFVTRFAFVHLRTRASV					
	:	:	:	:	:	:
g902	LRAAPYHDAVGGGLFEDGGGLRRSDVAVDPGRDVQTAFFGLGDEFVTRLAFVHLRARAPV					
		130	140	150	160	170
						180
m902.pep	180	190	200	210	220	230
	DGKGGDAAI FGD FGDGQVLNVVVPQTGTGFE GNGYACRTDDGFQNGGNQRLVLVHQ RATGL					
	:	:	:	:	:	:
g902	NGKGGNAAI FGD FGDGGQVLIVVVPQTGTGFE GNGYARRLDHRLQNGGNQRLVLVHQ RATGL					
		190	200	210	220	230
						240
m902.pep	240	250	260	270	280	290
	DIADFFSGTAHVVDVKLRPKADVTRGIRHLLRIASGNLHGNNAAFIGKIAAVQGFSSIS					
	:	:	:	:	:	:
g902	DVAHFLGGAHIDVDDL RPESDVVTRRI RHLFGVAAGNLHGNDAAFIGKITAVQGFSGIP					
		250	260	270	280	290
						300
m902.pep	300	310	320	330	340	350
	ERRVAGQHFAHRPTCAKISAKSAERFVGNARHRRKCDGVVDKIAADVHNHNGSAFQKSTPLY					
	:	:	:	:	:	:
g902	ERRIAGQHFAHRPTCAKRPTAAEGFVGNARHRRKCDGVVDKIADVHNHNGPAFQKSAPLY					
		310	320	330	340	350
						360
m902.pep	360					
	IFX					
g902	IFX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2713>:

a902.seq

```
1 TTGCACTTTC AAAGGATAAT CAAGTGTTCA GAAGGCATTT GGCGGGTAGG
51 CGCACGCCCC ACTGTCGETT TTTTCGGCAA GTCTTCAAG ATAACCTGCA
```


1288

```

101 AACATGTCGT ATTGCGCCGC CGCACTGTCC AAGCGGTTGA TTTCACGACG
151 TGTCTGTTTCG CCGTCGGGCA TTTCGTCGAT GTACCAGCCT ATGTGTTTGC
201 GTGCGATGCG CACACCGGCG GTGTCGCCGT AAAACGCGTG CATGGCTCGG
251 ATGTGTTTCA AAATAGTGGC GGTACATTCT GCCAACTCA AGGCAGGCGG
301 TAAACACCGG TGTTGGGCGT AATGTTTCAA ATCGCGGAAG AACCACGGTC
351 TGCTTGGGCG GCCGCGCCCT ATCATAATGC CGTCTGGGCG GGTGTTTGTG
401 AGGACGGCCTT GGGCTTTTTG CGGCGAGGTA ATGTCGCCGT TGACCCAGAC
451 CGGGATGTTT AGACGGCATT TGGTTTCGGC AATCAGGTCG TAAGCCGCTT
501 CGCCTTTGTA CATTGCGTG CGCGTGCGTC CGTGGACGGC AAGGGCGGCA
551 ATGCCGCAAT CTTCGGCGAT TTTGGCGATG ACGGGCAGGT TTTGATGGTC
601 GTCGTGCCAA CCCAACGGG TTTTGAGGGT AACGGGTACG CCCGCCGCTT
651 TGACCACCGC CTCCAAATG GCGCAACCA GCGGCTCGTT CTGCATCAGC
701 CGCCTTACCG CTGGACATT GCAGACTTTT TTAGCGGGAC AGCCCATGTT
751 GATGTCGATA AGCTGCGCCC CAAGGCTGAC GTTGTAACGC CGGCATCCG
801 CCATCTGCTG CGGATCGCTT CCGCAATCT GCACGGCAAC AATGCCGCCT
851 TCATCGGCAA AATCGCTGCG GTGCAAGGTT TTTCTAGTAT TTCTGAGCGT
901 CGGTCGCTG GTCAGCATT CGCACACCG CCAACCTGCG CCAAATCTC
951 GGCAAGTCG GCGGAACGGT TTGTCGGTAA TGCCCGCCAT CGGCGCAAGT
1001 GCGATGGGGT TGTGATAAA ATAGCCGCCG ATGTGCATAA TGGATCCGCG
1051 TTTCAAAAAA GTACGCCATT GTACATTTT TAA

```

This corresponds to the amino acid sequence <SEQ ID 2714; ORF 902.a>:

a902.pep

```

1 LHFQRIIKCS EGIWAVGARP TVGFFGKSFK ITCKHVVLRR RTVQAVDFTT
51 CLFAVGHFVD VPAYVFACDA HTGGVAVKRV HGSDVVQNSG GTFQCQTQGRR
101 *NTVFGVMFQ IAEPRSAALR AAPYHNAVCG GLFEDGLGFL RRGNVAVDPD
151 RDVQTAFGFG NQVVSRAFAV HLRARASVDG KGGNAIFGD FGDDGQVLMV
201 VVPTQTGFEG NGYARRFDHR LQNGGNQRLV LQQRATGLDI ADFFSGTAHV
251 DVDKLRPKAD VVTRGIRHLL RIASGNLHGN NAAFIGKIAA VQGFSSISER
301 RVAGQHFAHR PTCAKISAKS AERFVGNAHR RRKCDGVVDK IAADVHNGSA
351 FQKSTPLYIF *

```

m902/a902 94.7% identity in 360 aa overlap

	10	20	30	40	50	60
m902.pep	LHFQRIIKCS	EGIWAVGARPT	TVGFFGKSFK	ITCKHVVLRRRT	VQAVDFTTCL	FAVGHFVD
a902	LHFQRIIKCS	EGIWAVGARPT	TVGFFGKSFK	ITCKHVVLRRRT	VQAVDFTTCL	FAVGHFVD
	10	20	30	40	50	60
	70	80	90	100	110	120
m902.pep	VPAYVFACDA	HTGGVAVKRV	GADVQNSG	AFQCQTQGR	RQNTVFGIM	FQIAEPRPALR
a902	VPAYVFACDA	HTGGVAVKRV	HGSDVVQNS	GTFQCQTQ	GRXNTVFG	VMFQIAEPRSA
	70	80	90	100	110	120
	130	140	150	160	170	180
m902.pep	AAPYHNAV	GGGLFEDGL	FLRRSNVAV	DPDRDVQT	AFGFGDEF	VTFRFAFVHLR
a902	AAPYHNAV	GGGLFEDGL	FLRRSNVAV	DPDRDVQT	AFGFGN	QVVSRAFAFVHL
	130	140	150	160	170	180
	190	200	210	220	230	240
m902.pep	KGGDAAI	FGDFGDDG	QVLMVVVPT	QTGFEGNG	YACRTDDG	FQNGGNQRLV
a902	KGGNAAI	FGDFGDDG	QVLMVVVPT	QTGFEGNG	YARRFDHRL	QNGGNQRLV
	190	200	210	220	230	240
	250	260	270	280	290	300
m902.pep	ADFFSGTA	HVDVDKLR	PKADVVT	TRGIRHLL	RIASGNLH	GNNAAFI
a902	ADFFSGTA	HVDVDKLR	PKADVVT	TRGIRHLL	RIASGNLH	GNNAAFI
	250	260	270	280	290	300
	310	320	330	340	350	360
m902.pep	RVAGQHFA	HRPTCAK	ISAKSAER	FVGNAHR	RRKCDGV	VDKIAADV

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```

|||||
a902      RVAGQHFAHRPTCAKISAKSAERFVGNARHRRKCDGVVDKIAADVHNGSAFQKSTPLYIF
              310      320      330      340      350      360

m902.pep      X
                |
a902           X

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2715>:

```

g903.seq
1  ATGGCAACAC AGGTAGGCGG TGCAAattcG gatgaggCAA GCCCCTGCTT
51 TCCTATTTCT GAGGTGGAaT TGGTGGGTGA aGaaacggct aaATTCCGgt
101 tTGCCTcaaa ccaTGCCTTG tgccAAACAC ATTTTGtttc cGgcaagtgt
151 CTGcATGcgg gcgacatTAA TCAAAtcaTG TCCTTAGCAC AAAATGCTTT
201 GATCGGCAGG GGATATACCA CGACCCGTAT CTTGGCTGCG CCACAGGATT
251 TGAATAGTGG caaGCTTCAA TTAaccctga tgccggGCTA TCtgcgctcc
301 ATAcgaATCG atcgggtccaa cgatgatcaa ACCCATgcAG GACGTATTGC
351 AGCATTCCAA AACAAATTTC CCACCCGCTC GAACGATCTG TTGAATCTGC
401 GTGATTGGGA ACAAGGACTG GAAAATCTCA AATGTCTCCC GACTGCGGAA
451 GCCGATCTCC AAATCgttcc cgtAGAGAGA GAACcAAACC AAAGTGATGT
501 CGTGGTGCAA TGGCGGTAAC GTCTGCTGCC CTACTGTGTG AGTGTGGGA
551 TGGATAATTC GGGTAGTGAG GCGACAGGAA AATACCAAGG AAATATCACT
601 TTCTCTGCGG ACAATCCTTT TggactgAGT GATATGTTCT ATGTAAATTA
651 TGGACGTTCA ATTGGCGGTA CGcccgATGA GGAAAATTTT GACGGCCATC
701 GCAAAGAAGG CGGATCAAAC AATTACGCCG TACATTATTC AGCCCCTTTC
751 GGTAATGGA CATGGGCATT CAATCACAAT GGCTACCGTT ACCATCAGGC
801 GGTTCGGA TTATCGGAAG TCTATGACTA TAATGGAAAA AGTTACAACA
851 CTGATTTGGG CTCAACCGC CTGTTGTATC GTGATGCCAA ACGCAAAACC
901 TATCTCAGTG TAAAACGTG GACGAGGGAA ACAAAAAGTT ACATTGATGA
951 TGCCGAAC TGCTGACAAC GGCCTAAAC CACAGGTTGG TTGGCAGAAC
1001 TTTCCCAAA AGGATATATC GGTCGCAGTA CGGCAGATT TAAGTTGAAA
1051 TATAACACG GCACCGGCAT GAAAGATGCT CTGCGCGCGC CTGAAGAAGC
1101 CTTTGCGGAA GGCACGTCAC GTATGAAAT TTGGACGGCA TCGGCTGATG
1151 TAAATACTCC TTTTCAAATC GGTAAACAGC TATTTGCCTA TGACACATCC
1201 GTTCATGCAC AATGGAACAA AACCCCGCTA ACATCGCAAG ACAAACTGGC
1251 TATCGGCGGA CACCACCCG TACGTGGCTT CGACGGTGAA ATGAGTTTGC
1301 CTGCCGAGCG GGGATGGTAT TGGCGCAACG ATTTGAGCTG GCAATTAA
1351 CCAGGCCATC AGCTTTATCT TGGGGCTGAT GTAGGACATG TTTCAAGACA
1401 ATCCGCCAAA TGGTTATCGG GCCAACTCT AGCCGGCACA GCAATTGGGA
1451 TACGCGGGCA GATAAAGCTT GGCGGCAACC TGCATTACGA TATATTACC
1501 GGCCGTGCAT TGAAGAAGCC cgaatatatt cAGACGAAGA Aatgggtaac
1551 ggggtTCAG gtgggttatt cgTTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2716; ORF 903.ng>:

```

g903.pep
1  MATQVGANS DEASPCFPIS EVELVGEETA KFRFALNHAL CQTHFVSGKC
51 LHAGDINQIM SLAQNALIGR GYTTTRILAA PDLNSGKLQ LTLMPGYLRS
101 IRIDRSNDDQ THAGRIAAFQ NKFPTRNDL LNLRDLEQGL ENLKCLPTAE
151 ADLQIVPVER EPNQSDVVVQ WRXRLPYCV SVGMDNSGSE ATGKYQGNIT
201 FSADNPFGLS DMFYVNYGRS IGGTPDEENF DHRKEGGSN NYAVHYSAPF
251 GKWTWAFNHN GYRYHQAIVSG LSEVYDINGK SYNTDFGFNR LLYRDAKRKT
301 YLSVKLWTRT KSYIDDAEL TVQRRKTGW LAELSHKGYI GRSTADFKLK
351 YKHGTGMKDA LRAPEEAFGE GTSRMKIWTA SADVNTPFQI GKQLFAYDTS
401 VHAQWNKTPL TSQDKLAIIG HHTVRGFDGE MSLPAERGWE WRNDSWQFK
451 PGHQLYLGAD VGHVSGQSAK WLSGQTLAGT AIGIRGQIKL GGNLHYDIPT
501 GRALKKPEYF QTKKWTGFPQ VGYSF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2717>:

```

m903.seq
1  ATGCAGCGTC AGCAGCACAT AGATGCTGAA TTGTAACTG ATGCAAATGT
51 CCGTTTCGAG CAACCATGG AGAAGAACAA TTATGTCCTG ACTGAAGATG
101 AAACACCGTG TACTCGGTA AATTACATTA GTTTAGATGA TAAGACGGTG

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151 CGCAAATTTT CTTTCTTCC TTCTGTGCTC ATGAAAGAAA CAGCTTTTAA
201 AACTGGGATG TGTTTAGGTT CCAATAATTT GAGCAGGCTA CAAAAAGCCG
251 CGCAACAGAT ACTGATCGTG CGTGGCTACC TCACTTCCCA AGCTATTATC
301 CAaCCACAGA ATATGGATTG GGAATTCTG AAATTACGGG TATCAGCAGG
351 CGAAATAGGG GATATCCGCT ATGAAGAAAA ACGGGATGGG AAGTCTGCCG
401 AGGGCAGTAT TAGTGCAATC AATAACAAAT TTCCCTTATA TAGGAACAAA
451 ATTCTCAATC TTCGCGATGT AGAGCAGGGC TTGGAACC TGCGTCGTTT
501 GCCGAGTGT AAAACAGATA TTCAGATTAT ACCGTCCGAA GAAGAAGGCA
551 AAAGCGATTT ACAGATCAAA TGGCAGCAGA ATAAACCCAT ACGGTTCAGT
601 ATCGGTATAG ATGATGCGGG CGGCAAAACG ACCGGCAAAT ATCAAGGAAA
651 TGTGCTTTA TCGTTCGATA ACCCTTTGGG CTTAAGCGAT TTGTTtTATG
701 TTTTCATATG ACGCGGTTTG GCGCACAAA CGGACTTGAC TGATGCCACC
751 GGTACGGAAA CTGAAAGCGG ATCCAGAAGT TACAGCGTGC ATTATTGCGT
801 GCCCGTAAAA AAATGGCTGT TTCTTTTAA TCACAATGGA CATCGTTACC
851 ACGAAGCAAC CGAAGGCTAT TCCGTCAATT ACGATTACAA CGGCAACAAA
901 TATCAGAGCA GCCTGGCCGC CGAGCGCATG CTTTGGCGTA ACAGACTTCA
951 TAAAACTTCA GTCGAATGA AATTATGAC ACGCCAAACC TATAAATACA
1001 TCGACGATGC CGAAATCGAA GTACAACGCC GCCGCTCTGC AGGCTGGGAA
1051 GCCGAATTGC GCCACCGTGC TTACCTCAAC CGTTGGCAGC TTGACGGCAA
1101 GTTGTCTTAC AAACGCGGGA CCGGCATGCG CCAAAGTAGT CCTGCACCGG
1151 AAGAAAACGG CGGCGATATT CTTCAGGTA CATCTCGTAT GAAAATCATT
1201 ACTGCCAGTT TGGACGCAGC CGCCCCATTT AyTTTAGGCA AACAGCAGTT
1251 TTTCTACGCA ACCGCCATTC AAGCTCAATG GAACAAAACG CCGTTGGTTG
1301 CCCAAGATAA ATTGTCAATC GGCAGCCGCT ACACCGTTCG CGGATTTGAT
1351 GGGGAGCAGA GTCTTTTCGG AGAGCGAGGT TTCTACTGGC AGAATACTTT
1401 AACTTGGTAT TTTCATCCGA ACCATCAGTT CTATCTCGGT GCGGACTATG
1451 GCCGCGTATC TGGCGAAAGT GCACAATATG TATCGGGCAA GCAGCTGATG
1501 GGTGCAGTGG TCGGCTTCAG AGGAGGGCAT AAAGTAGGCG GTATGTTTGC
1551 TTATGATCTG TTGCGCGCA AGCCGCTTCA TAAACCCAAA GGCTTTCAGA
1601 CGACCAACAC CGTTTACGGC TCAACTTGA ATTACAGTTT CTAA

```

This corresponds to the amino acid sequence <SEQ ID 2718; ORF 903>:

```

m903.pep
1  MQRQQHIDAE LLTDANVRFE QPLEKNNYVL SEDETPCTRV NYISLDDKTV
51  RKFSFLPSVL MKETAFKTGM CLGSNNLSRL OKAAQQILIV RGYLTSQAI
101 QPONMDSGIL KLRVSAGEIG DIRYEKRDG KSAEGSISAF NKNFPLYRNN
151 ILNLRDVEQG LENLRLPSV KTDIQUIPSE BEGKSDLQIK WQONKPIRFS
201 IGIDDAGGKT TGKYQGNVAL SFDNPLGLSD LFYVSYGRGL AHKTDLTDAT
251 GTETESGSR S YSVHYSVPVK KWLFSFNHNG HRYHEATEGY SVNYDYNKQ
301 YQSSLAERM LWRNRLHKTS VGMKLWTRQT YKYIDDABIE VQRRRSAGWE
351 AELRHAYLN RWQLDGKLSY KRGTMRQSM PAPEENGDDI LPGTSRMKII
401 TASLDAAPF XLGKQFFYA TAIQAQWNKT PLVAQDKLSI GSRYTVRGFD
451 GEQSLFGERG FYWQNTLTWY FHPNHQFYL ADYGRVSGES AQYVSGKQLM
501 GAVVGRGGH KVGGMFAYDL FAGKPLHKPK GFQTTNTVYG FNLNYSF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 903 shows 48.9% identity over a 519 aa overlap with a predicted ORF (ORF 903.ng) from *N. gonorrhoeae*:

```

m903/g903
          10      20      30      40      50      60
m903.pep  MQRQQHIDAE LLTDANVRFE QPLEKNNYVL SEDETPCTRV NYISLDDKTV RKFSFLPSVL
          |:::| |:::| |:::| |:::| |:::|
g903      MATQVGGANSDEASPCFPISEVELVGEETAKFRFALNHA
          10      20      30
          70      80      90      100     110     120
m903.pep  MKETAFKTGMCLGSNNLSRLQKAAQQILIVRGYLT SQAIIPQNMDSGILKLRVSAGEIG
          : : | | | | : : : : : : : : : : : : : : : : : :
g903      LCQTHFVSGKCLHAGDINQIMSLAQNALIGRGYTTTRILAAPQDLNSGKQLQLTLMPGYLR
          40      50      60      70      80      90

```

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	130	140	150	160	170	180
m903.pep	DIRYEEKRDGKSAEGSISAFNNKFPLYRNKILNLRDVEQGLENLRLPSVKTIDIQIIPSE					
	: : : : : : : : : : : : : : : :					
g903	SIRIDRSNDDQTHAGRIAAFQNKFPTRSNLLNLRDLEQGLENLKCLPTAEADLQIVPVE					
	100	110	120	130	140	150
	190	200	210	220	230	
m903.pep	EE-GKSDLQIKWQONK-PIRFSIGIDDAGGKTTGKYQGNVALSFDNPLGLSDFVVSYGR					
	: : : : : : : : : : : : : : :					
g903	REPNSQSDVVVQWRXRLLPYCVSVGMDNSGSEATGKYQGNITFSADNPFGLSDMFYVNYGR					
	160	170	180	190	200	210
	240	250	260	270	280	290
m903.pep	GLAHKTDLTDATGTETESGSRYSVHYSPVVKWLFSPFNHNGHRYHEATEGYSVNYDYNG					
	: : : : : : : : : : :					
g903	SIGGTPDEENFDGHRKEGGSNNYAVHYSAPFGKWTWAFNHNHGYRYHQAVSGLSEVYDYNG					
	220	230	240	250	260	270
	300	310	320	330	340	350
m903.pep	KQYQSSLAERMLWRNRLHKTSSVGMKWLTRQTYKYIDDAEIEVQRRRSAGWEAELRHRAY					
	: : : : : : : : : : : : : : : :					
g903	KSYNTDFGFNRLLYRDAKRKTYLSVKLWTRETKSYIDDAELTVQRRKTTGWLAE LSHKGY					
	280	290	300	310	320	330
	360	370	380	390	400	410
m903.pep	LNRWQLDGLSYKRGTMQRQSMPEENGDDILPGTSMKIIITASLDAAAPFXLGKQQFF					
	: : : : : : : : : : :					
g903	IGRSTADFKLKYKHGTGMKDALARAPEEAFGE--GTSRMKIWTASADVNTPFQIGKQLFA					
	340	350	360	370	380	390
	420	430	440	450	460	470
m903.pep	YATAIQAWNKTPLVADKLSIGSRYTVRGFDGEOSLFGERGFYWQNTLTWYFHPNHQFY					
	: : : : : : : : : : : :					
g903	YDTSVHAQWNKTPLTSDQDKLAIGGHHTVRGFDGEMSLPAERGWYWRNDLSWQPKPGHQLY					
	400	410	420	430	440	450
	480	490	500	510	520	530
m903.pep	LGADYGRVSGESAQYVSGKQLMGAVVGFRGGHKVGGMFAYDLFAGKPLHKPKGFQTTNTV					
	: : : : : : : : : : : :					
g903	LGADVGHVSGQSAKWLSGQTLAGTAIGRQIKLGGNLHYDIFTGRALKKPEYFQTKKWV					
	460	470	480	490	500	510
	540					
m903.pep	YGFNLNYSFX					
	: :					
g903	TGFQVGYSFX					
	520					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2719>:

a903.seq

1	ATGCAGCGTC	AGCAGCACAT	AGATGCTGAA	TTGTAACTG	ATGCAAATGT
51	CCGTTTCGAG	CAACCATTGG	AGAAGAACAA	TTATGTCCTG	AGTGAAGATG
101	AAACACCGTG	TACTCGGGTA	AATTACATTA	GTTTAGATGA	TAAGACGGCG
151	CGCAAATTTT	CTTTCTTCC	TTCTGTGCTC	ATGAAAGAAA	CAGCTTTTAA
201	AACTGGGATG	TGTTTAGGTT	CCAATAATTT	GAGCAGGCTA	CAAAAAGCCG
251	CGCAACAGAT	ACTGATTGTG	CGTGGCTACC	TCACCTCCCA	AGCTATTATC
301	CAACCACAGA	ATATGGATTC	GGGAATCTCG	AAATTACGGG	TATCAGCAGG
351	CGAAATAGGG	GATATCCGCT	ATGAAGAAAA	ACGGGATGGG	AAGTCGCCG
401	AGGGCAGTAT	TACTGCATTC	AATAACAAAT	TTCCCTTATA	TAGGAACAAA
451	ATTCTCAATC	TTGCGCATGT	AGAGCAGGGC	TTGGAAGAAC	TGCGTCGTTT
501	GCCGAGTGTT	AAAACAGATA	TTCAGATTAT	ACCGTCCGAA	GAAGAAGGCA
551	AAAGCGATTT	ACAGATCAAA	TGGCAGCAGA	ATAAACCCAT	ACGGTTCAGT

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601 ATCGGTATAG ATGATGCGGG CGGCAAAACG ACCGGCAAAT ATCAAGGAAA
651 TGTCGCTTTA TCGTTCGATA ACCCTTTGGG CTTAAGCGAT TTGTTTTATG
701 TTTCATATGG ACGCGGTTTG GTGCACAAA CGGACTTGAC TGATGCCACC
751 GGTACGGAAA CTGAAAGCGG ATCCAGAAGT TACAGCGTGC ATTATTCGGT
801 GCCCGTAAAA AAATGGCTGT TTTCTTTTAA TCACAATGGA CATCGTTACC
851 ACGAAGCAAC CGAAGGCTAT TCCGTCAATT ACGATTACAA CGGCAAAACAA
901 TATCAGAGCA GCCTGGCCGC CGAGCGCATG CTTTGGCGTA ACAGGTTTCA
951 TAAAACTTCA GTCGGAATGA AATTATGGAC ACGCCAAACC TATAAATACA
1001 TCGACGATGC CGAAATCGAA GTGCAACGCC GCCGCTCTGC AGGCTGGGAA
1051 GCCGAATTGC GCCACCGTGC TTACCTCAAC CGTTGGCAGC TTGACGGCAA
1101 GTTGTCTTAC AAACGCGGGA CCGGCATGCG CCAAAGTATG CCCGCACCTG
1151 AAGAAAACGG CGCGGCTACT ATTCCAGGCA CATCCCGTAT GAAAATCATA
1201 ACCGCGGAT TGGATGCAGC GGCCCCGTTT ATGTTGGGCA AACAGCAGTT
1251 TTTCTACGCA ACCGCCATTC AAGCTCAATG GAACAAAACG CCTTTGGTTG
1301 CCAAGACAA GTTGTCTATC GGCAGCCGCT ACACCGTTNG CGGATTTGAT
1351 GGGAGCAGA GTCTTTTCGG AGAGCGAGGT TTCTACTGGC AGAATACTTT
1401 AACTTGGTAT TTTCATCCGA ACCATCAGTT CTATCTCGGT GCGGACTATG
1451 GCCGCGTATC TGGCGAAAAGT GCACAATATG TATCGGGCAA GCAGCTGATG
1501 GGTGCAGTGG TCGGNTTCAG AGGAGGNCAT AAAGTAGGCG GTATGTTTGC
1551 TTATGATCTG TTTGCCGGCA AGCCGCTTCA TAAACCCAAA GGCTTTCAGA
1601 CGACCAACAC CGTTTACGGC TTCAACTTGA ATTACAGTTT CTAA

```

This corresponds to the amino acid sequence <SEQ ID 2720; ORF 903.a>:

a903 .pep

```

1 MQRQQHIDAE LLTDANVRFE QPLEKNYVL SEDETPCTRV NYISLDDKTA
51 RKFSFLPSVL MKETAFTKGM CLGSNNLSRL QKAAQQILIV RGYLTSQAI
101 QPQNMDSGIL KLRVSAGEIG DIRYEEKRDG KSAEGSISAF NKFPLYRNK
151 ILNLRDVEQG LENLRLPSV KTDIQUIPSE EEGKSDLQIK WQONKEIRFS
201 IGIDTAGGKT TGKYQGNVAL SFDNPLGLSD LFYVSYGRGL VHKTDLTDAT
251 GTETESGSR SSVHYSPVK KWLFSFNHNG HRYHEATEGY SVNYDYNKGQ
301 YQSSLAERM LWRNRFHKT VGMKLWTRQT KYIDDAEIE VQRRRSAGWE
351 AELRHRAYLN RWQLDGKLSY KRGTGMRQSM PAPEENGSGT IPGTSRMKII
401 TAGLDAAAF MLGKQQFFYA TAIQAQWNKT PLVAQDKLSI GSRYTVXGFD
451 GEQSLFGERG FYWQNTLTWY FHPNHQFYLG ADYGRVSGES AQYVSGKQLM
501 GAVVGFRRGH KVGGMFAYDL FAGKPLHKPK GFQTTNTVYG FNLNYSF*

```

m903/a903 98.4% identity in 547 aa overlap

	10	20	30	40	50	60
m903 .pep	MQRQQHIDAE	LLTDANVRFE	QPLEKNYVL	SEDETPCTRV	NYISLDDKTV	RKFSFLPSVL
a903	MQRQQHIDAE	LLTDANVRFE	QPLEKNYVL	SEDETPCTRV	NYISLDDKTAR	KFSFLPSVL
	10	20	30	40	50	60
m903 .pep	70	80	90	100	110	120
m903 .pep	MKETAFKTM	CLGSNNLSRL	QKAAQQILIV	RGYLTSAII	QPQNMDSGIL	KLRVSAGEIG
a903	MKETAFKTM	CLGSNNLSRL	QKAAQQILIV	RGYLTSAII	QPQNMDSGIL	KLRVSAGEIG
	70	80	90	100	110	120
m903 .pep	130	140	150	160	170	180
m903 .pep	DIRYEEKRDG	KSAEGSISAF	NKFPLYRNK	ILNLRDVEQ	LENLRLPSV	KTDIQUIPSE
a903	DIRYEEKRDG	KSAEGSISAF	NKFPLYRNK	ILNLRDVEQ	LENLRLPSV	KTDIQUIPSE
	130	140	150	160	170	180
m903 .pep	190	200	210	220	230	240
m903 .pep	EEGKSDLQIK	WQONKEIRFS	IGIDTAGGKT	TGKYQGNVAL	SFDNPLGLSD	LFYVSYGRGL
a903	EEGKSDLQIK	WQONKEIRFS	IGIDTAGGKT	TGKYQGNVAL	SFDNPLGLSD	LFYVSYGRGL
	190	200	210	220	230	240
m903 .pep	250	260	270	280	290	300
m903 .pep	AHKTDLTDAT	GTETESGSR	SSVHYSPVK	KWLFSFNHNG	HRHYHEATEG	SVNYDYNKGQ
a903	VHKTDLTDAT	GTETESGSR	SSVHYSPVK	KWLFSFNHNG	HRHYHEATEG	SVNYDYNKGQ

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	250	260	270	280	290	300
	310	320	330	340	350	360
m903.pep	YQSSSLAAERMLWRNRLHKT SVGMKLWTRQTYKYIDDAEIEVQRRRSAGWEAELRHRAYLN					
a903	YQSSSLAAERMLWRNRFHKT SVGMKLWTRQTYKYIDDAEIEVQRRRSAGWEAELRHRAYLN					
	310	320	330	340	350	360
	370	380	390	400	410	420
m903.pep	RWQLDGKLSYKRGTGMRQSMPEENG DILPGTSRMKIITASLDAAAPFXLGKQQFFYA					
a903	RWQLDGKLSYKRGTGMRQSMPEENG GGTIPGTSRMKIITAGLDAAAPFMLGKQQFFYA					
	370	380	390	400	410	420
	430	440	450	460	470	480
m903.pep	TAIQAQWNKTPLVAQDKLSIGSRYTVRGFDGEQSLFGERGFYWQNTLTWYFHPNHQFYLG					
a903	TAIQAQWNKTPLVAQDKLSIGSRYTVXGFDGEQSLFGERGFYWQNTLTWYFHPNHQFYLG					
	430	440	450	460	470	480
	490	500	510	520	530	540
m903.pep	ADYGRVSGESAQYVSGKQLMGAVVGFRRGHKVGGMFAYDLFAGKPLHKPKGFQTTNTVYG					
a903	ADYGRVSGESAQYVSGKQLMGAVVGFRRGHKVGGMFAYDLFAGKPLHKPKGFQTTNTVYG					
	490	500	510	520	530	540
m903.pep	ENLNYSFX					
a903	ENLNYSFX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2721>:

g904.seq

```

1  ATGATGCAGC ACAATCGTTT CTTCGCGGTC GGGGCCGGTg gaGACGATGG
51  CGACCGGCGC GCGCAGACT TCTTCAATCC GTTTCAAATA TGCTTTGGCA
101 TTGGCAGGCA ATGCGTCGTA GCTTTTCACG CCGACAGTCG ATTCGCGCCA
151 GCCGGGCATG GTTTCGTAAA TCGGTTTGCA GGTTCACACC GCATCCGAAC
201 CGCAAGGCAG GATGTCGGTT TTGCCGCCGC CTGGCAATTC GTAGCCGACG
251 CAGATATTGA TGGTTTCAAC GCCGTCCATT ACATCGAGTT TGGTAATGCA
301 CATACCGGAA ATGCCGTTGA TTTGGATGGA GCGTTTCAGG GCGGCGGCAT
351 CAAACCAGCC GCAGCGGCGC GCGCGGCCGG TTACCGAACC GAATTCGTGT
401 CCGCGCTCCG CCAAACCTGC GCCTACTTCG TCGAACAAAT CGGTCCGGAA
451 CGGGCCCGAA CCGACGCCCG TGGTATAGGC TTGACGATG CCCAAACAT
501 AATCCAGCAT TTGAGGACCT ACGCCCGCGC CTGCCGAAGC CGCGCCGGCG
551 AGACAGTTGG ACGAGGTAAC GAAGGGGTAA GTGCCGTAGT CGATGTCCAA
601 CAACGCACCT TGC CGCCTT CAAACAGCAG TTTTTCGCCG TTTTGTGTTT
651 TTTCGTTCAA CACGCgggaC acgtcgGCAA TCATCGGCGC AATGCGCGGC
701 GCGACTTTT CGATAACCGC CATCACGTCT TCCGCTTTAA CCGGTCCGGC
751 GTTATGCAGG TATTGGAGTT GGACGTTGTA ATAGGCAAGG ACGGCATCCA
801 GTTTTTCACG CAGTTTTTCA GGATGCAGCA AATCGCGCGC GCGAATGGCG
851 CGGCGTGCCA CTTTGTCTTC GTAGGCAGGG CCGATGCCGC GGCCGTCGT
901 GCCGATTTTG CCTTTGCCGC GCGATGCTTC GCGGGCTTGG TCGAGCGCGA
951 TGTGGTAAGG CAGGATCAGC GGGCAGGTCG GCGCGATTTT CAGACGGCCT
1001 TCGACGTTTT TCACGCCCTGC CGCGTTCAAC TCGTCGATTT CGCCCAACAG
1051 GGCTTCGGGg gaaacgAcaa cGCCCCAACC gatGAAGCAA TCCAATCCTT
1101 CGTGCCAGGAT ACCGCTCGGA ATCAGGCGCA AAATGGTTTT TTTGCCGCCG
1151 ACGACCAAGG TATGCCCCGC ATTGTGGCCG CCTTGAAGC GCACgacGct
1201 gCCGGCTTCT TCCGCCAGCC AGTCAACGAT TTTACCTTTA CCCTCGTCGC
1251 CCCACTGTgc gccGATTACT ACAACATTTT TAGCCATAGC CATATAACCT
1301 ATCGatatTA A

```

This corresponds to the amino acid sequence <SEQ ID 2722; ORF 904.ng>:

g904.pep

```

1  MMQHNREFFAV GAGGDDGDRR AADFFNPFQI CFGIGRQCVV AFHADS RFAP

```

1294

```

51  AGHGFVNRFA GFHRIRTARQ DVGFAAAWQF VADADIDGFN AVHYIEFGNA
101 HTGNAVDLDG AFQGGGIKPA AAARAAGYRT EFVSALRQTC AYFVEQFGRE
151 RARTDARGIG FDDAQNI IQH LRTYARACRS RAGETVGRGN EGSAVVDVQ
201 QRTLRAFQKQ FFAVFVFFVQ HAGHVGNHRR NARRDFFDNR HHVFRFNRSR
251 VMQVLELDV IGKDGIOFFT QFFRMQIQG ANGAACHFVF VGRADAAAGR
301 ADFAFARCF AGLVERDVVR QDQAGRRDF QTAFDVFHAC RVQLVDFAAQ
351 GFGGNDNART DEAIQSFVQD TARNQAQNGF FAADDQGMAR IVAALEAHDA
401 AGFFRQPVND FTFTLVAPLC ADYYNIFSHS HITYRY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2723>:

m904.seq

```

1  ATGATGCAGC ACAATCGTTT CTTCTCGGTC GGGGCCGgTG GAGACGATGG
51  CGACCGGGCG GCCGCAGACT TCTTCAATCC GTTCAAATA TGCTTTGGCG
101 TTTTCGGGCA ATGCGCCGTA GTCCTTCACG CCGAAAGTGG ATTCGCGCCA
151 GCCGGGCATG GTTTCGTAAA TCGGCTTGCA GGTTCACACC GCATCGGAAC
201 CGCAAGGCAG GATGTCGGTT TTGCCGCGT CGGGCAATTC ATAGCCGACG
251 CAGATATTGA TGGTTTCAAC GCCGTCCATT ACATCGAGTT TAGTAATACA
301 CATACCGGAA ATGCCGTTGA TTTGGATGGA GCGTTTCAGG GCGGCGGCAT
351 CAAACAGACC GCAGCGGCGT GCGCGTCCG TTACCGAACC GAATTCGTGT
401 CCGCGTTCTG CCAAACCTAC GCCTACTTCG TCGAACCAAT CGGTGCGGAA
451 CCGGCCCCGA CCGACGCGCG TGGTATAGGC TTGACGATG CCCAAACAT
501 AATCCAGCAT TTGAGGACCT ACGCCCGCGC CTGCCCAAGC TGCGCCCGCC
551 AGACAGTTGG ACGAGGTAAC GAAGGGATAA GTGCCGTAGT CGATGTCCAA
601 CAACGCACCT TCGCGGCTT CAAACAGCAG TTTTTCGCGG TTTTGTGTTT
651 TCTCGTTCAA CACGCGGGAC ACGTCGGTAA TCATCGGCGC AATGCGCGGC
701 GCGACTTTTT CGATAACGCG CATCACGTCT TCCGCTTAA CCGGCTCGGC
751 ATTGTGCAGA TGTGTCAGTT GGACATTGTA ATAGGCAAGG ACGGCATCCA
801 GTTTTTCACG CAGTTTtTCA GGATGCAGCA AATCGGCGGC GCGAATGGCG
851 CGGCGTGCCA CTTGTCTTC GTAGGAGGG CCGATGCCGC GGCCGGTCGT
901 GCCGATTTTG CCTTGCCGC GCG.ATcTTC GCGGGCTTGG TCGAGCGCGA
951 TGTGGTAAGG CAGGATCAGC GGGCAGGTCG GCGCGATTTT CAGACGGCCT
1001 TCACGTTTTT TCACGCTGC CCGGTTCAAC TCGTCGATTT CGCCCAACAG
1051 GGCTTCGGGG GAGACGACAA CGCCGAACC GATGAAGCAG TCCAACTTT
1101 CATGCAGGAT GCCGCTCGGA ATCAGGCGCA AAATGGTTT TTTGCCGCG
1151 ACAACCAAGG TATGGCCCGC ATTGTGGCCG CCTTGGAGC GCACCAAGCC
1201 GCCGGCTTCT TCCGCCAGCC AGTCAACGAT TTTACCTTTA CCCTCGTCGC
1251 CCCACTGTGC GCCGATTast ACAACATTT TAGCCATAGC CATATAACCT
1301 ATCGATATTA A

```

This corresponds to the amino acid sequence <SEQ ID 2724; ORF 904>:

m904.pep

```

1  MMQHNRFVSFV GAGGDDGDRR AADFFNPFI CFCGVFGQCAV VLHAESGFAP
51  AGHGFVNRFA GFHRIGTARQ DVGFAAVGQF IADADIDGFN AVHYIEFSNT
101 HTGNAVDLDG AFQGGGIKPA AAACASGYRT BFVSAPCQTY AYFVEQFGRE
151 RARTDARGIG FDDAQNI IQH LRTYARACRS CARQTVGRGN EGISAVVDVQ
201 QRTLRAFQKQ FFAVFVFLVQ HAGHVGNHRR NARRDFFDNR HHVFRFNRLG
251 IVQMLQLDIV IGKDGIOFFT QFXRMQIQG ANGAACHFVF VGRADAAAGR
301 ADFAFAXIF AGLVERDVVR QDQAGRRDF QTAFDVFHAC RVQLVDFAAQ
351 GFGGDDNART DEAVQTFMQD AARNQAQNGF FAADNQGMR IVAALEAHHA
401 AGFFRQPVND FTFTLVAPLC ADXYNIFSHS HITYRY*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 904 shows 90.4% identity over a 436 aa overlap with a predicted ORF (ORF 904.ng) from *N. gonorrhoeae*:

m904/g904

	10	20	30	40	50	60
m904.pep	MMQHNRFVSFV GAGGDDGDRRAADFFNPFI CFCGVFGQCAV VLHAESGFAPAGHGFVNRFA					
	: : : : : : : :					
g904	MMQHNRFVAVGAGGDDGDRRAADFFNPFI CFCGIGRQCVVAFHADS RFAPAGHGFVNRFA					
	10	20	30	40	50	60
	70	80	90	100	110	120

1295

m904 . pep	GFHRIGTARQDVGFAAVGQFIADADIDGFNAVHYIEFSNHTGNVAVDLDGAFQGGGIKPA
g904	GFHRIRARQDVGFAAAWQFVADADIDGFNAVHYIEFGNAHTGNVAVDLDGAFQGGGIKPA
	70 80 90 100 110 120
m904 . pep	AAACASGYRTEFVS AFCQTYAYFVEQFGRERARTDARGIGFDDAQNI IQHLRTYARACRS
g904	AAARAAGYRTEFVSALRQTCAYFVEQFGRERARTDARGIGFDDAQNI IQHLRTYARACRS
	130 140 150 160 170 180
m904 . pep	CARQTVGRGNEGISAVVDVQQR TLRAFKQQFFAVFVFLVQHAGHVGNHRRNARRDFFDNR
g904	RAGETVGRGNEGVS AVVDVQQR TLRAFKQQFFAVFVFFVQHAGHVGNHRRNARRDFFDNR
	190 200 210 220 230 240
m904 . pep	HHVFRFNRLGIVQMLQLDIVIGKDG IQFFTQFXRMQQIGGANGAACHFV FVGRADAAAGR
g904	HHVFRFNRSVMQVLELDVVIGKDG IQFFTQFFRMQQIGGANGAACHFV FVGRADAAAGR
	250 260 270 280 290 300
m904 . pep	ADFAFAARIFAGLVERDVVRQDQ RAGRRDFQTA FDV FHACRVQLVDFAQQGFGGDDNART
g904	ADFAFAARCFAGLVERDVVRQDQ RAGRRDFQTA FDV FHACRVQLVDFAQQGFGGDDNART
	310 320 330 340 350 360
m904 . pep	DEAVQTFMQDAARNQAQNGFFAADNQGMARIVAAL EAHHAAGFFRQPVNDFTFTLVAPLC
g904	DEAIQSFVQDTARNQAQNGFFAADNQGMARIVAAL EAHDAAGFFRQPVNDFTFTLVAPLC
	370 380 390 400 410 420
m904 . pep	ADXYNIFSHSHITYRYX
g904	ADYYNIFSHSHITYRYX
	430

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2725>:

a904 . seq

1	ATGATGCAGC	ACAATCGTTT	CTTCGCGGTC	GGGGCCGGTG	GAGACGATGG
51	CGACCGGCGC	ACCGCAGACT	TCTTCAATCC	GTTTCAAATA	TGCTTTGGCA
101	TGGCAGGTA	ATGCGTCGTA	GCTTTTCACG	CCGAAAGTGG	ATTTCGCTCCA
151	ACCGGGCATG	GTTTCGTAAA	TCGGCTTGCA	GGCTTCTACC	GCATCAGAGC
201	CGCAAGGCAG	GATGTCGGTT	TTGCCGCCGT	CGGGCAATTC	GTAGCCGACG
251	CAGATATTGA	TGGTTTCAAC	GCCGTCCATT	ACATCGAGTT	TGGTAATACA
301	CATACCGGAA	ATGCCGTTGA	TTTGGATGGA	GCGTTTCAGG	GCGGCGGCAT
351	CAAACCAGCC	GCAGCGGCGT	GCGCGTCCGG	TTACCGAACC	GAATTCGTGT
401	CCGCGTTCTG	CCAAACCTGC	TCCGACTTCG	TCGAACAATT	CGGTCGGGAA
451	CGGGCCCGAA	CCGACGCGCG	TGGTATAGGC	TTTGACGATG	CCCAAAACAT
501	AATCCAGCAT	TTGAGGCGCT	ACGCCGCGC	CTGCCGAAGC	CGCGCCGGCG
551	AGCGAGTTGG	ACGAAGTAAC	GAAGGGGTAA	GTGCCGTAGT	CGATGTCCAA
601	CAACGCACCT	TGCGCGCCTT	CAAACAGCAG	TTTTTCGCCG	TTTTTGTTTT
651	TTTCGTTCAA	CACGCGGGAC	ACGTCGGTAA	TCATCGGCGT	AATGCGCGGC
701	GCGACTTTTT	CGATAACCGC	CATCACGTCT	TCCGCTTTCA	CCGACTCGGC
751	ATTGTGCAGA	TGTTGCAGTT	GGACGTTGTA	ATAAGCAAAG	ACGGCATCCA
801	GTTTTTCACG	CAGTTTTCAT	GCATGCAGCA	AATCGCGCGC	CCGAATGGCG
851	CGGCGTGCCA	CTTGTCTTTC	GTAGGCAGGG	CCGATGCCGC	GGCCGGTCGT
901	GCCGATTTTG	CCTTTGCCGC	GCGATGCTTC	TCGGGCTTGG	TCGAGCGCGA

1296

```

951 TGTGATAAGG CAGGATCAGC GGGCAGGTCG GCGCGATTTT CAGACGGCCT
1001 TCGACGTTTT TCACGCCTGC CGCGTTCAAC TCGTCGATTT CGCCCAACAG
1051 GGCTTCGGGG GAGACGACAA CGCCCGAACC GATGAAGCAG TCCAGACTTT
1101 CATGCAGGAT GCCGCTCGGA ATCAGGCGCA AAATGGTTTT TTTGCCGCCG
1151 ACAACCAAGG TATGACCCGC ATTGTGGCCG CCTTGAAGC GCACCAGCC
1201 TCCGGCTTCT TCCGCCAGCC AGTCAACGAT TTTACCTTTA CCCTCGTCGC
1251 CCCACTGTGC GCCGATTACT ACAACATTTT TAGCCATAGC CATATAACCT
1301 .TCGATATTA A

```

This corresponds to the amino acid sequence <SEQ ID 2726; ORF 904.a>:

a904.pep

```

1  MMOHNRFFAV GAGGDDGDRR TADFFNPFI CFIGR*CVV AFHAESGFAP
51  TGHGFVNRLA GFYRIRARQ DVGFVAVGQF VADADIDGFN AVHYIEFGNT
101 HTGNAVLDG AFQGGGKPA AACASGYRT EFVSAFCQTC SDFVEQFGRE
151 RARTDARGIG FDDAQNIIQH LRAYARACRS RAGEAVGRSN EGVSAVVDVQ
201 QRTLRAFKQQ FFAVVFVQVQ HAGHVGNHRR NARRDFFDNR HHVFRFHLG
251 IVQMLQLDVV ISKDGIOFFT QFFRMQQIGG ANGAACHFVF VGRADAAAGR
301 ADFAFAARCF SGLVERDVIR QDQAGRRDF QTAFDVFHAC RVQLVDFQQ
351 GFGDDNART DEAVQTFMQD AARNQAQNGF FAADNQGMR IVAALEAHHA
401 SGFRQPVND FTFTLVAPLC ADYNNIFSHS HITXRY*

```

m904/a904 91.3% identity in 436 aa overlap

m904.pep	10	20	30	40	50	60
	MMQHNRFFSVGAGGDDGDRRAADFFNPFI	CFI	GR	*CVV	AFHAESGFAPAGHGFVNRLA	
a904	10	20	30	40	50	60
	MMQHNRFFAVGAGGDDGDRRTADFFNPFI	CFI	GR	XC	VVAFHAESGFAPTGHG	GFVNRLA
m904.pep	70	80	90	100	110	120
	GFHRIGTARQDVGFVAVGQFIADADIDGF	NAVHYIEFSN	THTGNAV	DL	DGA	FGGGKIPA
a904	70	80	90	100	110	120
	GFYRIRARQDVGFVAVGQFVADADIDGF	NAVHYIEFGN	THTGNAV	DL	DGA	FGGGKIPA
m904.pep	130	140	150	160	170	180
	AAACASGYRTEFVSAFCQTYAYFVEQFGR	ERARTDARGIG	FDDAQNIIQ	HL	RTYARACRS	
a904	130	140	150	160	170	180
	AAACASGYRTEFVSAFCQTCSDVEQFGR	ERARTDARGIG	FDDAQNIIQ	HL	RAYARACRS	
m904.pep	190	200	210	220	230	240
	CARQTVGRGNEGISAVVDVQORTLRAFKQ	QFFAVFV	LVQ	HAGHVG	NHRRNARRD	FFDNR
a904	190	200	210	220	230	240
	RAGEAVGRSNEGVS	AVVDVQORTLRAFKQ	QFFAVFV	LVQ	HAGHVG	NHRRNARRD
m904.pep	250	260	270	280	290	300
	HHVFRFNLGIVQMLQLDIVIGKDGIOFFTQ	FXRMQQIGG	ANGAACHFV	FVGRADAAAGR		
a904	250	260	270	280	290	300
	HHVFRFHLGIVQMLQLDVVISKDGIOFFTQ	FXRMQQIGG	ANGAACHFV	FVGRADAAAGR		
m904.pep	310	320	330	340	350	360
	ADFAFAAXIFAGLVERDVVRQDQAGRRDFQ	TA	FDV	FHACRVQLVDF	AAQGGFGGDDNART	
a904	310	320	330	340	350	360
	ADFAFAARCFSGLVERDVIRQDQAGRRDFQ	TA	FDV	FHACRVQLVDF	AAQGGFGGDDNART	
m904.pep	370	380	390	400	410	420
	DEAVQTFMQDAARNQAQNGFFAADNQGMA	RIVA	AALEAHHAAGFFRQ	FPVNDFTFTLVAPLC		
a904	370	380	390	400	410	420
	DEAVQTFMQDAARNQAQNGFFAADNQMTR	IVA	AALEAHHAAGFFRQ	FPVNDFTFTLVAPLC		

430

1297

```

m904.pep      ADXYNIFSHSHITYRYX
               || ||||| |||| |||
a904          ADYYNIFSHSHITXRYX
               430

```

g906.seq not found yet
g906.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2727>:

```

m906.seq
1  ATGAAATATA TCGTATCAAT CTCTCTGGCT ATGGGATTGG CTGCCTGTTC
51  GTTTGGGGGA TTAAACCAA ATCCGTGGGA CGCCGCGTCA TTTTGGGAAT
101 TGAAAATTA CGCAATCCC TATCCGGGAT CAGCCTCGGC GGCATTGAC
151 CAATATCCAT CGAAAGCAAG ACGAAGGCAA CTGAAAGACA TGCAAGAGTG
201 CGGCTATGAC CCAATAGACG GCGGAAAGTC TGAAGCAGAT GCCTGCCTGA
251 GGAAAAAAGG CTGGTGTCTG AAGGGTTTCG ACCCTTATCC CGAAAAACAA
301 AAATACGAAT GGCCTCGAGA AGAAGGAAAA ACAAAATGA

```

This corresponds to the amino acid sequence <SEQ ID 2728; ORF 906>:

```

m906.pep
1  MKYIVSISLA MGLAACSFEG FKPNPWDAAS FWELKNYANP YPGSASAALD
51  QYPSKARRRQ LKDMQECGYD PIDGGKSEAD ACLRKKGWCR KGFDPPYPENK
101 KYEWPREEGK TK*

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2729>:

```

g907.seq (partial)
1  ATGAAAAAAC CGACCGATAC CCTACCCGTC AATCTGcaAC GCCGCCGCCT
51  GCTGTGTGCC GCCGGCGCGC TGTGTATCAG CCCGCTGCGC CACGCCGGCG
101 CGCAACGTGA AGAAACGctt gCCGACGATG TGGCTTCCGT GATGAGGAGT
151 TCTGTGCGCA GCGTCAATCC GCCGAGGCTG GTGTTGACA ATCCGAAAGA
201 GGGCGAACGT TGGTTGTCCG CGATGTCGGC ACGTTTGGA AGATTGCTCC
251 CCGACGAGGG GGAGCGGCGC AGGCTGCTGG TCAATATCCA ATACGAAAGC
301 AGCCGGGCGG GTTTGGATAC GCAGATTGTG TTGGGGCTGa ttgaagtgga
351 aagcgggtac cgagctcgaa tcatatca..

```

This corresponds to the amino acid sequence <SEQ ID 2730; ORF 907.ng>:

```

g907.pep (partial)
1  MKKPTDTLPV NLQRRRLCA AGALLISPLA HAGAQREETL ADDVASVMRS
51  SVGSVNPPRL VFDNPKEGER WLSAMSARLA RFVPDEGERR RLLVNIQYES
101 SRAGLDTQIV LGLIEVESGY RARIIS...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2731>:

```

m907.seq
1  ATGAGAAAAC CGACCGATAC CCTACCCGTT AATCTGCAAC GCCGCCGCCT
51  GTTGTGTGCC GCCGGTGCGT TGTGTCTCAG TCCTCTGGCG CACGCCGGCG
101 CGCAACGTGA GGAACGCTT GCCGACGATG TGGCTTCCGT GATGAGGAGT
151 TCTGTGCGCA GCGTCAATCC GCCGAGGCTG GTGTTTGACA ATCCGAAAGA
201 GGGCGAGCGT TGGTTGTCTG CCATGTCGGC ACGTTTGGA AGGTTGCTCC
251 CCGAGGAGGA GGAGCGGCGC AGGCTGCTGG TCAATATCCA GTACGAAAGC
301 AGCCGGGCGG GTTTGGATAC GCAGATTGTG TTGGGGCTGA TTGAGGTGGA
351 AAGCGCGTTC CGCCAGTATG CAATCAGCGG TGTGCGCGCG CGCGGCCTGA
401 TGCAGGTTAT GCCGTTktGG AAAAActACA TCGGCAAAAC GGCGCACAAc
451 CTGTTGACA TCCGCACCAA CCTGCGTTAC GGCTGTACCA TCCTGCGCCA
501 TTACCGGAAT CTTGAAAAAG GCAACATCGT CCGCGCGCTT GCCGCTTTA
551 ACGGCAGCTT GGGCAGCAAT AAATATCCGA ACGCCGTTTT GGgCGCGTGG
601 CGCAACCGCT GGCAGTGGCG TTGA

```

This corresponds to the amino acid sequence <SEQ ID 2732; ORF 907>:

```

m907.pep
1  MKKPTDTLPV NLQRRRLCA AGALLLSPLA HAGAQREETL ADDVASVMRS
51  SVGSVNPPRL VFDNPKEGER WLSAMSARLA RFVPEEEERR RLLVNIQYES
101 SRAGLDTQIV LGLIEVESAF RQYAISGVGA RGLMQVMPXW KNYIGKPAHN

```

1298

151 LFDIRTNLRY GCTILRHYRN LEKGNIVRAL ARFNGSLGSN KYPNAVLGAW
201 RNRWQWR*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 907 shows 92.9% identity over a 126 aa overlap with a predicted ORF (ORF 907.ng) from *N. gonorrhoeae*:

g907/m907

	10	20	30	40	50	60
g907.pep	MKKPTDTLPVNLQRRRLCAAGALLISPLAHAGAQREETLADDVASVMRSSVGSVNPRL					
	:	:	:	:	:	:
m907	MRKPTDTLPVNLQRRRLCAAGALLSPLAHAGAQREETLADDVASVMRSSVGSVNPRL					
	10	20	30	40	50	60
	70	80	90	100	110	120
g907.pep	VFDNPKEGERWLSAMSARLARFVPEDEGERRRLLVNIQYESSRAGLDTQIVLGLIEVESGY					
m907	VFDNPKEGERWLSAMSARLARFVPEEEERRLLVNIQYESSRAGLDTQIVLGLIEVESAF					
	70	80	90	100	110	120
	130	140	150	160	170	180
g907.pep	RARIIS					
m907	RQYAIISGVGARGLMQVMPXWKNYIGKPAHNLFDIRTNLRYGCTILRHYRNLEKGNIVRAL					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2733>:

a907.seq

```

1  ATGAAAAAAC CGACCGATAC CCTACCCGTC AATCTGCAAC GCCGCCGCTT
51  ATGTGTGTGCT GCCGGCGCGC TGTGTGCTCAG CCCGCTGGCA CAAGCCGGCG
101 CGCAACGTGA AGAAACGCTT GCCGACGATG TGGCTTCCGT GATGAGGAGC
151 TCTGTGCGCA GCATAATCC GCCGAGGCTG GTGTTGACA ATCCGAAAGA
201 GGGCGAGCGT TGGCTGTCCG CGATGTCTGC TCGGTTGGCA AGGTTCTGCC
251 CCGATGAGGA GCAGCGGCGC AGGCTGCTGG TCAATATCCA GTACGAAAGC
301 AGCCGGGCGG GTTTGGATAC GCAGATTGTG TTGGGGCTGA TTGAGGTGGA
351 AAGCGCGTTC CGCCAGTATG CAATCAGCGG TGTCGGCGCG CGCGGCCTGA
401 TGCAGGTATG GCCGTTTIGG AAAAATACA TCGGCAAACC GGCGCACAAC
451 CTGTTGACA TCCGCACCAA CCTGCGTTAC GGCTGTACCA TCCTGCGCCA
501 TTACCGGAAT CTTGAAAAAG GCAACATCGT CCGCGCACTC GCCCGTTTTA
551 ACGGTAGCCT CGGCAGCAAT AAATATCCGA ACGCCGTTTT GGGCGCGTGG
601 CGCAACCGCT GGCAGTGGCG TTGA

```

This corresponds to the amino acid sequence <SEQ ID 2734; ORF 907.a>:

a907.pep

```

1  MKKPTDTLPV NLQRRRLCA AGALLSPLA QAGAOREETL ADDVASVMRS
51  SVGSINPRL VFDNPKEGER WLSAMSARLA RFVPDEEERR RLLVNIQYES
101 SRAGLDTQIV LGLIEVESAF RQYAIISGVA RGLMQVMPFW KNYIGKPAHN
151 LFDIRTNLRY GCTILRHYRN LEKGNIVRAL ARFNGSLGSN KYPNAVLGAW
201 RNRWQWR*

```

m907/a907 97.6% identity in 207 aa overlap

	10	20	30	40	50	60
m907.pep	MRKPTDTLPVNLQRRRLCAAGALLSPLAHAGAQREETLADDVASVMRSSVGSVNPRL					
	:	:	:	:	:	:
a907	MKKPTDTLPVNLQRRRLCAAGALLSPLAQAGAOREETLADDVASVMRSSVGSINPRL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m907.pep	VFDNPKEGERWLSAMSARLARFVPEEEERRLLVNIQYESSRAGLDTQIVLGLIEVESAF					
a907	VFDNPKEGERWLSAMSARLARFVPEEEERRLLVNIQYESSRAGLDTQIVLGLIEVESAF					

1299

	70	80	90	100	110	120
	130	140	150	160	170	180
m907 . pep	RQYAISGVGARGLMQVMPXWKNYIGKPAHNLFDIRTNLRYGCTILRHYRNLEKGNIVRAL					
a907	RQYAISGVGARGLMQVMPFWKNYIGKPAHNLFDIRTNLRYGCTILRHYRNLEKGNIVRAL					
	130	140	150	160	170	180
	190	200				
m907 . pep	ARFNGSLGSNKYPNAVLGAWRNRWQWRX					
a907	ARFNGSLGSNKYPNAVLGAWRNRWQWRX					
	190	200				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2735>:

```

g908 . seq
1  ATGAG . AAAA GCCGTCTAAG CCGGTATAAA CAAAATAAAC TCATTGGGCT
51  ATTTGTCGCA GGTGTAAC TG CAAGAACAGC GGCAGAGTTG GTAGGCATTA
101 ATAAAAATAC CGCAGCCTAT GATTTTCATC GTTTACGATG ACTGATTTAT
151 CAAAACGGTC CGCATTTAGA AATGTTTGAT GGCGAAGTAG AAGCAGATGA
201 AAGTTATTTT GGCGGACAAC GCAAAGGCAA ACGCGGTCGC GGTGCTGCCG
251 GTAAAGTCGC CGTATTCGGT CTTTGAAGC GAAATGGTAA GGTTTATACG
301 GTTACAGTAC CGAATACTCA AACCGCTACT TTATTTCCCTA TTATCCGTGA
351 acaagtgaac cctgacagta ttgtttatac ggattgttat CgTAGCTATG
401 ATGTATTAGA Tgtgagcgaa tttagccatT TTagcttcgc tgaaacttcg
451 ttttcgtaTC AATCACAGCA CACATTTTGC CGAACGACAA AACCATATTA
501 A

```

This corresponds to the amino acid sequence <SEQ ID 2736; ORF 908.ng>:

```

g908 . pep
1  MXKSRLSRYK QNKLIGLFVA GVTARTAAEL VGINKNTAAY DFHRLR*LIY
51  QNGPHLEMF D GEVEADESYF GGQRKGKRGR GAAGKVAVFG LLKRNGKVYT
101 VTVPNTQTAT LFPPIREQVK PDSIVYTD CY RSYDVL DVSE FSHFSFAETS
151 FSYQSQHTFC RTTKPY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2737>:

```

m908 . seq
1  ATGAGAAAAA GTCGTCTAAG CCAGTATAAA CAAAmTAAAC TCATTGAACT
51  GTTTGTCACA GGTGTAAC TG CAAGAACGCG AGCAGAGTTA GTAGGCGTTA
101 ATAAAAATAC CGCAGCCTAT TATTTTCATC GTTTACGATT ACTTATTTAT
151 CAAAACAGTC CGCATTTGGA AATGTTTGAT GGCGAAGTAG AAGCAGATGA
201 AAGTTATTTT GGCGGACAAC GCAAAGGCAA ACGCGGTCGC GGTGCTGCCG
251 GTAAAGTCGC CGTATTCGGT CTTTGAAGC GAAATGGTAA GGTTTATACG
301 GTTACAGTAC CGAATACTCA AACCGCTACT TTATTTCCCTA TTATCCGTGA
351 ACAAGTGAAA CCTGACAGCA TTTTTTATAC GGATTGTTAT CGTAGCTATG
401 ATGTATTAGA TGTGCGCGAA TTTAGCCATT TTAGCTTCGC TGAAACTTCG
451 TTTTCGTATC AATCACAGCA CACATTTTGC CGAACGACAA AACCATATTA
501 A

```

This corresponds to the amino acid sequence <SEQ ID 2738; ORF 908>:

```

m908 . pep
1  MRKSRLSRYK QXKLIELFVT GVTARTAAEL VGVNKNTAAY YFHRLRLLIY
51  QNSPHLEMF D GEVEADESYF GGQRKGKRGR GAAGKVAVFG LLKRNGKVYT
101 VTVPNTQTAT LFPPIREQVK PDSIFYTD CY RSYDVL DVRE FSHFSFAETS
151 FSYQSQHTFC RTTKPY*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 908 shows 93.4% identity over a 166 aa overlap with a predicted ORF (ORF 908.ng) from *N. gonorrhoeae*:

```

g908/m908
10      20      30      40      50      60
g908 . pep  MXKSRLSRYKONKLIGLFVAGVTARTAAELVGINKNTAAYDFHRLRLXIYQNGPHLEMF D

```

1300

```

      |||||:|||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m908  MRKSRLSQYKQXKLIELFVTGVTARTAAELVGVNKNNTAAAYFHRLRLLIYQNSPHLEMPD
      10      20      30      40      50      60

      70      80      90      100     110     120
g908.pep GEVEADESYFGGQRKGKRGGAAGKVAVFGLLKRNGKVYTVTPNTQTATLFPPIIREQVK
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m908  GEVEADESYFGGQRKGKRGGAAGKVAVFGLLKRNGKVYTVTPNTQTATLFPPIIREQVK
      70      80      90      100     110     120

      130     140     150     160
g908.pep PDSIVYTDYRSYDVLVDVREFSHFSAETSFSYQSQHTFCRRTTKPYX
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m908  PDSIFYTDCYRSYDVLVDVREFSHFSAETSFSYQSQHTFCRRTTKPYX
      130     140     150     160

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2739>:

```

a908.seq
1  ATGAGAAAAA GTCGTCTAAG CCAGTATAAA CAAAATAAAC TCATTGAGCT
51  ATTTGTCGCA GGTGTAAC TG CAAGAACGGC AGCAGAGTTA CTAGGCGTTA
101 ATAAAAATAC CGCAGCCTAT TATTTTCATC GTTTACGATT ACTTATTAT
151 CAAAACAGTC CGCATTGGGA AATGTTTGAT GGCGAAGTAG AAGCAGATGA
201 AAGTTATTTT GCGGACAAAC GCAAAGGCAA ACGCGGTGCG GGTGCTGCCG
251 GTAAAGTCGC CGTATTCGGT CTTTGAAGC GAAATGGTAA GGTATATACG
301 GTTACAGTAC CGAATACTCA AACCGCTACT TTATTTCCTA TTATCCGTGA
351 ACAAGTGAAG CCTGACAGCA TTGTTTATAC GGATTGTTAT CGTAGCTATG
401 ATGTATTAGA TGTGCGCGAA TTAGCCATT TTAGCTTCGC TGAAACTCG
451 TTTTCGTATC AATCACAGCA CACATTTTGC CGAACGACAA AACCATATTA
501 A

```

This corresponds to the amino acid sequence <SEQ ID 2740; ORF 908.a>:

```

a908.pep
1  MRKSRLSQYK QNKLIELFVA GVTARTAAEL VGVNKNNTAA YFHRLRLLIY
51  QNSPHLEMPD GEVEADESYF GGQRKGKRG GAAGKVAVFG LLKRNGKVYT
101 VTPNTQTAT LFPPIIREQVK PDSIVYTDY RSYDVLVDVRE FSHFSAETS
151 FSYQSQHTFC RRTTKPY*

```

m908/a908 98.2% identity in 166 aa overlap

```

      10      20      30      40      50      60
m908.pep MRKSRLSQYKQXKLIELFVTGVTARTAAELVGVNKNNTAAAYFHRLRLLIYQNSPHLEMPD
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a908  MRKSRLSQYKQNKLIELFVAGVTARTAAELVGVNKNNTAAAYFHRLRLLIYQNSPHLEMPD
      10      20      30      40      50      60

      70      80      90      100     110     120
m908.pep GEVEADESYFGGQRKGKRGGAAGKVAVFGLLKRNGKVYTVTPNTQTATLFPPIIREQVK
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a908  GEVEADESYFGGQRKGKRGGAAGKVAVFGLLKRNGKVYTVTPNTQTATLFPPIIREQVK
      70      80      90      100     110     120

      130     140     150     160
m908.pep PDSIFYTDCYRSYDVLVDVREFSHFSAETSFSYQSQHTFCRRTTKPYX
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a908  PDSIVYTDYRSYDVLVDVREFSHFSAETSFSYQSQHTFCRRTTKPYX
      130     140     150     160

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2741>:

```

g909.seq (partial)
1  atgcgtaaaa ccgtacttat cCTgaccatc tccgcgcgcc ttttgtcggg
51  ctgcacatgG gaaacttatc aagacggcag cggcaaaacc gccgtccgtg
101 caaatgttc caccggcacg ccgctgtgtt ggcaagacgg gcgcggctcg

```

1301

```

151 aaaaaggtgg actgcgacga gtacgggtggc gaacgccggg ccgtgttgcg
201 caaccaaaag cgggggaagc ccgcgacgag gagagccgca acgctgggga
251 aaccgagttt ccgggcgagg gacggggggg ggcgggtgaa cagggcagaa
301 acgggggagg ggaagcgatc ggcgagg..

```

This corresponds to the amino acid sequence <SEQ ID 2742; ORF 909.ng>:

g909.pep (partial)

```

1 MRKTVLILTI SAALLSGCTW ETYQDGSgKT AVRACSTGT PLCWQDGRGS
51 KKVDCDEYGG ERRAVLNRNQK RGKPATRRAA TLGKPSFRAR DGGGRVNRAE
101 TGEgKRSAR..

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2743>:

m909.seq

```

1 ATGCGTAAAA CCTTCCTCTT CTGACCGCT GCCGCGCCC TTTGTGCGG
51 CTGCGCGTGG GAAACTTATC AAGACGGCAA CGGCAAGACC GCCGTCCGTC
101 AAAAATATCC CGCCGGCACG CCCGTTTATT ACCAAGACGG CAGCTACTCG
151 AAAAATATGA ACTACAACCA ATACCGTCCC GAACGCCATG CCGTGTACC
201 CAATCAAACC GGCAACAACG CCGACGAAGA GCATCGCCAA CACTGGCAAA
251 AACCAAAGTT TCAAAACCGA TAA

```

This corresponds to the amino acid sequence <SEQ ID 2744; ORF 909>:

m909.pep

```

1 MRKTFLEFLTA AAALLSGCAW ETYQDNGKKT AVRQKYPAGT PVYYQDGSYS
51 KNNMNYQYRP ERHAVLPNQT GNNADEEHRQ HWQKPKFQNR *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 909 shows 53.3% identity over a 90 aa overlap with a predicted ORF (ORF 909.ng) from *N. gonorrhoeae*:

m909/g909

	10	20	30	40	50	60
m909.pep	MRKTFLEFLTAALLSGCAWETYQDNGKKTAVRQKYPAGTPVYYQDGSYSKNNMNYQYRP					
	: : : : : : : : :					
g909	MRKTVLILTI SAALLSGCTWETYQDGSgKTAVRAKSTGTPLCWQDGRGSKKVDCDEYGG					
	10	20	30	40	50	60

	70	80	90
m909.pep	ERHAVLPNQTGNNADEEHRQHWQKPKFQNRX		
	: : : : : : :		
g909	ERRAVLRNQKRGKPATRRAATLGKPSFRARDGGGRVNRAETGEGKRSAR		
	70	80	90 100

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2745>:

a909.seq

```

1 ATGCGTAAAA CCTTCCTTAT CCGATGACT GCCCGCGCCC TTTGTGCGG
51 CTGCGCGTGG GAAACTTATC AAGACGGCAA CGGCAAGACC GCCGTCCGTC
101 AAAAATATCC CGCCGGCACG CCCGTTTATT ACCAAGACGG CAGCTACTCG
151 AAAAATATGA ACTACAACCA ATACCGTCCC GAACGCCATG CCGTGTACC
201 CAACCAAACC GGCAACAACG CCGACGAAGA GCATCGCCAA CACTGGCAAA
251 AGCCCAAATT TCAAAACCGA TAA

```

This corresponds to the amino acid sequence <SEQ ID 2746; ORF 909.a>:

a909.pep

```

1 MRKTFILILMT AAALLSGCAW ETYQDNGKKT AVRQKYPAGT PVYYQDGSYS
51 KNNMNYQYRP ERHAVLPNQT GNNADEEHRQ HWQKPKFQNR *

```

m909/a909 96.7% identity in 90 aa overlap

	10	20	30	40	50	60
m909.pep	MRKTFLEFLTAALLSGCAWETYQDNGKKTAVRQKYPAGTPVYYQDGSYSKNNMNYQYRP					
	: : : : : : : : :					
a909	MRKTFILILMTAAALLSGCAWETYQDNGKKTAVRQKYPAGTPVYYQDGSYSKNNMNYQYRP					
	10	20	30	40	50	60

1302

```

              70      80      90
m909 . pep    ERHAVLPNQTGNNADEEHRQHWQKPKFQNRX
              |||||
a909          ERHAVLPNQTGNNADEEHRQHWQKPKFQNRX
              70      80      90

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2747>:

```

g910 . seq
1  ATGAAAAAAC TGTATTGGC CGCGTTGTT TCCTAAATG CCGCAACCGC
51  ATTTGCCGGC GACTCTGCCG AGCGTCAGAT TTACGGCGAT CCCCATTTTG
101 AACAAAACCG CACAAAAGCC GTGAAATGT TGAACAGCG CGGTTATCAG
151 GTTTACGATG TCGATGCCGA CGACTACTGG GGCAAACCTG TTTTGAAGT
201 GGAAGCCTAT AAAGACGGCC GCGAATACGA CATCGTGTG TCTTACCCCG
251 ACCTGAAAAT CATCAAAGAG CAGCTCGATC GCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2748; ORF 910.ng>:

```

g910 . pep
1  MKKLLLAADV SLNAATAFAG DSAERQIYGD PHFEQNRTKA VKMLEQRGYQ
51  VYDVDADDYW GKPVLEVEAY KDGREYDIVL SYPDLKIIKE QLDR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2749>:

```

m910 . seq
1  ATGAAAAAAC TGTATTGGC TGCCGTTGTT TCTCTGAGTG CCGCTGCCGC
51  ATTTGCCGGC GACTCTGCCG AGCGTCAGAT TTACGGCGAT CCCCATTTTG
101 AACAAAACCG CACAAAAGCT GTGAAATGT TGGAGCAGCG CGGTTATCAG
151 GTTTACGATG TCGATGCCGA CGACCATGG GGTAAGCCTG TGCTGGAAGT
201 GGAAGCCTAT AAAGACGGCC GCGAATACGA CATCGTGTG TCTTACCCCG
251 ACCTGAAAAT CATCAAAGAG CAGCTCGATC GCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2750; ORF 910>:

```

m910 . pep
1  MKKLLLAADV SLNAAAFAG DSAERQIYGD PHFEQNRTKA VKMLEQRGYQ
51  VYDVDADDHW GKPVLEVEAY KDGREYDIVL SYPDLKIIKE QLDR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 910 shows 96.8% identity over a 94 aa overlap with a predicted ORF (ORF 910.ng) from *N. gonorrhoeae*:

```

g910/m910
              10      20      30      40      50      60
g910 . pep    MKKLLLAADVSLNAAAFAGDSAERQIYGDPHFEQNRTKAVKMLEQRGYQVYDVDADDYW
              |||||:|:|:|
m910          MKKLLLAADVSLNAAAFAGDSAERQIYGDPHFEQNRTKAVKMLEQRGYQVYDVDADDHW
              10      20      30      40      50      60

              70      80      90
g910 . pep    GKPVLEVEAYKDGREYDIVLSYPDLKIIKEQLDRX
              |||||
m910          GKPVLEVEAYKDGREYDIVLSYPDLKIIKEQLDRX
              70      80      90

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2751>:

```

a910 . seq
1  ATGAAAAAAC TGTATTGGT CGCGTTGTT TCCTTGAGTG CCGCAACCGC
51  ATTTGCCGGC GACTCTGCCG AGCGTCAGAT TTACGGCGAT CCTATTTTG
101 AACAAAACCG CACAAAAGCC GTGAAATGT TGAACAGCG CGGTTATCAG
151 GTTACGATG TCGATGCCGA CGACCATGG GGCAAACCTG TTTTGAAGT
201 GGAAGCCTAT AAAGACGGCC GCGAATACGA CATTGTGTTG TCTTACCCCG
251 ACCTGAAAAT CATCAAAGAG CAGCTCGATC GCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2752; ORF 910.a>:

```

a910 . pep

```

1 MKKLLLVAVV SLSAATAFAG DSAERQIYGD PYFEQNRTKA VKMLEQRGYQ
51 VHDVDADDDHW GKPVLEVEAY KDGREYDIVL SYPDLKIIKE QLDR*

	10	20	30	40	50	60
m910.pep	MKKLLLA	VVLSAAA	FAGDS	SAERQ	IYGD	PHFEQ
		:	:	:	:	:
a910	MKKLLLV	AVVLSA	ATAFAG	DSAERQ	IYGD	PYFEQ
		:	:	:	:	:
	10	20	30	40	50	60
	70	80	90			
m910.pep	GKPVLE	VEAYK	DGREY	DIVLS	YPDLK	IIKEQ
a910	GKPVLE	VEAYK	DGREY	DIVLS	YPDLK	IIKEQ
	70	80	90			

```
g911.seq
  1  ATGAAAAAGA ACATATTGGA ATTTTGGGTC GGACTGTTCC TCTTGATCGG
 51  CGCGGCGGCG GTTGCCCTTTC TCGCTTTCGG CGTGGCGGGC GGCGCGGCGT
101  TCGGCGGGTT GGACAAAATC TACCGCGTTT ATGCGGATTT CGGCGACATC
151  GGGCGGTTGA AGGTCAAATG CCCCGTCAAA TCCGCAAGGT TATTGTTCGG
201  GCGCGTCGGC GCTATCGGGC TTGACCCGAA ATCCTATCAG GCGAGGTGTC
251  GCCTTGATTT GGACGGCAAG TATCAGTTCA GCAGTGACGT TTCGCGCAA
301  ATCCTGACTT CGGGACTTTT GGGCGAACAG TACATCGGGC TGCAGCAGGG
351  CGGCGATACG GAAACCTTTC CTGCGGGCGA CACCATCTCC GTAACCAGTT
401  CTGCAATGGT TCTGGAAAAC CTGATCGGTA AATTCATGAC CAGCTTCGCC
451  GAGAAAAACG CTGAGGGCGG CAATGCGGAA AAAGCCGcaq aAtaa
```

g911.pep

1	MKKNILEFPW	GLFVLIGAAA	VAFLAFRVAG	GAAFGGSDKT	YAVYADFQDI
51	GGLKVNAPVK	SAGVLVGRVG	AIGLDPKSYQ	ARVRLDLGDK	YQFSSEVSAQ
101	ILTSGLLGEQ	YIGLQQGGDT	ENLAAGDTIS	VTSSAMVLEN	LIGKFMTSFA
151	EKNAEGGNAE	KAEE*			

```
m911.seq
      1  ATGAAGAAGA  ACATATTGGA  ATTTTGGGTC  GGACTGTTTC  TCCTGATTGG
     51  CGCGGCGGCG  GTTGCTTTT  TCGCTTTCCG  CGTGGCCGGC  GGTGCGGCGT
    101  TCGGCGGTTT  GGACAAAAC  TACGCCGTTT  ATGCCGATT  CGGCGACATC
    151  GGCGGTTTGA  AGGTCAATG  CCCCCTCAA  TCCGCAAGGC  TATTGGTCGG
    201  GCGCGTCGGC  GCTATCGGAC  TTGACCCGAA  ATCCTATCAG  GCGAGGGTGC
    251  GCCTCGATTT  GGACGGCAAG  TATCAGTTCA  GCAGCGACGT  TTCCGCGCAA
    301  ATCCTGACTT  CGGGACTTTT  GGGCGAGCAG  TACATCGGGC  TGACGACGGG
    351  CGGCGACACG  GAAAACTTT  CTGCCGGCGA  CACCATCTCC  GTAACCAATT
    401  CTGCAATGGT  TCTGGAAAA  TTATCGGCA  AAATCATGAC  GAGTTTTCCT
    451  GAGAAAAATG  CCGACGGCGG  CAATGCGGAA  AATGCGCGCG  AATAA
```

```
m911.pep
  1  MKKNILEFWV GLFVLIGAAA VAFLAFRVAG GAAFGGSDKT YAVYADFGDI
51  GGLKVNAPVK SAGVLVGRVG AIGLDPKSYQ ARVRLDLGK YQFSSDVSQA
101 ILTSGLLGEQ YIGLQQGGDT ENLAAGDTIS VTSSAMVLEN LIGKFMTSFA
151 EKNADGGNAE KAAE*
```

q911/m911

10 20 30 40 50 60

1304

```

g911.pep  MKKNILEFWVGLFVLIGAAVAFLAFRVAGGAAPGSDKTYAVYADFGDIGGLKVNAPVK
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
m911      MKKNILEFWVGLFVLIGAAVAFLAFRVAGGAAPGSDKTYAVYADFGDIGGLKVNAPVK
          10      20      30      40      50      60

          70      80      90      100     110     120
g911.pep  SAGVLVGRVGAIGLDPKSYQARVRLLDLGKYQFSSDVSAQILTSGLLGEQYIGLQQGGDT
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
m911      SAGVLVGRVGAIGLDPKSYQARVRLLDLGKYQFSSDVSAQILTSGLLGEQYIGLQQGGDT
          70      80      90      100     110     120

          130     140     150     160
g911.pep  ENLAAGDTISVTSSAMVLENLIGKFMTSFAEKNADGGNAEKAEX
          ||||||||||||||||||||||||||||||||||||||||:|||||||
m911      ENLAAGDTISVTSSAMVLENLIGKFMTSFAEKNADGGNAEKAEX
          130     140     150     160

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2757>:

```

a911.seq
1  ATGAAAAAGA ACATATTGGA ATTTGGGTC GGA CTGTTTCG TCCTGATTGG
51 CGCGCGGCGC GTTGCCCTTC TCGCTTCCG CGTGGCCGCG GGTGCGGCGT
101 TCGGCGGTTT GGACAAACT TACGCCGTT ATGCCGATT CGGCGACATC
151 GCGCGTTTGA AGGTCAATGC CCCCGTCAA TCCGCAGGCG TATTGGTCGG
201 GCGCGTCGGC GCTATCGGAC TTGACCGAA ATCCTATCAG GCGAGGGTGC
251 GCCTCGATTT GGACGGCAAG TATCAGTTCA GCAGCGACGT TTCCGCGCAA
301 ATCCTGACTT CGGGACTTTT GGGCGAGCAG TACATCGGCG TGCAGCAGGG
351 CGGCGACACG GAAAACCTTG CTGCCGGCGA CACCATCTCC GTAACCAAGT
401 CTGCAATGGT TCTGGAAC CTTATCGGCA AATTCATGAC GAGTTTTGCC
451 GAGAAAAATG CCGACGGCGG CAATGCGGAA AAAGCCGCGG AATAA

```

This corresponds to the amino acid sequence <SEQ ID 2758; ORF 911.a>:

```

a911.pep
1  MKKNILEFWV GLFVLIGAAA VAFLAFRVAG GAAFGGSDKT YAVYADFGDI
51 GGLKVNAPVK SAGVLVGRVG AIGLDPKSYQ ARVRLLDLGK YQFSSDVSAQ
101 ILTSGLLGEQ YIGLQQGGDT ENLAAGDTIS VTSSAMVLEN LIGKFMTSFA
151 EKNADGGNAE KAAE*

```

m911/a911 100.0% identity in 164 aa overlap

```

          10      20      30      40      50      60
m911.pep  MKKNILEFWVGLFVLIGAAVAFLAFRVAGGAAPGSDKTYAVYADFGDIGGLKVNAPVK
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a911      MKKNILEFWVGLFVLIGAAVAFLAFRVAGGAAPGSDKTYAVYADFGDIGGLKVNAPVK
          10      20      30      40      50      60

          70      80      90      100     110     120
m911.pep  SAGVLVGRVGAIGLDPKSYQARVRLLDLGKYQFSSDVSAQILTSGLLGEQYIGLQQGGDT
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a911      SAGVLVGRVGAIGLDPKSYQARVRLLDLGKYQFSSDVSAQILTSGLLGEQYIGLQQGGDT
          70      80      90      100     110     120

          130     140     150     160
m911.pep  ENLAAGDTISVTSSAMVLENLIGKFMTSFAEKNADGGNAEKAEX
          ||||||||||||||||||||||||||||||||||||||||
a911      ENLAAGDTISVTSSAMVLENLIGKFMTSFAEKNADGGNAEKAEX
          130     140     150     160

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2759>:

```

g912.seq
1  gtgAAAAaat cctcctTcat cagcGCATTG GGCATCGgtA TTTTGAGCAT
51 CGGCATGGCA TTTGCCTCCC CGGCCGACGC AGTGGGACAA ATCCGCCAAA
101 ACGCCACACA GGTTTTGACC ATCCTCAAAA GCGGCGACGC GGCTTCTGCA

```

151	CGCCCAAAAG	CCGAAGCCTA	TGCGGTTCCC	TATTTCGATT	TCCAACGTAT
201	GACCGCATTG	GGCGTTCGCA	ACCCTTGGCG	TACCGCGTCC	GACGCGCAAA
251	AACAAGCGTT	GCCCAAAAGAA	TTTCAAACCC	TGCTGATCCG	CACCTATTCC
301	GGCAGCATGC	TGAAATTCAA	AAGCGCGACC	GTCAACGTCA	AAGACAATCC
351	CATCGTCAAT	AAGGCGCGCA	AGGAATTCGT	CGTCCGTGCC	GAGCATCGCA
401	TCCC CGGTCA	GAAGCCCGTC	AATATGGACT	TTACCACCTA	CCAAAGCGGC
451	GGCAAATACC	GTACCTACAA	CGTCGCCATC	GAAGGCACGA	GCTTGGTTAC
501	CGTGATCCGC	AACCAATTCC	GCGAAATCAT	CAAGGCCAAA	GGCATCGACG
551	GGTGTATTGC	CGAGTTGAAA	GCCAAAAACG	CGGGCAATA	A

This corresponds to the amino acid sequence <SEQ ID 2760; ORF 912.ng>:

q912.pep

```

1  VKKSSFISAL GIGILSIGMA FASPADAVGQ IRQATQVLT ILKSGDAASA
51  RPKAEAYAVP YDFFORMTAL AVGNPWRITAS DAQKQALAKE FQTLILRTYS
101 GTMLKFKNAT VNVKDNPIVN KGGKEIVVRA EVGIPGQKPV NMDFTTYQSG
151 GKYRTYNVAI EGTSLVTVYR NQFGEIHKAK GIDGLIAELK AKNGGK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2761>:

m912.seq

1	ATGAAAAAAT	CCTCCCTCAT	CAGCGCATTG	GGCATCGGTA	TTTGTAGCAT
51	CGGCATGGCA	TTTGCCGCCC	CTGCCGACGC	GGTAAGCCAA	ATCCGTCAAA
101	ACGCCACTCA	AGTATTGAGC	ATCTTAAAAA	ACGGCGATGC	CAACACCGCT
151	CGCCAAAAAG	CCGAAGCCTA	TGCGATTCCC	TATTTGGAAT	TCCAACGTAT
201	GACCGCATTG	GCGTCCGCA	ACCTTGGCG	CACCGCGTCC	GACGCGCAAA
251	AACAAAGCGT	GGCCAAAGAA	TTTCAAAACC	TGCTGATCCG	CACCTATTCC
301	GGCACGATGC	TGAAATTAAA	AAACGCCAAC	GTCACGTCGA	AAGACATCC
351	CATCGTCAAT	AAAGGCGGCA	AAGAAATCAT	CGTCCGCGCC	GAAGTCGGCG
401	TACCCGGGCA	AAAACCCGTC	AACATGGACT	TCACCACCTA	CCAAGCGGC
451	GGTAAATACC	GTACCTACAA	CGTGCCATT	GAAGGCGCGA	GGCTGTTTAC
501	CGGTGTACCG	AACCAATTCC	CGGAAATCAT	CAAAAGCAAA	GCCGTGGACG
551	GACTGATTGC	CGAGTTGAAA	GCCAAAAACG	CGGGCAATA	A

This corresponds to the amino acid sequence <SEQ ID 2762; ORF 912>:

m912.pcp

1 MKKSSLSIAL GIGILSIGMA FAAPADAVSQ IRQATQVLS ILKNGDANTA
51 RQKAEAYAIP YFDFQRMAL AVGNPWRAS DAQKQALAKE FQTLIRTY
101 GTMLKLKLAN VNVKDNPIVN KGGKEIIVRA EVGVPQKPV NMDFTTYQSG
151 GKYRTYNVAI EGASLVTVYR NQFGEIHKAK GVDGLIAELK AKNGGK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 912 shows 91.8% identity over a 196 aa overlap with a predicted ORF (ORF 912.ng)

from *N. gonorrhoeae*:

q912/m912

	10	20	30	40	50	60
g912.pep	VKKSSFISALGIGILSIGMAFASPADAVGOIRONATQVLTILKSGDAASARPKAEAYAVP					
m912	MKKSSLISALGIGILSIGMAFAAPADAVSQIRONATQVLSILKNGDANTARQKAEYAIIP					
	70	80	90	100	110	120
g912.pep	YFDIFORMTALAVGNPWRTASDAQQALAKEFQTLLIRTYSGMTLKFKNATVNVKDNPIVN					
m912	YFDIFORMTALAVGNPWRTASDAQQALAKEFQTLLIRTYSGMTLKLKNANVNVKDNPIVN					
	130	140	150	160	170	180
g912.pep	KGGKEIVRAEVGIPGQKPVMNMDFTTYQSGGKYRTYNVAIEGTSLVTVYRNQFGEI IKAK					
m912	KGGKEIIVRAEVGVPGQKPVMNMDFTTYQSGGKYRTYNVAIEGASLVTVYRNQFGEI IKAK					
	190					
g912.pep	GIDGLIAELKAKNGGKX					

1306

```

      |||||||||
m912  GVDGLIAELKAKNGGKX
      190

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2763>:

```

a912.seq
1   ATGAAAAAAT CCTCCTTCAT CAGCGCATTG GGCATCGSTA TTTTGAGCAT
51  CGGCATGGCA TTTGCCGCCC CTGCCGACGC GGTAAACCAA ATCCGTCAAA
101 ACGCCACTCA AGTATTGAGC ATCTTAAAAA GCGGTGATGC CAACACCGCC
151 CGCCAAAAAG CCGAAGCCTA TCGGATTCCC TATTTGATT TCCAACGTAT
201 GACCGCATTG GCGGTCGGCA ACCCTTGGCG CACCGCGTCC GACGCGCAA
251 AACACGCGTT GGCCAAAGAA TTTCAAACCC TGCTGATCCG CACCTATTCC
301 GGCACGATGC TGAATTATAA AAACGCCAAC GTCAACGTCA AAGACAATCC
351 CATCGTCAAT AAAGGCGGCA AAGAAATCAT CGTCCGCGCC GAAGTCGGCG
401 TACCGGGGCA AAAACCCGTC AACATGGACT TCACCACCTA CCAAAGCGGC
451 GGTAATATAC GTACCTACAA CSTCGCCATC GAAGGCGCGA GCCTGGTTAC
501 CGTGTACCGC AACCAATTCG GCGAAATTAT CAAAGCGAAA GGCGTGGACG
551 GACTGATTGC CGAGTTGAAG GCTAAAAACG GCAGCAAGTA A

```

This corresponds to the amino acid sequence <SEQ ID 2764; ORF 912.a>:

```

a912.pep
1   MKKSSFISAL GIGILSIGMA FAAPADAVNQ IRQNATQVLS ILKSGDANTA
51  RQKAEAYAIP YFDFQRM TAL AVGNPWRTAS DAQKQALAKE FQTLIRITYS
101 GTMLKLKNAN VNVKDNPIVN KGGKEIIVRA EVGVPQKPV NMDFTTYQSG
151 GKYRTYNVAI EGASLVTYR NQFGEIIRAK GVDGLIAELK AKNGSK*

```

m912/a912 98.0% identity in 196 aa overlap

```

      10      20      30      40      50      60
m912.pep  MKKSSLISALGIGILSIGMAFAAPADAVSQIRONATQVLSILKNGDANTARQKAEAYAIP
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a912      MKKSSFISALGIGILSIGMAFAAPADAVNQIRONATQVLSILKSGDANTARQKAEAYAIP
      10      20      30      40      50      60

      70      80      90      100     110     120
m912.pep  YFDFQRM TALAVGNPWRTASDAQKQALAKEFQTLIRITYSGTMLKLKNANVNVKDNPIVN
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a912      YFDFQRM TALAVGNPWRTASDAQKQALAKEFQTLIRITYSGTMLKLKNANVNVKDNPIVN
      70      80      90      100     110     120

      130     140     150     160     170     180
m912.pep  KGGKEIIVRAEVGVPQKPVNMDFTTYQSGGKYRTYNVAIEGASLVTYRNVQFGEIIRAK
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a912      KGGKEIIVRAEVGVPQKPVNMDFTTYQSGGKYRTYNVAIEGASLVTYRNVQFGEIIRAK
      130     140     150     160     170     180

      190
m912.pep  GVDGLIAELKAKNGGKX
      |||:|||||:|||||:|||||
a912      GVDGLIAELKAKNGSKX
      190

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2765>:

```

g913.seq
1   atGAAAAAAA CCGCCTACGC CATCCTCCTG CTGATCGGGT TCGCTTCCGC
51  CCTGCAATTG GCAGAAACCC GCCCCGCCGA CCCTTATGAA GGCTACAACC
101 GCGCGGTTTC CAAATTCAAC GACCAAGCCG ACCGCTACAT TTTCGCCCTT
151 GCGCGCGCGG GCTACCGCAA AGTTACGCCG AAACCCGTCC GCGCCGGCGT
201 GTCCAATTTT TTTAACAACC TCGCGGACGT GGTCACTTTC GGCAGCAATA
251 TCTTGCGTTT GGACatCAAA cgcgcAAGcg aAGACctcgT CCGcgtcggc
301 atCAATACCA CCTTCGTTT GGcgcGGCTC ATTGATATTG CCGGcgcGGg
351 cggcgttccc gacaataaaa AcacTttgGg cgacacgttt gcctcgtGGG
401 GctgGAAAAa cagcaATTAT TTCGTgttgc CCGtcttagg cccgtccacc

```

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```

451 gtccgcgacg cgctcggcac gggcattacc tCTGTTTATC CGCccaagaa
501 tategttttc catacccctg ccggacgctg GGgcacgact gCCGCTGCCG
551 CCGTcagtac gcgcgaaggc ctctcgcatt tgaccgacag Tctggacgaa
601 gccgccatCG ACAAATACAG CTACACGCGc gacctctata tgAAAGTCCG
651 CGcacgGCag AccgGTGCAA CACCTGCCGA AGgtacggaa gataacatcg
701 acatcgacat cgACGAATTG GTCGAAAGTG CCGAAACCGG CGCGGCAGAG
751 CCCGCCGTTC ACGAAGATTG CGTATCCGAA ACACAGGCAG AAGCAGCAGG
801 GGAAGCCGAA ACGCAACCTG GAACACAACC CTAA

```

This corresponds to the amino acid sequence <SEQ ID 2766; ORF 913.ng>:

```

g913.pep
  1 MKKTAYAILL LIGFASAPAF AETRPADPYE GYNRAVSKFN DQADRYIFAP
 51 AARGYRKVTP KPVRAVSNNF FNNLRDVVSF GSNILRLDIK RASEDLVRVG
101 INTTFGLGGL IDIAGAGGVP DNKNTLGDTF ASWGWNKSNY FVLPVLGPST
151 VRDALGTGIT SVYPPKNIVF HTPAGRWTGT AAAAVSTREG LLDLTDSLDE
201 AAIDKYSYTR DLYMKVRRAR TGATPAEGTE DNIDIDIDEL VESAETGAEE
251 PAVHEDSVSE TQAEAAEGAE TQPGTQP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2767>:

```

m913.seq
  1 ATGAAAAAAA CCGCCTATGC CTTCCTCCTG CTGATCGGGT TCGCTTCCGC
 51 CCCTGCATTT GCCGAAACCC GCCCGCCGA CCCTTATGAA GGCTACAACC
101 GCGCCGTTTT CAAATTCAAC GACCAAGCCG ACCGCTACAT TTTCGCCCTT
151 GCCGCGCGCG GCTACCGCAA AGTTGCGCGG AAACCCGTCC GCGCCGCGCT
201 GTCCAATTTT TTTAACAACC TGTGCGACGT GGTGAGCTTC GGCAGCAATA
251 TCTTGCCTTT GGACATCAAA CGCGCAAGCG AAGACCTTGT CCGCGTCGGC
301 ATCAACACCA CTTTCGGTTT GGGCGGGCTT ATCGACATCG CCGGCGCGGG
351 CCGGATTCCC GACAATAAAA ACACCTTGGG CGACACGTTT GCCTCGTGGG
401 GATGGAAAAA CAGCAATTAT TTCGTGTTGC CCGTCTTAGG GCCGTCCACC
451 GTCCGCGACG CGCTCGGCAC GGGTATTACC TCCGTTTATT CGCCCAAGAA
501 TATCGTCTTC CGCACCCCTG TCGGACGCTG GGGCACGACT GCGGTATCCG
551 CCGTCAGTAC GCGCGAAGGC CTgCTCGATT TGACCGACAG TCTGGACGAA
601 GCCGCCATCG ACAAATACAG CTACACGCGC GACCTCTATA TGAAAGTCCG
651 TGCGCGGCAG ACCGGTGCAA CACCTGCCGA AGgTACGAA GATAACATCG
701 ACATCGACGA ATTGGTCGAA AGTGCCGAAA CCGGCGCGGC GGAAACTGCC
751 GTTCAAGAAG ATTCCGTATC CGAAACACAG GCAGAAGCAG CAGGGGAAGC
801 CGAAACGCAA CCTGGAACAC AACCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2768; ORF 913>:

```

m913.pep
  1 MKKTAYAFLL LIGFASAPAF AETRPADPYE GYNRAVSKFN DQADRYIFAP
 51 AARGYRKVAP KPVRAVSNNF FNNLRDVVSF GSNILRLDIK RASEDLVRVG
101 INTTFGLGGL IDIAGAGGIP DNKNTLGDTF ASWGWNKSNY FVLPVLGPST
151 VRDALGTGIT SVYSPKNIVF RTPVGRWTGT AVSAVSTREG LLDLTDSLDE
201 AAIDKYSYTR DLYMKVRRAR TGATPAEGTE DNIDIDELVE SAETGAAETA
251 VQEDSVSETQ AEAAGEAETQ PGTQP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 913 shows 94.9% identity over a 277 aa overlap with a predicted ORF (ORF 913.ng) from *N. gonorrhoeae*:

```

g913/m913
      10      20      30      40      50      60
g913.pep  MKKTAYAILLLIGFASAPAF AETRPADPYE GYNRAVSKFN DQADRYIFAPAARGYRKVTP
          |||||:|||||
m913      MKKTAYAFLLLIGFASAPAF AETRPADPYE GYNRAVSKFN DQADRYIFAPAARGYRKVAP
          |||||:|||||
      10      20      30      40      50      60

      70      80      90     100     110     120
g913.pep  KPVRAVSNNFNNLRDVVSFGSNILRLDIK RASEDLVRVGINTTFGLGGLIDIAGAGGVP
          |||||:|||||
m913      KPVRAVSNNFNNLRDVVSFGSNILRLDIK RASEDLVRVGINTTFGLGGLIDIAGAGGIP
          |||||:|||||
      70      80      90     100     110     120

```

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	130	140	150	160	170	180
g913 . pep	DNKNTLGDTFASWGWKNSNYFVL	PVLGPSTVRDALGTGITSVYPPKNIVFHTPAGRWGTT				
m913	DNKNTLGDTFASWGWKNSNYFVL	PVLGPSTVRDALGTGITSVYSPKNIVFRTVPVGRWGTT				
	130	140	150	160	170	180
	190	200	210	220	230	240
g913 . pep	AAAVSTREGLLDLTDSLDEAAIDKYSYTRDLYMKVRRARQTGATPAEGTEDNIDIDIDEL					
m913	AVSAVSTREGLLDLTDSLDEAAIDKYSYTRDLYMKVRRARQTGATPAEGTEDNIDI--DEL					
	190	200	210	220	230	
	250	260	270			
g913 . pep	VESAETGAAEPAVHEDSVSETQAEAAGEAETQPGTQPX					
m913	VESAETGAAETAVQEDSVSETQAEAAGEAETQPGTQPX					
	240	250	260	270		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2769>:

```

a913 . seq
1  ATGAAAAAAA CCGCCTATGC CTTCTCCTG CTGATCGGGT TCGCTTCCGC
51  CCCTGCATTT GCCGAAACCC GCCCGCCGA CCCTTATGAA GGCTACAACC
101 GCGCGGTTT CAAATCAAC GACCAAGCG ACCGCTACAT TTTGCCCCCT
151 GCGCGCGCG GCTACCGCAA AGTTGCGCG AAACCCGTC GCGCCGGCGT
201 GTCCAATTT TTTAACAACC TGTGCGACG GTCAGCTTC GGCAGCAATA
251 TCTTGCGCTT AGACATCAA CGCGCAAGC AAGACCTGT CCGCGTCGGT
301 ATCAACACCA CTTTCGGTTT GGGCGGGCTT ATCGACATCG CCGGCGCGGG
351 CGGCATTCCC GACAATAAAA ACACCTTGGG CGACACGTT GCTTCGTGGG
401 GATGGAAAA CAGCAATTAT TTCGTGTTGC CCGTCTTAGG GCCGTCCACC
451 GTCCGCGACG CGCTCGGCAC GGGTATTACC TCCGTTTATT CGCCCAAGAA
501 TATCGTCTTC CGCACCCCTG TCGGACGCTG GGGCAGGACT GCCGTATCCG
551 CCGTCAGTAC GCGCGAAGGC CTGCTCGATT TGACCGACAG TCTGGACGAA
601 GCCGCCATCG ACAATAACAG CTACACGCGC GACCTCTATA TGAAAGTCCG
651 TGC GCGGCGAG ACCGTTGCAA CACCTGCCGA AGGTACGGAA GATAACATCG
701 ACATCGACGA ATTGGTCGAA AGTGCCGAAA CCGGCGCGGC GGAACTGCC
751 GTTCAAGAAG ATTCCGTATC CGAAACACAG GCAGAAGCAG CAGGGGAAGC
801 CGAAACGCAA CCTGGAACAC AACCTGGAAC ACAACCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2770; ORF 913.a>:

```

a913 . pep
1  MKKTAYAFLL LIGFASAPAF AETRPADPYE GYNRAVFKFN DQADRYIFAP
51  AARGYRKVAP KPVRAVSNNF FNNLCDVVSF GSNILRLDIK RASEDLVRVG
101 INTTFGLGL IDIAGAGGIP DNKNTLGDTF ASWGWKNSNY FVLPLVGPST
151 VRDALGTGIT SVYSPKNIVF RTPVGRWGTT AVSAVSTREG LLDLTDSLDE
201 AAIDKYSYTR DLYMKVRRARQ TGATPAEGTE DNIDIDELVE SAETGAAETA
251 VQEDSVSETQ AEAAGEAETQ PGTQPGTQP*

```

m913/a913 100.0% identity in 275 aa overlap

	10	20	30	40	50	60
m913 . pep	MKKTAYAFLL	LIGFASAPAF	AETRPADPYE	GYNRAVFKFN	DQADRYIFAP	AARGYRKVAP
a913	MKKTAYAFLL	LIGFASAPAF	AETRPADPYE	GYNRAVFKFN	DQADRYIFAP	AARGYRKVAP
	10	20	30	40	50	60
	70	80	90	100	110	120
m913 . pep	KPVRAVSNNF	FNNLCDVVSF	GSNILRLDIK	RASEDLVRVG	INTTFGLGL	IDIAGAGGIP
a913	KPVRAVSNNF	FNNLCDVVSF	GSNILRLDIK	RASEDLVRVG	INTTFGLGL	IDIAGAGGIP
	70	80	90	100	110	120
	130	140	150	160	170	180
m913 . pep	DNKNTLGDTFASWGWKNSNYFVL	PVLGPSTVRDALGTGITSVYSPKNIVFRTVPVGRWGTT				
a913	DNKNTLGDTFASWGWKNSNYFVL	PVLGPSTVRDALGTGITSVYSPKNIVFRTVPVGRWGTT				

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	130	140	150	160	170	180
	190	200	210	220	230	240
m913.pep	AVSAVSTREGLDLTDSLDEAAIDKYSYTRDLYMKVRARQTGATPAEGTEDNIDIDELVE					
a913	AVSAVSTREGLDLTDSLDEAAIDKYSYTRDLYMKVRARQTGATPAEGTEDNIDIDELVE					
	190	200	210	220	230	240
	250	260	270			
m913.pep	SAETGAAETAVQEDSVSETQAEAAGEAETQPGTQPX					
a913	SAETGAAETAVQEDSVSETQAEAAGEAETQPGTQPX					
	250	260	270	280		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2771>:

g914.seq

```

1  ATGAAAAAAT GTATTTTGGG CATTTTGACC GCGTGTGCCG CCATGCCTGC
51  ATTTGCCGAC AGAATCAGCG ATTTGGAAGC ACGTCTGGCG CAGTTGGAAC
101 ACCGTGTCCG CGTATTGGAA AGCGGCGGCA ATACCGTCAA AATCGACCTT
151 TTCGGTTCAA ATTCCACCAT GTATGTATGC AGCGTTACGC CTTTTCAGAA
201 GacgtttGag gCAAGCGATC GGAATGAAGG CGTGGCGCGG CAGAAAGTGC
251 GTCAGGCGTG CAACCGCGAA ACTTCGGCAA TGTTTTGCGG AGATGAGGCA
301 ATCCGATGCA GAAAATTCGA TTGATGTATC GGTTGGACGG ATAAAGAAAC
351 GGATACGGAG CTGGGCTTCC GTCTCTGTTT TTCTCTGCCC GATTTTCCAT
401 GCATCGGGTT TCAGACGGCA TTGGAGTGTC AGTCGTGTTT TGCCGATTCT
451 taggctTCGA CGATTTTTCG CACCAGAGGA TGCCGGACAA CGTCTTCGCC
501 GGTGAAGGTA TGGAAATACA GTCTTGCCAC GCCGTGCAGT TTCTCACGTG
551 CGTCTTTCAA TCCCGATTG ATGTTTTTGG GCAGGTcgaT TTGGCTGGTG
601 TCGCCGGTAA TGACGGCTTT CGCgcccgaag ccGATGCGGG TCAGGAACAT
651 TTTCATTTGT TCGGGCGTGg tgTtttGcgC TTCGTGAGG ATGATGTATG
701 CGCCGTTGAg cgTCCTGCCG CGCATATAG

```

This corresponds to the amino acid sequence <SEQ ID 2772; ORF 914.ng>:

g914.pep

```

1  MKKCILGILT ACAAMPAPAD RISDLEARLA QLEHRVAVLE SGGNTVKIDL
51  FGSNSTMYVC SVTPFQKTFE ASDRNEGVAR QKVRQACNRE TSAMFCGDEA
101 IRCRKFD*CI GWTDKETDTE LGFRLCFSLP DFPCIGFQTA LECQSCSADS
151 *ASTIFCTRG CRTTSSPVKV WKYSPATPCS PSRASFPNDL MFLGRSIWL
201 SPVMTAFAPK PMRVRNIFIC SGVVFCASSR MMYAPLSVLP RI*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2773>:

m914.seq

```

1  ATGAAAAAAT GTATTTTGGG CATTTTGACC GCGTGTGCCG CCATGCCTGC
51  ATTTGCCGAC AGAATCGGCG ATTTGGAAGC ACGTCTGGCG CAGTTGGAAC
101 ACCGTGTCCG CGTATTGGAA AGCGGCGGCA ATACCGTCAA AATCGACCTT
151 TTCGGTTCAA ATTCCACCAT GTATGTATGC AGCGTTACGC CTTTTCAGAA
201 GACGTTTGAG GCAAGCGATC GGAATGAAGG CGTGGCGCGG CAGAAAGTGC
251 GTCAGGCGTG CAACCGCGAA ACTTCGGCAA TGTTTTGCGA AGATGAGGCA
301 ATCCGATGCA GAAAATTCGA TTGATGTATC GGTTGGACGG ATAAAGAAAC
351 GGATACGGAT ACGGAGCTTG GCTTCGTAT CTGTTTTTCT CTGCCTGATT
401 TTCCATGCAT CGGGTTTCAG ACGGCATTGG AATGTCAGTC GTGTTCTGCC
451 GATTCGTAGG CTTCGACGAT TTTTGCACC AAAGGATGCC GGACAACGTC
501 TTCGCCGGTA AAGGTGTGGA AATACAGCCC TTCCACGTTG TGCAGTTTCT
551 CACGCGCATC TTTTAATCCC GATTGTATGT TTTTGGGCAG GTCGATTTGG
601 CTGGTGTCG CCGTAATGAC GGCTTTCGCG CCGAAGCCGA TCGCGGTCAG
651 GAACATTTTC ATTTGTTTCG GCGTGGTGTT TTGCGCTTCC TCGAGGATGA
701 TGTATGCGCC GTTGAGCGTC CTGCCGCGCA TATAG

```

This corresponds to the amino acid sequence <SEQ ID 2774; ORF 914>:

m914.pep

```

1  MKKCILGILT ACAAMPAPAD RIGDLEARLA QLEHRVAVLE SGGNTVKIDL
51  FGSNSTMYVC SVTPFQKTFE ASDRNEGVAR QKVRQACNRE TSAMFCEDEA
101 IRCRKFDXCI GWTDKETD TD TELGFRICFS LPDFPCIGFQ TALECQSCSA

```

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151 DSXASTIFCT KGCRTTSSPV KVKYSPSTL CSFSRASFPN DIMFLGRSIW
 201 LVSPVMTAFA PKPMRVNIF ICSGVVFCAS SRMMYAPLSV LPRI*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 914 shows 96.7% identity over a 244 aa overlap with a predicted ORF (ORF 914.ng) from *N. gonorrhoeae*:

g914/m914

	10	20	30	40	50	60
g914.pep	MKKCILGILTACAAMPADFADRIDLEARLAQLEHRVAVLESGGNTVKIDLFGSNSTMYVC					
m914	MKKCILGILTACAAMPADFADRIDLEARLAQLEHRVAVLESGGNTVKIDLFGSNSTMYVC					
	10	20	30	40	50	60
	70	80	90	100	110	119
g914.pep	SVTPFQKTFEASDRNEGVARQKVRQACNRETSAMFCDEAIRCRKFDXCIGWTDKETD-					
m914	SVTPFQKTFEASDRNEGVARQKVRQACNRETSAMFCDEAIRCRKFDXCIGWTDKETD					
	70	80	90	100	110	120
	120	130	140	150	160	170
g914.pep	-ELGFRLCFSLPDFPCIGFQTALEQCSCSADSXASTIFCTRGCRRTSSPVKVKYSPATP					
m914	TELGFRICFSLPDFPCIGFQTALEQCSCSADSXASTIFCTKGCRRTSSPVKVKYSPSTL					
	130	140	150	160	170	180
	180	190	200	210	220	230
g914.pep	CSFSRASFPNPDLMFLGRSIWLVSPVMTAFAPKPMRVNIFICSGVVFCASSRMMYAPLSV					
m914	CSFSRASFPNPDLMFLGRSIWLVSPVMTAFAPKPMRVNIFICSGVVFCASSRMMYAPLSV					
	190	200	210	220	230	240
	240					
g914.pep	LPRIX					
m914	LPRIX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2775>:

a914.seq

1	ATGAAAAAT	GTATTTTG3G	CATTTTGACC	GCGTGTGCCG	CCATGCCTGC
51	ATTTGCCGAC	AGAATCGGCG	ATTGGAAGC	ACGTCTGGCG	CAGTTGGAAC
101	ACCGTGTCGC	CGTATTGGAA	AGCGGCAGCA	ATACCGTCAA	AATCGACCTT
151	TTCGGTTCAA	ATTCCACCAT	GTATGTATGC	AGCGTTACGC	CTTTTCAGAA
201	GACGTTTGAG	GCAAGCGATC	GGAATGAAGG	CGTGGCGCGG	CAGAAAGTGC
251	GTCAGGCGTG	CAACCGCGAA	ACTTCGGCAA	TGTTTTGCGA	AGATGAGGCA
301	ATCCGATGCA	GAAAAATCGA	TTGATGTATC	GTTTGGACGG	ATAAAGAAAC
351	GGATACGGAG	CTTGGCTTCC	GTATCTGTTT	TTCTCTGCCC	GATTTTCCAT
401	GCATCGGGTT	TCAGACGGCA	TTGGAATGTC	AGTCGTGTTC	TGCCGATTCTG
451	TAGGCTTCGA	CGATTTTTTG	CACCAAAGGA	TGCCGACAA	CGTCTTCGCC
501	GGTAAAGGTG	TGGAAATACA	GCCCTTCCAC	GCCGTGCAST	TTCTCACGCG
551	CATCTTTTAA	TCCCGATTG	ATGTTTTTGG	GCAGGTCGAT	TTGGCTGGTG
601	TCGCCGGTAA	TGACGGCTTT	CGCGCCGAAG	CCGATGCGGG	TCAGGAACAT
651	TTTCATTGT	TCGGGCGTGG	TGTTTTCGCG	TTCGTCGAGG	ATGATGTATG
701	CGCCGTTGAG	CGTCTGCCG	CGCATATAG		

This corresponds to the amino acid sequence <SEQ ID 2776; ORF 914.a>:

a914.pep

1	MKKCILGILT	ACAAMPADFAD	RIGDLEARLA	QLEHRVAVLE	SGSNTVKIDL
51	FGSNSTMYVC	SVTPFQKTFE	ASDRNEGVAR	QKVRQACNRE	TSAMFCEDEA
101	IRCRKFD*CI	GWTDKETDTE	LGFRICFSLP	DFPCIGFQTA	LEQCSCSADS
151	*ASTIFCTKG	CRTTSSPVKV	WKYSPSTPCS	FSRASFPNPD	MFLGRSIWLV
201	SPVMTAFAPK	PMRVNIFIC	SGVVFCASSR	MMYAPLSVLP	RI*

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m914/a914 98.4% identity in 244 aa overlap

	10	20	30	40	50	60
m914 . pep	MKKCILGILTACAAMPAFADRIGDLEARLAQLEHRVAVLES GGNTVKIDLFGSNSTMYVC					
a914	MKKCILGILTACAAMPAFADRIGDLEARLAQLEHRVAVLES GGNTVKIDLFGSNSTMYVC					
	10	20	30	40	50	60
	70	80	90	100	110	120
m914 . pep	SVTPFQKTFEASDRNEGVARQKVRQACNRETSAMFCEDEAIRCRKFDXCIGWTDKETD					
a914	SVTPFQKTFEASDRNEGVARQKVRQACNRETSAMFCEDEAIRCRKFDXCIGWTDKETD--					
	70	80	90	100	110	
	130	140	150	160	170	180
m914 . pep	TELGRICFSLPDFPCIGFQTALEQCSCSADXSASTIFCTKGCRTTSSPVKVKYSPSTL					
a914	TELGRICFSLPDFPCIGFQTALEQCSCSADXSASTIFCTKGCRTTSSPVKVKYSPSTP					
	120	130	140	150	160	170
	190	200	210	220	230	240
m914 . pep	CSFSRASFPDLMFLGRSIWLVPVMTAFAPKPMVRNIFICSGVVFCASSRMMYAPLSV					
a914	CSFSRASFPDLMFLGRSIWLVPVMTAFAPKPMVRNIFICSGVVFCASSRMMYAPLSV					
	180	190	200	210	220	230
m914 . pep	LPRIX					
a914	LPRIX					
	240					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2777>:

g915 . seq

```

1  ATGAAGAAAA CCCTGTTGGC AATTGTTGCC gtTTTCGCCT TAAGTGCCTG
51  CCGGCaggcg gaAGaggcac cgccgCCTTT ACCCCGGCAG AtTAGCGacc
101 gttcggtcgg aCACTAttgC Agtatgaacc tgaccgaaca caacggcccc
151 aaagcccaga tttttttgaa cGGCAAACCC GATCAGCCCG TTTGGTTCTC
201 CACCGTcaag cagatgttcg GCTATACCAA GCTGCCCCGAA GAGCCCAAAG
251 GCATCCGCGT GATTACGTT ACCGATATGG GCAATGTTAC CGATTGGACG
301 AATCCTAATG CCGACACGGA GTGGATAGAT GCGAAAAAAG CCTTTTACGT
351 CATCGACAGC GGCTTTATCG GCGGTATGGG CGCGGAAGAC GCGCTGCCGT
401 TCGGCAACAA GGAGCAGGCT GAAAAATTG CAAAGGATAA AGGCGGCAAG
451 GTCGTCGGTT TTGACGATAT GCCCGATGCT TACATTTTCA AGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2778; ORF 915.ng>:

g915 . pep

```

1  MKKTLAIVA VFALSACRQA EEAPPLPRQ ISDRSVGHYC SMNLTEHNGP
51  KAQIFLNGKP DQPVWFSTVK QMFGYTKLPE EPKGIRVIYV TDMGNVTDWT
101 NPNADTEWID AKKAFYVIDS GFIGGMGAED ALPFGNKEQA EKFAKDKGGK
151 VVGFDMPDA YIFK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2779>:

m915 . seq

```

1  ATGAAAAAAA CCCTGTTGGC AATTGTTGCC GTTTCGCCT TAAGTGC .tg
51  CCGGCAGGCG GAAGAGGGAC CGCCGCCTTT ACCcGGCAG ATTAGCGACC
101 GTTCGGTCGG ACATATTGTC AGTATGAACC TGACCGAACA CAACGGCCCC
151 AAAGCCCAGA TTTTCTTGAA CGGCAAACCC GATCAGCCCG TtTGTTCTC
201 CACCATCAAG CAGATGTTTCG GCTATACCAA GCTGCCCCGAA GAGCCTAAAG
251 GCATCCGCGT GATTACGTT ACCGATATGG GCAATGTTAC CGATTGGACG
301 AATCCCAATG CCGACACGGA GTGGATGGAT GCGAAAAAAG CCTTTTACGT
351 CATCGACAGC GGCTTTATCG GCGGTATGGG TGCGGAAGAC GCGCTGCCGT
401 TCGGCAACAA AGAGCAGGCT GAGAAATTG CAAAGGATAA AGCGGTAAG

```


1312

451 GTTGTTCGGTT TCGACGATAT GCCTGATACC TATATTTTCA AATAA

This corresponds to the amino acid sequence <SEQ ID 2780; ORF 915>:

m915.pep

1 MKKTLAIVA VSALSACRQA EEGPPPLPRQ ISDRSVGHYC SMNLTEHNGP
 51 KAQIFLNGKP DQPVWFSTIK QMFGYTKLPE EPKGIRVIYV TDMGNVTDWT
 101 NPNADTEWMD AKKAFYVIDS GFIGGMAED ALPFGNKEQA EKFAKDKGGK
 151 VVGFDMPDT YIFK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 915 shows 97.0% identity over a 164 aa overlap with a predicted ORF (ORF 915.ng) from *N. gonorrhoeae*:

m915/g915

	10	20	30	40	50	60
m915.pep	MKKTLAIVAVSALSACRQAEEGPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP					
g915	MKKTLAIVAVFALSACRQAEEAPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m915.pep	DQPVWFSTIKQMFYTKLPEEPKGIRVIYVTDMGNTDWTNPNADTEWMDAKKAFYVIDS					
	:					
g915	DQPVWFSTVKQMFYTKLPEEPKGIRVIYVTDMGNTDWTNPNADTEWIDAKKAFYVIDS					
	70	80	90	100	110	120
	130	140	150	160		
m915.pep	GFIGGMAEDALPFGNKEQA EKFAKDKGGKVVGFDMPDTYIFKX					
g915	GFIGGMAEDALPFGNKEQA EKFAKDKGGKVVGFDMPDAYIFKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2781>:

a915.sec

1 ATGAAAAA CCCTGTTGGC AATTGTTGCC GTTCCGCCT TAAGTGCCTG
 51 CCGGCAGGCG GAAGAGGGAC CGCCGCTTT ACCCGGCAG ATTAGCGACC
 101 GTTCGGTCGG AACTATTGC AGTATGAACC TGACCGAACA CAACGGCCCC
 151 AAAGCCAGA TTTCTTGAA CGGCAAACCC GATCAGCCCG TTTGGTCTC
 201 CACCATCAAG CAGATGTTTC GCTATACCAA GCTGCCCCGAA GAGCCTAAG
 251 GCATCCGCGT GATTACGTT ACCGATATGG GCAATGTTAC CGATTGGACG
 301 AATCCCAATG CCGACACGGA GTGGATGGAT GCGAAAAAAG CCTTTTACGT
 351 CATCGACAGC GGCTTTATCG GCGGTATGGG TCGGGAAGAC GCGCTGCCGT
 401 TCGGCAACAA AGAGCAGGCT GAGAAATTG CAAAGGATAA AGCGGTAAG
 451 GTTGTTCGGTT TCGACGATAT GCCTGATACC TATATTTTCA AATAA

This corresponds to the amino acid sequence <SEQ ID 2782; ORF 915.a>:

a915.pep

1 MKKTLAIVA VSALSACRQA EEGPPPLPRQ ISDRSVGHYC SMNLTEHNGP
 51 KAQIFLNGKP DQPVWFSTIK QMFGYTKLPE EPKGIRVIYV TDMGNVTDWT
 101 NPNADTEWMD AKKAFYVIDS GFIGGMAED ALPFGNKEQA EKFAKDKGGK
 151 VVGFDMPDT YIFK*

m915/a915 99.4% identity in 164 aa overlap

	10	20	30	40	50	60
m915.pep	MKKTLAIVAVSALSACRQAEEGPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP					
a915	MKKTLAIVAVSALSACRQAEEGPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m915.pep	DQPVWFSTIKQMFYTKLPEEPKGIRVIYVTDMGNTDWTNPNADTEWMDAKKAFYVIDS					
a915	DQPVWFSTIKQMFYTKLPEEPKGIRVIYVTDMGNTDWTNPNADTEWMDAKKAFYVIDS					

1313

	70	80	90	100	110	120
	130	140	150	160		
m915.pep	GFIGGMGAEDALPFGNKEQAEKFAKDKGGKVVGFDMPDTYIFKX					
a915	GFIGGMGAEDALPFGNKEQAEKFAKDKGGKVVGFDMPDTYIFKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2783>:

g917.seq

```

1  ATGGTCAAac atctgccacT cgcCGTCctg actgctTtgc tgcttgCagc
51  gtgcGGCGGT Tcggacaaac cgcctgccga Aaaaccggca ccggcgGaAA
101  accaaAacgt atTgaAAATT TataACTGGT CGGAATACGT CGATCCGGAA
151  ACCGTTGCCG ATTTTGAAAA GAAAAACGGC ATCAAGGTTA CTTATGATGT
201  GTACGACAGT GATGAAACGC TGGAAAGCAA GGTGCTGACC GGAAATCCG
251  GTTACGACAT TGTGCGCGCG TCCAATGCGT TTGTGGGCAG GCAGATTAAG
301  GCAGGTGCGT ATCAGAAAAT CGATAAGTCG ATGATTCCCA ATTATAAACA
351  TCTCAACCCT GAAATGATGA GGCTGATGGA CGGGGTCGAT CCCGACCAG
401  AATACGCCGT GCCGTTTAT TGGGGGACAA ATACCTTCGC CATCAATACC
451  GAACGCGTGA AAAAGGCTTT GGGTACGGAC AAGCTGCCGG ACAACCAGTG
501  GGATTTGGTG TTCAACCCCG AATACACGTT CAAACTCAAA CAATGCGGCA
551  TCAGCTATTT GGACAGCGCG GCGGAAATTT ATCCCATGGT GTTGAACAT
601  TTGGGCAAAA ACCCGAACAG CAGCAATACG GAAGACATCA GGGAGGCAAC
651  CGCCCTGCTC AAGAAAAACC GCCCAATAT CAAACGCTT ACTTCGTCG
701  GCTTTATCGA TGATTGGCG CGCGGCGATA CCTGCGTAAC AATCGGTTTC
751  GGCGGAGATT TGAACATCGC CAAACGCCGT GCCGAAGAAG CGGGCGGCAA
801  GGAaaaaATC CGCGTGATGA TGCCGAAAGA GGGCGTGGG ATTGGGTGG
851  ATTCCTTCGT GATTCGAAA GATGCGAAA ACGTCGCCAA CGGCACAAA
901  TACATCAACG ACTTCCTCGA TCCGGAAGTG TCGGCGAAAA ACGGCAATTT
951  cgttacCTAC GCGCTTCGA GCAAGCCGGC GCGCGATTG ATGGAGGACG
1001  AATTTAAAAA CGACAATACG ATTTTCCCGA CGGGGGAAGA TTGAAAAAC
1051  AGCTTTATCA TGGTGCCTAT CCGGCCGGCG GCATTGAAGT TTATGGTGGC
1101  CCAGTGGCAG GATGTGAAGG CGGGGAAAT A

```

This corresponds to the amino acid sequence <SEQ ID 2784; ORF 917.ng>:

g917.pep

```

1  MVKHLPLAVL TALLLAACGG SDKPPAEKPA PAENQNVLKI YNWSEYVDPE
51  TVADFEKKNG IKVTYDVYDS DETLESKVL T GSKGYDIVAP SNAFVGRQIK
101  AGAYQKIDKS MIPNYKHLNP ENMLMDGVD PDHEYAVPFY WGTNTFAINT
151  ERVKKALGTD KLPDNQWDLV FNPEYTFKLK QCGISYLSA AEIYPMVLNY
201  LGKNPNSSNT EDIREATALL KKNRPNIKRF TSSGFIDDLA RGDTCVTIGF
251  GGDNLIAKRR AEBAGGKEKI RVMPKEGVG IWVDSFVIPK DAKNVANAHK
301  YINDFLDPEV SAKNGNFVTY APSSKPARDL MEDEFKNDNT IFPSGEDLKN
351  SFIMVPIRPA ALKFMVRQWQ DVKAGK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2785>:

m917.seq

```

1  ATGACCAAAC ATCTGCCCTT GGCCGTCCTG ACTGCTTTGC TGCTTGCAAGC
51  GTGCGGCGGT TCGGACAAAC CGCCTGCCGA AAAACCGGCA CCGGCGGAAA
101  ACCAAAACGT ATTGAAAATT TACAACGGT CGGAATATGT CGATCCGGAA
151  ACCGTTGCCG ATTTTGAAAA GAAAAACGGC ATCAAGGTTA CTTATGATGT
201  GTACGACAGC GATGAAACGC TGGAAAGCAA GGTGCTGACA GGCAAGTCCG
251  GTTACGACAT TGTGCGCGCG TCCAATGCGT TTGTGGGCAG GCAGATTAAG
301  GCAGGTGCGT ATCAGAAAAT CGATAAGTCG CTGATTCCCA ATTATAAACA
351  CCTCAACCCC GAAATGATGA GGCTGATGGA CGGGGTCGAT CCCGCCACG
401  AATACGCCGT GCCGTTTAT TGGGGGACAA ATACCTTCGC CATCAATACC
451  GAACGCGTGA AAAAGGCTTT GGGTACGGAC AAGCTGCCGG ACAACCAGTG
501  GGATTTGGTG TTCGACCCCG AATACACGTC CAAACTCAAG CAATGCGGCA
551  TCAGCTATTT GGACAGCGCG GCGGAAATCT ATCCTATGGT GTTGAACAT
601  TTGGGTAAAA ACCCGAACAG CAGCAATACG GAAGACATCA GGGAGGCAAC
651  CGCCCTACTC AAGAAAAACC GCCCAATAT CAAACGCTT ACTTCGTCG
701  GCTTTATCGA TGATTGGCG CGCGGCGATA CCTGCGTAAC AATCGGTTTC

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1314

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751 GCGGCGGATT TGAACATCGC CAAACGCCGT GCCGAAGAAG CGGGCGGCAA
801 GGAAAAAATC CGCGTGATGA TGCCCAAAGA GGGCGTGGGG ATTTGGGTGG
851 ATTCTTTCGT GATTCCGAAA GATGCGAAAA ACGTCGCCAA CGCGCACAAA
901 TACATCAACG ACTTCCTCGA CCCGGAAGTG TCGGCGAAAA ACGGCAATTT
951 CGTTACTTAC GCGCCTTCGA GCAAGCCTGC GCGTGAGCTG ATGGAAGACG
1001 AATTTAAAAA CGACAATACG ATTTTCCCAA CCGAGGAGGA TTTGAAAAAC
1051 AGCTTTATCA TGGTGCCTAT CCAGCCGGCG GCATTGAAGT TTATGGTGGC
1101 CCAATGGCAG GATGTGAAGG CGGGGAATA A

```

This corresponds to the amino acid sequence <SEQ ID 2786; ORF 917>:

```

m917.pep
  1 MTKHLPLAVL TALLLAACGG SDKPPAEKPA PAENQNVLKI YNWSEYVDPE
 51 TVADFEKKNG IKVTYDVYDS DETLESKVLT GKSGYDIVAP SNAFVGRQIK
101 AGAYQKIDKS LIPNYKHLNP EMMRLMDGVD PGHEYAVPFY WGTNTFAINT
151 ERVKKALGTD KLPDNQWDLV FDPEYTSKLK QCGISYLSA AEIYPMVLNY
201 LGKNPNSSNT EDIREATALL KKNRPNIKRF TSSGFIDDLA RGDTCVTIGF
251 GGDNLIAKRR AEEAGGKEKI RVMPKEGVI IWVDSFVIPK DAKNVANAHK
301 YINDFLDPEV SAKNGNFVTY APSSKPAREL MEDEFKNDNT IFPTEEDLKN
351 SFIMVPIQPA ALKFMVRQWQ DVKAGK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 917 shows 97.6% identity over a 376 aa overlap with a predicted ORF (ORF 917.ng) from *N. gonorrhoeae*:

m917/g917

m917.pep	10	20	30	40	50	60
	MTKHLPLAVLTALLLAACGGSDKPPAEKPAPAENQNVLKIYNWSEYVDPETVADFEKKNG					
g917	MVKHLPLAVLTALLLAACGGSDKPPAEKPAPAENQNVLKIYNWSEYVDPETVADFEKKNG					
m917.pep	70	80	90	100	110	120
	IKVTYDVYDSDETLESKVLTGKSGYDIVAPSNFVGRQIKAGAYQKIDKSLIPNYKHLNP					
g917	IKVTYDVYDSDETLESKVLTGKSGYDIVAPSNFVGRQIKAGAYQKIDKSMIPNYKHLNP					
m917.pep	130	140	150	160	170	180
	EMMRLMDGVDPGHEYAVPFYWGNTNTFAINTERVKKALGTDKLPDNQWDLVFDPEYTSKLK					
g917	EMMRLMDGVDPDHEYAVPFYWGNTNTFAINTERVKKALGTDKLPDNQWDLVFNPEYTFKLK					
m917.pep	190	200	210	220	230	240
	QCGISYLSAAEYPMVLNLYLGKNPNSSNTEDIREATALLKKNRPNIKRFTSSGFIDDLA					
g917	QCGISYLSAAEYPMVLNLYLGKNPNSSNTEDIREATALLKKNRPNIKRFTSSGFIDDLA					
m917.pep	250	260	270	280	290	300
	RGDTCVTIGFPGDNLIAKRRAEAGGKEKIRVMPKEGVGIWVDSFVIPKDAKNVANAHK					
g917	RGDTCVTIGFPGDNLIAKRRAEAGGKEKIRVMPKEGVGIWVDSFVIPKDAKNVANAHK					
m917.pep	310	320	330	340	350	360
	YINDFLDPEVSAKNGNFVTYAPSSKPARELMEDEFKNDNTIFPTEEDLKN SFIMVPIQPA					
g917	YINDFLDPEVSAKNGNFVTYAPSSKPARELMEDEFKNDNTIFPTEEDLKN SFIMVPIQPA					
	370					

1315

m917.pep ALKFMVRQWQDVKAGKX
 |||||
 g917 ALKFMVRQWQDVKAGKX
 370

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2787>:

a917.seq
 1 ATGACCAAAC ATCTGCCCTT GCGCGTCTG ACTGCTTTGC TGCTTGACG
 51 GTGCGGCGGT TCGGACAAAC CGCTGCCGA AAAACCGGCG CCGGCGGAAA
 101 ACCGAAACGT ATTTGAAATT TACAACGTG CGGAATACGT CGATCCGGAA
 151 ACCGTTGCCG ATTTGAAAA GAAAAACGGC ATCAAGGTTA CTTATGATGT
 201 GTACGACAGC GATGAAACGC TGGAAAGCAA GGTGCTGACC GGAAAACTCTG
 251 GTTACGACAT TGTGCGCGCG TCCAATGCGT TTGTGGGCAG GCAGATTAAG
 301 GCAGGTGCGT ATCAGAAAAT CGATAAGTCG CTGATTCCCA ATTATAAACA
 351 CCTCAACCCC GAAATGATGA GGCTGATGGA CCGGGTCGAT CCCGGCCACG
 401 AATACGCCGT GCCGTTTAT TGGGGGACAA ATACCTTCGC CATCAATACC
 451 GAACGCGTGA AAAAGGCTTT GGGTACGGAC AAGCTGCCGG ACAACCAAGTG
 501 GGATTTGGTG TTCGACCCCG AATACACGTC CAACTCAAG CAATGCGGCA
 551 TCAGCTATTT GGACAGCGCG GCGGAAATCT ATCCTATGGT GTTGAACATAT
 601 TTGGGTAAAA ACCGAAACAG CAGCAATACG GAAGACATCA GGGAGGCAAC
 651 CGCCCTACTC AAGAAAAACC GCCCCAATAT CAAACGCTTT ACTTCGTCGG
 701 GCTTTATCGA TGATTTGGCG CGCGGCATA CCTGCGTAAC AATCGGTTTC
 751 GCGGCGGATT TGAACATCGC CAAACGCGGT GCCGAAGAAG CCGGCGGCAA
 801 GGAAAAAATC CGCGTGATGA TGCCCAAAGA GGGCGTGGGG ATTTGGGTGG
 851 ATTCTTTCGT GATTCCGAAA GATGCGAAAA ACGTCGCCAA CGCGCACAAA
 901 TACATCAACG ACTTCCTCGA CCGGAAGTG TCGGCGAAAA ACGGCAATTT
 951 CGTTACTTAC GCGCCTTCGA GCAAGCCTGC GCGTGAGCTG ATGGAAGACG
 1001 AATTTAAAAA CGACAATACG ATTTCCCAA CCGAGGAGGA TTTGAAAAAC
 1051 AGCTTTATCA TGGTGCCTAT CCAGCCGCGG GCATTGAAGT TTATGGTGCG
 1101 CCAGTGGCAG GATGTGAAGG CGGGGAATA A

This corresponds to the amino acid sequence <SEQ ID 2788; ORF 917.a>:

a917.pep
 1 MTKHLPLAVL TALLLAACGG SDKPPAEKPA PAENRNVLKI YNWSEYVDPE
 51 TVADFEKKNG IKVTYDVYDS DETLESKVLK GKSGYDIVAP SNAFVGRQIK
 101 AGAYQKIDKS LIPNYKHLNP EMMRLMDGVD PGHEYAVPFY WGTNTFAINT
 151 ERVKKALGTD KLPDQWDLV FDPEYTSKLG QCGISYLSA AEIYPMVLNY
 201 LGKNPNSSNT EDIREATALL KKNRPNIKRF TSSGFIDDLA RGDTCVTIGF
 251 GGDNLNIAKRR AEEAGGKEKI RVMPKEGVG IWVDSFVIPK DAKNVANAHK
 301 YINDFLDPEV SAKNGNEVTY APSSKPAREL MEDEFKNDNT IFPTEDDLKN
 351 SFIMVPIQPA ALKFMVRQWQ DVKAGK*

m917/a917 99.7% identity in 376 aa overlap

	10	20	30	40	50	60
m917.pep	MTKHLPLAVLTALLLAACGGSDKPPAEKPAPAENQNVLKIYNWSEYVDPETVADFEKKNG					
a917	MTKHLPLAVLTALLLAACGGSDKPPAEKPAPAENRNVLKIYNWSEYVDPETVADFEKKNG					
	10	20	30	40	50	60
m917.pep	IKVTYDVYDSDETLESKVLTKGSGYDIVAPSNFVGRQIKAGAYQKIDKSLIPNYKHLNP					
a917	IKVTYDVYDSDETLESKVLTKGSGYDIVAPSNFVGRQIKAGAYQKIDKSLIPNYKHLNP					
	70	80	90	100	110	120
m917.pep	EMMRLMDGVDPGHEYAVPFYWGNTNTFAINTERVKKALGTDKLPDQWDLVFDPEYTSKLG					
a917	EMMRLMDGVDPGHEYAVPFYWGNTNTFAINTERVKKALGTDKLPDQWDLVFDPEYTSKLG					
	130	140	150	160	170	180
m917.pep	QCGISYLSAAEIYPMVLNLYLGKNPNSSNTEDIREATALLKKNRPNIKRTSSGFIDDLA					
a917	QCGISYLSAAEIYPMVLNLYLGKNPNSSNTEDIREATALLKKNRPNIKRTSSGFIDDLA					
	190	200	210	220	230	240
m917.pep						
a917						

1316

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a917      QCGISYLDAAEIFYMVLNLYGKNPNSSNTEDIREATALLKKNRPNIKRTSSGFIDDLA
           190      200      210      220      230      240

           250      260      270      280      290      300
m917.pep  RGDTCTVTIGFGGDLNIAKRRAEEAGGKEKIRVMMPEKGVGIWVDSFVIPKDAKNVANAHK
           |||||||
a917      RGDTCTVTIGFGGDLNIAKRRAEEAGGKEKIRVMMPEKGVGIWVDSFVIPKDAKNVANAHK
           250      260      270      280      290      300

           310      320      330      340      350      360
m917.pep  YINDFLDPEVSAKNGNFVTYAPSSKPARELMEDEFKNDNTIFPTEEDLKNSFIMVPIQPA
           |||||||
a917      YINDFLDPEVSAKNGNFVTYAPSSKPARELMEDEFKNDNTIFPTEEDLKNSFIMVPIQPA
           310      320      330      340      350      360

           370
m917.pep  ALKFMVRQWQDVKAGKX
           |||||||
a917      ALKFMVRQWQDVKAGKX
           370

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2789>:

```

g919.seq
1  ATGAAAAAAC ACCTGCTCCG CTCCGCCCTG TACGGcatCG CCGCCgccAT
51  CctcgCCGCC TGCCAAAgca gGAGCATCCA AACCTTTCCG CAACCCGACA
101 CATCCGTCAT CAACGGCCCG GACCGGCCG CCGGCATCCC CGACCCCGCC
151 GGAACGACGG TTGCCGGCGG CGGGGCCGTC TATACCGTTG TGCCGCACCT
201 GTCCATGCCC CACTGGGCGG CGCaggATT TGCCTTTCAG CTGCAATCCT
251 TCCGCTCCG CTGCGCCAAT TTGAAAAACC GCCAAGGCTG GCAGGATGTG
301 TGCGCCCAAG CCTTCAAAC CCCCGTGCAT TCCTTTCAGG CAAAGcGgTT
351 TTTTGAACGC TATTTCACGC cgtGGCagg tgcaggcaAC GGAAGcCTTG
401 CaggtaaggT TACCGGCTAT TACGAACCGG TGCTGAAGGG CGACGGCAGG
451 CGGACGGAAC GGGCCCGCTT CCCGATTTC GGTATTCCCG ACGATTTTAT
501 CTCCGTCCCG CTGCCTGCCG GTTTCGGGG CGGAAAAAAC CTTGTCCGCA
551 TCAGGCAGAc ggGAAAAAAC AGCGGCACGA TCGACAATGC CGGCGGCACG
601 AACACGCGCG ACCTCTCCCG ATTCCCCATC ACCGCGCGCA CAACGGcaat
651 caaaGGCAGG TTTGAaggAA GCCGCTTCCT CCCTTACCAC ACGCGCAACC
701 AAAtcaacGG CGGCGgcgCT GACGGCAAag cccCCATCCT CggttaagcC
751 GAagaccCcg tcgaacttTT TTTTCATGCAC AtccaaggCT CGGGCCGCCT
801 GAAAAACCcg tccggcaaat acatCCGCAt cggaTaccgc gacAAAAACG
851 AACATccgTa tgtttccatc ggACGctaTA TGGCGGACAA AGGCTACCTC
901 AAGctcgggc agACCTCGAT GCAGGgcac aaagcCTATA TGCGGCAAAA
951 TCCGCAACGC CTCGCCGAAG TTTTGGGTCA AAACCCAGC TATATCTTTT
1001 TCCGCGAGCT TGCCGGAAGC GGCAATGAGG GCCCGCTCGG CGCACTGGGC
1051 ACGCCACTGA TGGGGGAATA CGCCGGCGCA ATCGACCGGC ACTACATTAC
1101 CTTGGGCGCG CCCTTATTTG TCGCCACCGC CCATCGGTT ACCCGCAAAG
1151 CCCTCAACCG CCTGATTATG GCGCAGGATA CAGGCAGCGC GATCAAAGGC
1201 GCGGTGCGCG TGGATTATTT TTGGGGTTAC GCGGACGAAG CCGGCGAACT
1251 TGCCGGCAAA CAGAAAACCA CGGATACGT CTGGCAGCTC CTGCCCAACG
1301 GCATGAAGCC CGAATACCGC CCGTGA

```

This corresponds to the amino acid sequence <SEQ ID 2790; ORF 919.ng>:

```

g919.pep
1  MKKHLRLSAL YGIAAAILAA CQSRSIQTFP QPDTSVINGP DRPAGIPDPA
51  GTTVAGGGAV YTVVPHLSMP HWAQDFAKS LQSFRLGCAN LKNRQWQDV
101 CAQAFQTPVH SFQAKRFFER YFTPNQVAGN GSLAGTVTGY YEPVLKGDGR
151 RTEARFPIY GIPDDFISVP LPAGLRGGKN LVRIQTGKN SGTIDNAGGT
201 HTADLSRFPI TARTTAIKGR FEGSRFLPYH TRNQINGGAL DGKAPILGYA
251 EDPVELFFMH IQSGRLKTP SKYIRIGYA DKNEHPYVSI GRYMADKGYL
301 KLGQTSMQGI KAYMRQNPQR LAEVLGQNPS YIFFRELGS GNEGPGVAGL
351 TPLMGEYAGA IDRHYITLGA PLFVATAHPV TRKALNRLIM AQDTGSAIKG
401 AVRVDYFWGY GDEAGELAGK QXTTGYVWQL LPNGMKPEYR P*

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1	ATGAAAAAAT	ACCTATTCCG	CGCGCCCTG	TACGGCATCG	CGCGCCCAT
51	CCTCGCGGCC	TGCGAAAGCA	AGAGCATCCA	AACCTTTCGG	CAACCCGACA
101	CATCCGTCAT	CAACGCGCCG	GACCGCGCCG	TCGGCATCCC	CGACCCCGCC
151	GGAAAGCAGG	TCGGCGCGCG	CGGGGCCGTG	TATACCGTTG	TACCGCACTT
201	GTCCCTGCCC	ACTGGGGCGG	CGCAGGATTT	CGCCAAAAGC	CTGCAATCTT
251	TCCGCTCGG	CTGCGCCAAT	TTGAAAAACC	GCCAAAGGCTG	CGAGGATGTG
301	TGCGCCCAAG	CCTTTCAAAC	CCCCGTCCAT	TCCTTTCAGG	CAAAACAGTT
351	TTTTGAACGC	TATTTACGCG	CGTGGCAGGT	TGCAGGCAAC	GGAAGCCTTG
401	CCGGTACCGT	TACCGGCTAT	TACGAACCGG	TGCTGAAGGG	CGACGACAGG
451	CGGACGGCAC	AAGCCCGCTT	CCCGATTATC	GGTATTCCCG	ACGATTTTAT
501	CTCCGTCCCC	CTGCGTCCGG	GTTCGCGGAG	CGGAAAAGCC	CTTGTCCGCA
551	TCAGGCAGAC	GGGAAAAAAC	AGCGGCACAA	TCGACAATAC	CGCGCGCACA
601	CATACGCGCG	ACCTCTCCcG	ATTCCCCATC	ACCGCGCGCA	CAACAGCAAT
651	CAAGCGCAGG	TTTGAAGGAA	GCCGCTTCCT	CCCCTACCAC	ACGCGCAACC
701	AAATCAACGG	CGGCGCGCTT	GACGGCAAGG	CCCCGATAGT	CGGTTACGCC
751	GAAAGCCCTG	TGCAACTTTT	TTTTATGCAC	ATCCAAGGCT	CGGGCCGTCT
801	GAAAACCCCG	TCCGGCAAAT	ACATCCGCAT	CGGCTATGCC	GCAAAAAGCG
851	AACATCCyTA	CGTTTCCATC	GGACGCTATA	TGGCGGATAA	GGGCTACCTC
901	AAACTCGGAC	AAACCTCCAT	GCAGGGCATT	AAGTCTTATA	TGCGGCAAAA
951	TCCGCAACGC	CTCGCCGAAG	TTTTGGGTGA	AAACCCCAGC	TATATCTTTT
1001	TCGGCGAGCT	TGCCGGAAGC	AGCAATGACG	GCCCTGTCCG	CGCATCTGGG
1051	ACGCGCGTGA	TGGGGGAATA	TGCCGGCGCA	GTGCAACGGC	ACTACATTAC
1101	CTTGGGTGCG	CCCTTATTTG	TCGCCACCBC	CCATCCGGTT	ACCCGCAAAG
1151	CCCTCAACCG	CCTGATTATG	GCGCAGGATA	CCGGCAGCGC	GATTAAAGGC
1201	GCGGTGCGCG	TGGAATATTT	TTGGGGATAC	GGCGACGAAG	CCGGCGAACT
1251	TGCCCGGCAA	GACAAAACCA	CGGGATATGT	CTGGCAGCTC	CTACCCAACG
TGAAGCG CGAATACCGc CCGTAA					

m919.pep

1	<u>KKKYLFRAL</u>	<u>YGIAAILAA</u>	CQSKSIQTFP	QPDTSVINGP	DREPVGIPDPA
51	GTTVGGGGA	YTVVPHLSLP	HWAAQDFAKS	LQSFRLGCAN	LKNRQGWQDV
101	CAQAFQTPVH	SPQAKQFFER	YFTPWQVAGN	GSLAGTVTGY	YEPVLKGGDR
151	RQAQTFPIY	QIPDDFISVP	LPAGLRSKGA	LVRIRQTKGN	SGTIDNTGGT
201	HTADLSRFPI	TARTTAIKGR	PEGSRFLPYH	TRNQINGGAL	DGKAPILGYA
251	EDPVLFPMH	IQGSGRLKTP	SGKYIRIGYA	DKNEHPYVSI	GRYMADRGYL
301	KLQGTSMQGI	KSYMQRNPQR	LAEVLGQNPS	YIFFRELASG	SNDGPVGALG
351	TPLMGEYAGA	VDRHYITLGA	PLFVATAHPV	TRKALNRLIM	AQDTGSAIKG
401	AVRVDFYFWG	GDEAGELAGK	QKTTGYVWQL	LPNGMKPEYR	P*

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N.gonorrhoeae*
ORF 919 shows 95.9 % identity over a 441 aa overlap with a predicted ORF (ORF 919.ng) from *N. gonorrhoeae*:
m919/q919

	10	20	30	40	50	60
m919.pep	MKKYLFR	AALYGIA	AAAILAAC	QSKSIQT	FPQPDTS	VINGPDRP
	:	:	:	:	:	:
g919	MKKHLLR	SALYGIA	AAAILAAC	QSRSIQT	FPQPDTS	VINGPDRP
	:	:	:	:	:	:
	10	20	30	40	50	60
	70	80	90	100	110	120
m919.pep	YTVVPHL	SLPHWAA	QDFAKSL	QSFRLGC	ANLKNRQ	GWQDVCA
	:	:	:	:	:	:
g919	YTVVPHL	SMPHWAA	QDFAKSL	QSFRLGC	ANLKNRQ	GWQDVCA
	:	:	:	:	:	:
	70	80	90	100	110	120

```

a919.seq
1  ATGAAAAAAT  ACCTATTCCG  CGCCGCCCTG  TCGGGCATCG  CCGCCGCCAT
51  CCTCGCGTCT  TGCCAAAGCA  AGAGCATCCA  AACCTTTCGC  CAACCCGACA
101  CATCCCGTCAT  CAACGGCCCG  GACCGGCCGG  TCGGCATCCC  CGACCCCGCC
151  GGAACGACGG  TCGGCGGCGG  CGGGGCGGTT  TATACCGTTG  TGCCGCACCT
201  GTCCCTGCCC  CTGCGGGCGG  CGCAGGATTT  CGCAAAGACG  CTGCAATCCT
251  TCCGCCTCGG  CTCGCGCAAT  TTGAAAAAAC  GCCAAGGCTG  GCAGGATGTG
301  TGGCGCCAAG  CCTTTCAAAC  CCGCGTCCAT  TCGGTCAGG  AAAACAGTT
351  TTTTGAACGC  TATTTACGCG  CGTGGCAGGT  TGCAGGCAAC  GGAAGCTTTG
401  CCGGTACGGT  TACCGGCTAT  TACGAGCCGG  TGCTGAAGGG  CGACGACAGG
451  CGGACGGCAC  AAGCCCGCTT  CCGGATTTAC  GGTATTCCCG  ACGATTTTAT
501  CTCGCTCCCC  CTGCTGCGG  GTTTCGGGAG  CGGAAAAGCC  TTGTGTCGCA
551  TCAGGCAGAC  GGGAAAAAAC  AGCGGCACAA  TCGACAATAC  CGGCGGCACA
601  CATACCGCCG  ACCTCTCCCA  ATTCCCATC  ACTGCGCGCA  CAACGGCAAT
651  CAAGGCGACG  TTTGAAGGAA  GCGGCTTCTT  CCCCTACCAC  CGCGTCAACC
701  AAATCAACGG  CGGCGCGCTT  GACGGCAAAG  CCCCAGTACT  ACCTTAGCCG
751  GAAGACCCCG  TCGAACTTTT  TTTTATGCAC  ATCCAAGGCT  CGGGCCGTCT
801  GAAACCCCG  TCCGGCAAA  ACATCCGCAT  CGGCTATGCC  GACAAAAACG
851  AACATCCCTA  CGTTTCCAT  GCACGTATA  TGCGGACAA  AGGCTACCTC
901  AAGCTCGGCG  AGACCTCGAT  CAGGGCATC  AAAGCCTATA  TGCAGCAAAA
951  CCCGCAACG  CTCGCCAAG  TTTTGGGCA  AAACCCAGC  TATATCTTTT
1001  TCCGAGAGCT  TACCGGAAG  AGCAATGAC  GCCTGTCCG  CGCATGGGG
1051  ACGCGCTGA  TGGCGGAGTA  CGCGCGAGCA  GTCCAGCCGC  ACTACATTAC
1101  CTTGGGCGCG  CCCTATTATT  TCGCCACCGC  CCATCCGGTT  ACCCGGAAAG

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1319

```

1151 CCTCAACCG CCTGATTATG GCGCAGGATA CCGGCAGCGC GATTAAAGGC
1201 GCGGTGCGCG TGGATTATTT TTGGGGATAC GGCGACGAAG CCGGCCAACT
1251 TGCCGGCAAA CAGAAAACCA CGGGATATGT CTGGCAGCTT CTGCCCAACG
1301 GTATGAAGCC CGAATACCGC CCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2794; ORF 919.a>:

a919.pep

```

      1 MKKYLFRAL CGIAAAILAA CQSKSIQTFP QPDTSVINGP DRPVGIPDPA
    51 GTTVGGGAV YTVVPHLSLP HWAAQDFAKS LOSFRLGCAN LKNRQGWQDV
   101 CAQAFQTPVH SVQAKQFFER YFTPWQVAGN GSLAGTVTGY YEPVLKGDDR
   151 RTAQAFFPIY GIPDDFISVP LPAGLRSGKA LVRIRQTGKN SGTIDNTGGT
   201 HTADLSQFPI TARTTAIKGR FEGRFLPYH TRNQINGGAL DGKAPILGYA
   251 EDPVELFFMH IQSGRLKTP SGKYIRIGYA DKNEHPYVSI GRYMADKGYL
   301 KLGQTSMQGI KAYMQQNQR LAEVLGQNPS YIFFRELTS SNDGPVGALG
   351 TPLMGEYAGA VDRHYITLGA PLFVATAHPV TRKALNRLIM AQDTGSAIKG
   401 AVRVDYFWGY GDEAGELAGK QKTGYVWQL LPNGMKPEYR P*

m919/a919 98.6% identity in 441 aa overlap
      10      20      30      40      50      60
m919.pep MKKYLFRALYGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
||||||| ||||||| ||||||| ||||||| ||||||| |||||||
a919      MKKYLFRALYGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
      10      20      30      40      50      60

      70      80      90     100     110     120
m919.pep YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
||||||| ||||||| ||||||| ||||||| ||||||| |||||||
a919      YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSVQAKQFFER
      70      80      90     100     110     120

      130     140     150     160     170     180
m919.pep YFTPWQVAGNGSLAGTVTGYEPVLKGDDRRRTAQAFFPIYGIPDDFISVPLPAGLRSGKA
||||||| ||||||| ||||||| ||||||| ||||||| |||||||
a919      YFTPWQVAGNGSLAGTVTGYEPVLKGDDRRRTAQAFFPIYGIPDDFISVPLPAGLRSGKA
      130     140     150     160     170     180

      190     200     210     220     230     240
m919.pep LVRIRQTGKNSGTIDNTGGTHTADLSRFPITARTTAIKGRFEGRFLPYHTRNQINGGAL
||||||| ||||||| ||||||| ||||||| ||||||| |||||||
a919      LVRIRQTGKNSGTIDNTGGTHTADLSQFPITARTTAIKGRFEGRFLPYHTRNQINGGAL
      190     200     210     220     230     240

      250     260     270     280     290     300
m919.pep DGKAPILGYAEDPVELFFMHIIQSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
||||||| ||||||| ||||||| ||||||| ||||||| |||||||
a919      DGKAPILGYAEDPVELFFMHIIQSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
      250     260     270     280     290     300

      310     320     330     340     350     360
m919.pep KLGQTSMQGIKSYMQRNPQRLAEVLGQNPSYIFFRELTSNDGPVGALGTPLMGEYAGA
||||||| ||||||| ||||||| ||||||| ||||||| |||||||
a919      KLGQTSMQGIKAYMQQNQRLEAEVLGQNPSYIFFRELTSNDGPVGALGTPLMGEYAGA
      310     320     330     340     350     360

      370     380     390     400     410     420
m919.pep VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
||||||| ||||||| ||||||| ||||||| ||||||| |||||||
a919      VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
      370     380     390     400     410     420

      430     440
m919.pep QKTGYVWQLLPNGMKPEYREX
||||||| ||||||| ||||||| ||||||| ||||||| |||||||
a919      QKTGYVWQLLPNGMKPEYREX
      430     440

```


Expression of ORF 919

The primer described in Example 1 for ORF 919 was used to locate and clone ORF 919. This sequence was purified and expressed in *E. coli* as provided in Figure 1 #. The hydrophilicity plots, antigenic index, and amphipathic regions of ORF 919 is provided in Figure 5 #. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 919 is provided in Exhibit C #.

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2795>:

```
g920.seq (partial)
1  ..ccgatgcagc tggttaccga aaaAGGTAAG GAAAACATGA TTCAACGCGG
51  CACATACAAC TACCAATACC GCAGCAACCG TCCCGTCAAA GACGGCAGCT
101 ACCTCGTTAC CGCCGAATAT CAGCCTACTT TCCGGTCAAA AAACAAAGCA
151 GGCTGGAAAC AGGCTGGCAT CAAAGAAATG CCTGACGCAA GCTATTGCGA
201 ACAAACCCGT ATGTTTCGTA AAAACATTGT CAACGTGGGA CACGAAAGCG
251 CGGACACCGC CATCATCACC AAACCGGTGC GACAAAACCT GGAAATCGTC
301 CCGCTGGACA ATCccgcccga caTTCACgtg ggctaacgCt tcaaaGTccg
351 cgttCtgttc cgtGGCgaac cgCTGcccaa tgccACCgtt accgCtacaT
401 TTGacggctt cGAcaccagc gaccgcagca aaacgcacaa Aaccgaagcc
451 caagcctTCT ccgacaccac cgacggcgaa ggcgaaagtgg acatcatCCC
501 CTGCGcccaa GGCTTtttga aAgcGAGTGT CGAATAcaaa gccgAttccc
551 CCGATcaaAG CCTGTGccga AAACAggcga ACTACaCaac TTtaaccttc
601 caaatcgccc attctCacca tTaa
```

This corresponds to the amino acid sequence <SEQ ID 2796; ORF 920.ng>:

```
g920.pep (partial)
1  ..PMQLVTEKGK ENMIQRGTYN YOYRSNRPVK DGSYLVTAEY QPTFRSKNKA
51  GWKQAGIKEM PDASYCEQTR MFGKNIVNVG HESADTAIIT KPVGQNLEIV
101 PLDNPAIDHV GXRFKVRVLF RGEPLPNATV TATFDGFDTS DRSKTHKTEA
151 QAFSDTIDGE GEVDIIPLRQ GFWKASVEYK ADFPDQSLCR KQANYTTLTf
201 QIAHSHH*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2797>:

```
m920.seq
1  ATGAAGAAAA CATTGACACT GCTCTCCGTT TCCGCCCTAT TTGCCACATC
51  CGCCCACGCC CACCGmGTCT GGGTCGAAAC CGCCCACACG CACGGCGGCG
101 AATACCTTAA AGCCGACTTG GGCTACGGCG AATTTCCTCGA ACTCGAACCC
151 ATCGCCAAAG ACCGCCTGCA CATCTTCAGC AAACCGATGC AGCTGGTTAC
201 CGAAAAAGGC AAGGAAAAACA TGATTCAACG CGGCACATAC AACTACCACT
251 ACCGAAGCAA CCGTCCCGTT AAGGACGGCA GTTACCTCGT CATCGCCGAA
301 TATCAGCCTA CTTTCTGGTC AAAAwACAAA GCAGGCTGGA AACAGGCGGG
351 CATCAAAGAA ATGCCTGACG CAAGCTATTG CGAACAAACC CGAATGTTCTG
401 GCAAAAACAT CGTCAACGTC GGACACGAAA GCGCGGACAC CGCCATCATC
451 ACCAArCCGG TCGGACAAAA CTTGGAAATC GTCCCGCTGG ACAATCCCGC
501 CAACATTACG GTAGGCGAAC GCTTCAAAGT CCGCGTTCTG TTCCGTGGCG
551 AACCGCTGCC CAATGCCACC GTTACCGCCA CCTTTGACGG CTTCGACACC
601 AGCGACCGCA GCAAAACGCA CAAwmCCGAA GCACAGGCTT TCTCCGACAG
651 CACAGACGAC AAAGGCGAAG TGGACATCAT CmCCTTGCGC CAAGGCTTCT
701 GGAAAGCCAA TGTCGAACAC AAAACCGACT TCCCGATCA AAGCGTGTGC
751 CAAAAACAGG CGAACTACTC GACTTTAACC TTCCAAATCG GTCATTGCGA
801 CCATTAA
```

This corresponds to the amino acid sequence <SEQ ID 2798; ORF 920>:

```
m920.pep
1  MKKTLTLHSV SALFATSAHA HRVWVETAHT HGGEYLKADL GYGEFPELEP
51  IAKDRLHIFS KPMQLVTEKG KENMIQRGTY NYOYRSNRPV KDGSYLVIAE
101 YOPTFWSKKK ACWKQAGIKE MPDASYCEQT RMFGKNIVNV GHESADTAII
151 TKPVGQNLEI VPLDNPAIDH VGERFKVRVL FRGEPLPNAT VTATFDGFDT
```

Homology with a predicted ORF from *N. gonorrhoeae*

from *N. gonorrhoeae*:

q920/m920

[illegible]

a920.seq

1	TGAAAGAAAA	CAATTGACACT	GCTCGCGGTT	TCCGCCCTAT	TTGCCGCATC
51	CGCCCCACGC	CACCGCGTCT	GGGTGGAAC	CGCCCCACAG	CACGGCGGCG
101	AATACCTTAA	AGCGACTTGT	GGCTACGGCG	AAATTTCCCA	AGTCGAACCC
151	ATCGCCAAAG	ACCGCTGCA	CATCTTCAG	AAACCGATGC	ACTCGGTTAC
201	CGAAAAAGGC	AAGGAAAAACA	TGATTCAACG	CGGCACATAC	AACTACCACT
251	ACCGAAGCAA	CCGTCCCGTT	AAGGACGGCA	GTTACCTCGT	CATCGCCGAA
301	TATCAGCCTA	CTTTCTGGCT	AAAAAACAA	GCAGGCTGGA	AACAGGCGGG
351	CATCAACAAC	ATGCTGTACG	CAAGCTATTG	CGAACAAACC	CGAATGTTCT
401	GCAAAAAACAT	CGTCACACGTC	GGACACGAA	GCGCGGACAC	CGGCATCATC
451	ACCAAACCGG	TGCGACAAAA	CTTGGAATC	GTCCCGCTGG	ACAATCCCGC
501	CAACATCTCAC	TGAGGCGAAC	GCTTCAAAGT	CCGCGTTCTG	TTCCGTTGGC
551	AACCGCTGCC	CAATGCCACC	GTTAACCGCA	CCTTTGACGG	CTTCGACACC
601	AGCGACCGCA	GCAAAACGCA	GTAAACCGAA	GCACAGGCTT	TCTCCGACAG
651	CACAGACGAC	AAAGGCGAAG	TGGACATCAT	CCCTTGCGC	CAAGGCTTCT
701	GGAAAGCCAA	TGTCGAACAC	AAAGCCGACT	TCCCGATCA	AAGCGTGTGC
751	CAAAAACAGG	CGAACTACTC	GACTTTAACC	TTCAAATCG	GCCATTGCGA
801	CAATTAA				

a920.pep

1	*KKTLLTLLA	<u>SALFAASAHA</u>	HRVWVETAHT	HGGEYLKADL	CYGEFPELEP
51	IAKDRLHISK	KPMQLVTEKG	KENMIZQRGT	NYQYRSNRFP	KDGSYLVAIE
101	YQPTFWSHFN	AGWKQAGIKQ	MPDASQEQT	RMFGKNIVNV	HGESADTAII
151	TKPVGQNLFI	VPLDNPAHNI	VGERFKVRVL	FRGEPLPNAT	VTATFDGFDI
201	SDRSKTHKTE	AQAFSDSTHD	KGEVDIIPLR	QGFWKANVEH	KADFPDQSVC
251	OKOANYSTIL	FOIGHSH**			

m920/a920 97.0% identity in 267 aa overlap

	10	20	30	40	50	60
m920.pep	MKKTLTLLSVSALFATSAHAHRVWVETAHTHGGEYLKADLGYGEFPELEPIAKDRLHIFS					
a920	XKKTLTLLVSAFSAHAHRVWVETAHTHGGEYLKADLGYGEFPELEPIAKDRLHIFS					
	10	20	30	40	50	60
m920.pep	70	80	90	100	110	120
	KPMQLVTEKGKKNMIQRTYNYQYRSNRPVKDGSYLVIAEYQPTFWSKKKAGWKQAGIKE					
a920	KPMQLVTEKGKKNMIQRTYNYQYRSNRPVKDGSYLVIAEYQPTFWSKKNAGWKQAGIKQ					
	70	80	90	100	110	120
m920.pep	130	140	150	160	170	180
	MPDASYCEQTRMFQKNIIVNVGHESADTAITKPVGQNLIVPLDNPANIHVGERFKVRVL					
a920	MPDASYCEQTRMFQKNIIVNVGHESADTAITKPVGQNLIVPLDNPANIHVGERFKVRVL					
	130	140	150	160	170	180
m920.pep	190	200	210	220	230	240
	FRGEPLPNATVTATFDGFDTSDRSKTHXEAQAFSDSTDGKGEVDIIXLRQGFWKANVEH					
a920	FRGEPLPNATVTATFDGFDTSDRSKTHKTEAQAFSDSTDGKGEVDIIPLRQGFWKANVEH					
	190	200	210	220	230	240
m920.pep	250	260	269			
	KTDFPDQSVQKQANYSTLTFOIGHSHHX					
a920	KADFPDQSVQKQANYSTLTFOIGHSHHX					
	250	260				

g920-1.seq

1	ATGAAGAA	CAATTGACACT	GCTCGCggtt	TcCGCACTAT	TTGCCACATc
51	cgCACACCCC	CACCGCTCT	GGGTCCGAAC	CgcCACACAg	cAcgGCGCCG
101	AATACCTTAA	AGCCGACTTG	GGTTCACGGC	AATTCCCGCA	ACTCGAACCC
151	ATCGcCAAG	ACGcctTGCA	CATCTTCAGC	AAACCGATGC	AGCTGGTTAC
201	CGAAaaAGGT	AAGGAaaACA	TGATTCAACG	CGGCACATAC	AACTACCAAT
251	ACCGCAGCA	CCGTCCGCTC	AAAGCAGCGA	GCTACTCTGT	TACCGCCGAA
301	TATCAGCTA	CTTTCCGCTC	AAAAAACATA	GCAGGCTGGA	ACAAGCCTGG
351	CATCAAGAA	ATGCTTGACG	CAGCTATCTT	CGAACAAACC	CGTATGTTTC
401	GTAaaAACAT	TGTCACCGTG	GGACACGAAA	GC CGCGACAC	CGCATCATCG
451	ACCAAAACCG	TCCGACGAAA	CTTGGAATCT	GTCCCGCTGG	ACAATCCCGC
501	CAACATTCA	GTAGCGCAAA	GCTTCAAAGT	CCGCGTCTGT	TTCCGTGGCG
551	AACCGCTGCC	CAATGCCACC	GTTACCGCTA	CATTTCAGCG	CTTCGACACC
601	AGCGACGCGA	CGAAAAACGA	CAAAACCGCA	CCCCAAGCTC	TCTCCGACAC
651	CACCGACGGC	AAAGCGCAAG	TGCATCATAT	CCCTTCGCC	CAGGCTTTT
701	GGAAGCGCAG	TGTCGAATAC	AAAGCCGATT	TCCCGCATCA	AAGCGTGTGC
751	CAAAAACAGG	CGAACTACAC	AACTTTAACC	TTCAAATCG	GCCATTCTCA
801	CCATTAA				

g920-1.pep

1	<u>MKKTLTLA</u>	<u>SALFATSAPH</u>	HRVWVETAHT	HGGEYLKADL	GYGEFPELEP
51	IAKRLDHIFS	KPMQLVTEKG	KENMIQRCTY	RYQFNSRNPV	KDGSYLVA7E
101	YQPTFRSKNG	AQWQAGIKE	KPDASISCEQ	NMFKGKINVV	GHESDATAI I
151	TKPVGQNLEI	VPLDNPANIH	VGERFKVRVL	FRGEPLPNAT	VTATDFDGFDT
201	SDRSKTHKE	QAQSDTTDG	KGEVDII PLR	QGFWKASVEY	KADDFDQGLC
251	OKQANYTTLT	FOFGSHH*			

m920-1.seq

1	ATGAAGAAAA	CATTGACACT	GCTCGCCGTT	TCCGCCCTAT	TTGCCACATC
51	CGCCACGCCG	CACCGCGTCT	GGGTACGAAAC	CGCCCAACAG	CACGCGCGGG
101	AATACCTTAA	AGCGCACTTG	GGGTACGCGC	AGTTTCCCGA	ACTCGAACCC
151	ATCGCCAAAG	ACCGCTTGCA	CATCTTCAGC	AAACCGATGC	AGCTGGTTAC
201	CGAAAAAGG	CAGGAAAAACA	TGATTCAACG	CGGCACATAC	AATCTACGAT
251	ACCGAAGCAA	CCGTCCCGTT	AAGACGCGCA	GTTACTCTGT	CACCTCCGAA

1323

```

301 TATCAGCCTA CTTTCTGGTC AAAAAACAAA GCAGGCTGGA AACAGGCGGG
351 CATCAAGAA ATGCCTGACG CAAGCTATTG CGAACAAACC CGAATGTTCTG
401 GCAAAAACAT CGTCAACGTC GGACACGAAA GCGCGGACAC CGCCATCATC
451 ACCAAACCGG TCGGACAAAA CTTGGAATC GTCCCGCTGG ACAATCCCGC
501 CAACATTAC GTAGGCGAAC GCTTCAAAGT CCGCGTTCTG TTCCGTGGCG
551 AACCGCTGCC CAATGCCACC GTTACCGCCA CCTTTGACGG CTTCGACACC
601 AGCGACCGCA GCAAAACGCA CAAAACCGAA GCACAGGCTT TCTCCGACAG
651 CACAGACGAC AAAGGCGAAG TGGACATCAT CCCCTTGCGC CAAGGCTTCT
701 GGAAGCCAA TGTCGAACAC AAAGCCGACT TCCCGGATCA AAGCGTGTGC
751 CAAAAACAGG CGAACTACTC GACTTTAACC TTCCAAATCG GTCATTTCGA
801 CCATTAA

```

This corresponds to the amino acid sequence <SEQ ID 2804; ORF 920-1>:

m920-1.pep

```

1 MKKTLTLLAV SALFATSAHA HRVWVETAHT HGGEYLKADL GYGEFFPELEP
51 IAKDRLHIFS KPMQLVTEKG KENMIQRGTY NYQYRSNRPV KDGSYLIVIAE
101 YQPTFWSKNK AGWKQAGIKE MPDASYCEQT RMFGKNIVNV GHESADTAII
151 TRPVQNLEI VPLDNPANIH VGERFKVRVL FRGEPLPNAT VTATFDGFD
201 SDRSKTHKTE AQAFSDSTDD KGEVDIIPLR QGFWKANVEH KTDFFDQSV
251 KQANYSTLT FQIGHSHH*

```

m920-1/g920-1 96.3% identity in 268 aa overlap

	10	20	30	40	50	60
m920-1.pep	MKKTLTLLAVSAI	FATSAHAHRVWVETAHT	HGGEYLKADL	GYGEFFPELEPI	IAKDRLHIFS	
g920-1	MKKTLTLLAVSALFATSAH	PHRVWVETAHTHGGEYLKADL	GYGEFFPELEPI	IAKDRLHIFS		
	10	20	30	40	50	60
	70	80	90	100	110	120
m920-1.pep	KPMQLVTEKG	KENMIQRGTY	NYQYRSNRPV	KDGSYLIVIAE	YQPTFWSKNK	AGWKQAGIKE
g920-1	KPMQLVTEKG	KENMIQRGTY	NYQYRSNRPV	KDGSYLIVIAE	YQPTFRSKNK	AGWKQAGIKE
	70	80	90	100	110	120
	130	140	150	160	170	180
m920-1.pep	MPDASYCEQTR	MFEGKNIVNVGHESADTAII	TKPVQNLEIV	VPLDNPANIH	VGERFKVRVL	
g920-1	MPDASYCEQTR	MFEGKNIVNVGHESADTAII	TKPVQNLEIV	VPLDNPANIH	VGERFKVRVL	
	130	140	150	160	170	180
	190	200	210	220	230	240
m920-1.pep	FRGEPLPNAT	VTATFDGFDTS	DRSKTHKTEA	QAFSDSTDD	KGEVDIIPLR	QGFWKANVEH
g920-1	FRGEPLPNAT	VTATFDGFDTS	DRSKTHKTEA	QAFSDTDG	KGEVDIIPLR	QGFWKASVEY
	190	200	210	220	230	240
	250	260	269			
m920-1.pep	KTDFFDQSV	CQKQANYSTLT	FQIGHSHHX			
g920-1	KADFFDQSL	CQKQANYTTL	FQIGHSHHX			
	250	260				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2805>:

a920.seq

```

1 TGAAAGAAAA CATTGACACT GCTCGCCGTT TCCGCCCTAT TTGCCGCATC
51 CGCCACAGCC CACCGCTCTT GGTGCGAAAC CGCCACACAG CACGGCGGGC
101 AATACCTTAA AGCCGACTTG GGCTACGGCG AATTCCCGA ACTCGAACCC
151 ATCGCCAAAG ACCGCTGCA CATCTTCAGC AAACCGATGC AGCTGGTTAC
201 CGAAAAAGGC AAGGAAAACA TGATTCAACG CGGCACATAC AACTACCACT
251 ACCGAAGCAA CCGTCCCGTT AAGGACGGCA GTTACCTCGT CATCGCCGAA
301 TATCAGCCTA CTTTCTGGTC AAAAAACAAA GCAGGCTGGA AACAGGCGGG
351 CATCAACAA ATGCCTGACG CAAGCTATTG CGAACAAACC CGAATGTTCTG
401 GCAAAAACAT CGTCAACGTC GGACACGAAA GCGCGGACAC CGCCATCATC
451 ACCAAACCGG TCGGACAAAA CTTGGAATC GTCCCGCTGG ACAATCCCGC
501 CAACATTAC GTAGGCGAAC GCTTCAAAGT CCGCGTTCTG TTCCGTGGCG
551 AACCGCTGCC CAATGCCACC GTTACCGCCA CCTTTGACGG CTTCGACACC
601 AGCGACCGCA GCAAAACGCA CAAAACCGAA GCACAGGCTT TCTCCGACAG
651 CACAGACGAC AAAGGCGAAG TGGACATCAT CCCCTTGCGC CAAGGCTTCT
701 GGAAGCCAA TGTCGAACAC AAAGCCGACT TCCCGGATCA AAGCGTGTGC
751 CAAAAACAGG CGAACTACTC GACTTTAACC TTCCAAATCG GCCATTTCGA
801 CCATTAA

```

This corresponds to the amino acid sequence <SEQ ID 2806; ORF 920-1.a>:

```
a920.pep
1  *KKLTLLAV SALFAASAHA HRVWVETAHT HGGEYLKADL GYGEFPELEP
51  IAKDRLHIFS KPMQLVTEKG KENMIQRGTY NYQYRSNRPV KDGSYLVAIE
101 YQPTFWSKNK AGWKQAGIKQ MPDASYCEQT RMFGKNIVNV GHESADTAII
151 TKPVGQNL EI VPLDNPANIH VGERFKVRVL FRGEPLPNAT VTATFDGFDT
201 SDRSKTHKTE AQAFSDSTDD KGEVDIIPLR QGFWKANVEH KADFPDQSVC
251 KQQANYSTLT FQIGHSHH*
```

m920-1/a920 98.9% identity in 267 aa overlap

	10	20	30	40	50	60
m920-1.pep	MKKTLTLLAVSALFATS	SAHAHRVWVETAHTHG	GEYLKADLGYGEFPE	LEPIAKDRLHIFS		
a920	KKKTLTLLAVSALFAA	SAHAHRVWVETAHTHG	GEYLKADLGYGEFPE	LEPIAKDRLHIFS		
	10	20	30	40	50	60
	70	80	90	100	110	120
m920-1.pep	KPMQLVTEKGKENMI	QRGTYNQYRSNRPVK	DGSYLVAIEYOPTF	WSKNKAGWKQAGIKE		
a920	KPMQLVTEKGKENMI	QRGTYNQYRSNRPVK	DGSYLVAIEYOPTF	WSKNKAGWKQAGIKQ		
	70	80	90	100	110	120
	130	140	150	160	170	180
m920-1.pep	MPDASYCEQTRMFGK	NIVNVGHESADTAII	TKPVGQNL EIVPLD	NPANIHVGERFKVRVL		
a920	MPDASYCEQTRMFGK	NIVNVGHESADTAII	TKPVGQNL EIVPLD	NPANIHVGERFKVRVL		
	130	140	150	160	170	180
	190	200	210	220	230	240
m920-1.pep	FRGEPLPNATVTATF	DGFDTSDRSKTHKTE	AQAFSDSTDDKGEVD	IIPLRQGFWKANVEH		
a920	FRGEPLPNATVTATF	DGFDTSDRSKTHKTE	AQAFSDSTDDKGEVD	IIPLRQGFWKANVEH		
	190	200	210	220	230	240
	250	260	269			
m920-1.pep	KTDFPDQSVCKQQAN	YSTLTTFQIGHSHHX				
a920	KADFPDQSVCKQQAN	YSTLTTFQIGHSHHX				
	250	260				

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2807>:

```
g921.seq
1  ATGAAAAAAT ACCTTATCCC TCTTTCCATT GCGGCAGTCC TTTCCGggtG
51  Ccagtcattt tatGtgccca cattgacggA aatccccgTg aatcccatca
101 ataCCgtcaa aacggaagCA CCTGCAAAAG GTTTTCGCCT CGCCCCCTCG
151 CATTGGGCGG ATGTTGCCAA AATCAGCGAT GAAGCGACGC GCTTGGGCTA
201 TCAGGTGGGT ATCGGTAAAA TGACCAAGGT TCAGGcgGCG CAATATCTGA
251 ACAACTTCAG AAAACGCCTG GTCGGACGCA ATGCCGTCTGA TGACAGTATG
301 TATGAAATCT ACCTGCGTTC GCGGTAGAC AGCCAGCGCG GCGAAATCAA
351 TACGGAACAG TCCAAGCTGT ATATCGAGAA TGCCTTGCGC GGCTGGCAGC
401 AGCGTtggAA AAATATGGAT GCCAAACCCG ATAATCCCGC ATTTACCAAC
451 TTTTGTATGG AAGTGATGAA GATGAGCCCC TTGAAATGA
```

This corresponds to the amino acid sequence <SEQ ID 2808; ORF 921.ng>:

```
g921.pep
1  MKKYLPLSI AAVLSGCQSI YVPTLTEIPV NPINTVKTEA PAKGFRLAPS
51  HWADVAKISD EATRLGYQVG IGKMTKVQAA QYLNFRKRL VGRNAVDDSM
101 YEIYLRSAVD SQRGEINTEQ SKLYIENALR GWQQRWKNMD AKPDNPAFTN
151 FLMEVMMQMP LK*
```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2809>:

```
m921.seq
1  ATGAAAAAAT ACCTTATCCC TCTTTCCATT GCGGCAGTTC TTTCCGGCTG
51  CCAGTCTATT TATGTGCCCA CATTGACGGA AATCCCCGTG AATCCTATCA
101 ATACCGTCAA AACGGAAGCA CCTGCAAAAG GTTTCCGCCT TGCTCTTTCG
151 CATTGGACGG ATGTTGCCAA AATCAGCGAT GAAGCGACGC GCTTGGGCTA
201 TCAGGTGGGT ATCGGTAAAA TGACCAAGGT TCAGGCGGCG CAATATCTGA
```

251 ACAACCTTCAG AAAACGCGCTG GTCGGACGCA ATGCCGTGCGA TGACAGTATG
301 TATGAAATCT ACCTGCGTTC GGCATAGACAG AGCCAGCGGG GCGCATCAAA
351 TACGGAAACAG TCCAAGTGT ATATCCAGAA TGCGTTGCGC GGCTGGCAGC
401 AGCGTTGGAA AATATGGAT GTCAAAACCA CCAACCCGC ATTTACCAAC
451 TTTTGTATGG AAGTGATGAA GATGCAGCCC TTGAAATGA

```

1  MKKYLIPLSI AAVLSGCQSI YVPTLTEIPV NPINTVKTEA PAKGFRCLASS
51  HWTDVAKISD EATRLGYQVG IGMKTKVQAA QYLNFRKRL VGRNAVDDSM
101 YBIYLRSAID SQRGAINTEQ SKLYIQNALR GWQQRWKNMD VKPNNPFTN
151 FLMEVMKMQP LK*

```

m921/g921

1	ATGAAAAAA	ACCTTATCCC	TCTTTCATT	GTGCGAGTTC	TTTCCGGCTG
51	CCAGTCTATT	TATGTGCCCA	CATTGACGGA	AATCCCCGTG	AATCCTATCA
101	ATACCGTCAA	AACGGAAGCA	CCTGCAAAG	GTTTCCGCCT	TGCTCTTCG
151	CATTGGACGG	ATGTTGCCAA	AACGACGAT	GAAGCGACGC	GCTTGGGCTA
201	TCAGGTGGGT	ATCGGTAAAA	TGACCAAGT	TACGGCGCGG	CAATACGTGA
251	ACAACCTTCAG	AAAACGCCTG	GTCGGACGCA	ATGCCGTCGA	TGACAGTATG
301	TATGAAATCT	ACCTGCGTTC	GGCGATAGAC	AGCCAGCGGG	GCGCAATCAA
351	TACGGAACAG	TCCAAGCTGT	ATATCCAGAA	TGCCTTCCGC	GGCTGGCAGC
401	AGCGTTGGAA	AAATATGGAT	GTCAAACCCA	ACAACCCCGC	ATTTACCAAC
451	TTTTTGATGG	AAGTGATGAA	GATCAGCCCC	TTGAAATGA	

```

1  MKKYLIPLSI VAVLSGCQSI YVPTLTEIPV NPINTVKTEA PAKGFRCLASS
51 HWTDVAKISD EATRLGYQVG IGMKTKVQAA QYLNNFRKRL VGRNAVDDSM
101 YEIYLRSAID SORGAINTEQ SKLYIQNALR GWQQRWKNMD VKPNNPAFTN
151 FLMEVMKMQP LK*

```

m921.pep
MKKYLIPLSLAAVLSCQSIYVPTLTEIPVNPINTVKTEAPAKGFRLASSHWTDVAKISD
|||||:::|||||
a921
MKKYLIPLSIVAVLSCQSIYVPTLTEIPVNPINTVKTEAPAKGFRLASSHWTDVAKISD
10 20 30 40 50 60

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	70	80	90	100	110	120
m921.pep	EATRLGYQVGIGKMTKVQAAQYLNNFRKRLVGRNAVDDSMYEIYLRSAIDSQRGAINTEQ					
a921	EATRLGYQVGIGKMTKVQAAQYLNNFRKRLVGRNAVDDSMYEIYLRSAIDSQRGAINTEQ					
	70	80	90	100	110	120
	130	140	150	160		
m921.pep	SKLYIQNALRGWQQRWKNMDVKPNNPAFTNFLMEVMKMQPLKX					
a921	SKLYIQNALRGWQQRWKNMDVKPNNPAFTNFLMEVMKMQPLKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2813>:

g922.seq

```

1  ATGGAAGA GAAAATACT GCCGCTGGCA ATTTGTTTGG CGGCTTTGTC
51  TGCCTGTACG GCGATGGAGG CCCGCACACC CCGGGCAAAT GAAGCCCAAG
101  CCCCCCGCGC GGATGAAATG AAAAAAGAAA GCCGCCCGC GTTTGACGCG
151  GCAGCCGTAC CGGTATCCGA CAGCGGGTTT GCCGCCAATG CAAATGTCCG
201  CCGTTTGTG GACGATGAAG TCGGGAAGG GGATTTTTC CAGGCGGAAT
251  GGCAGGATTT TTTTGACAAA GCGGCTTACA AGGCGGACAT CGTCAAGATT
301  ATGCACCGAC CCTCCACATC GCGtCCGTGG TATGtgttcc gCacggGAAa
351  ttcGGgcagg gcgaaAtttc ACggcgCGCG Caggttttat GcggaaAacc
401  gcgcggttat cgatgatgtg gcgCAAAaT acggcgTGCC TGCCGAGCTT
451  ATCGTGGCGA TTATCGGGAT TGAACGAAT TACGGCAAAA ATACGGGCAG
501  TTTCGTGTG GCGGACGCAT TGGCGACTTT AGGCTTTGAT TATCCCCGCC
551  GC3CCGGGTT TTTCCAAAAA GAATTGGTCG AGCTTTTAAA GCTGGCAAAA
601  GAAGAAGGCG GTGATGTTTT CGCCTTTAAG GGCagcTATG CGGGTGCAAT
651  GGGTATGCCG CAATTTATGC CTTCGAGCTA CCGGAAATGG GCGGTGGATT
701  ATGAcgggga cggacatCGG GATATAtggg GCAACGTcgg tgatgtcgcg
751  gcatcggTTG CCAATTatcT gaagCAGCAC GGTGGCGCA CgggcggTAA
801  AATGTTGGTG TCGGCGAcgt tggcgccggg tgccgATGTT CAggcAATCA
851  TTGGCGAATA ACCGCCCTG ACGCGGACGG TGGCGGATTT GAagcCGTAc
901  ggcacatccc ccggggaaac GCTCGCAGAT GATGAAAAGg cgGTTTGTGTT
951  CAACTGGAA ACCGCACCCG GCGTGTTTGA ATATTATTTG GGCTTGAACA
1001  ATTTTATATC GGTATGGCAG TACAACCACA GCCGGATGTA TGTAACGgcg
1051  gtcaggGACA TTGCCAATTC GCTCGGCGGC CCGGGATTGT Aa

```

This corresponds to the amino acid sequence <SEQ ID 2814; ORF 922.ng>:

g922.pep

```

1  MEKRKILPLA ICLAALSACT AMEARTPRAN EAQAPRADEM KKERPAFPA
51  AAVPVSDSGF AANANVRRFV DDEVGKGDFS QAEWQDFFDK AAYKADIVKI
101  MHRPSTSRPW YVFRGTNSGR AKFHGARRFY AENRAVIDDV AQKYGVPAEL
151  IVAIIGIETN YGKNTGSFRV ADALATLGFD YPRRAGFFQK ELVELLKLAK
201  EGGDVFAFK GSYAGAMGMP QFMPSSYRKW AVDYDGDGHR DIWGNVGDVA
251  ASVANYMKQH GWRTGGKMLV SATLAPGADV QAIIGECTAL TRTVADLKAY
301  GIIPGETLAD DEKAVLFKLE TAPGVFEYLL GLNNFYTVWQ YNHSRMVYTA
351  VRDIANSLGG PGL*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2815>:

m922.seq

```

1  ATGAAAAAGA GAAAATACT GCCGCTGGCA ATTTGTTTGG CGGCTTTGTC
51  TGCCTGTACG GCGATGGAGG CACGCCACACC CCGGGCAAAT GAAGCCCAAG
101  CCCCCCGCGC GGTGAAATG AAAAAAGAAA GCCGCCCGC GTTTGACGCG
151  GCAGCCGTAT TTGACGCGGC AGCCGTACCG GTATCCGACA GCGGGTTTGC
201  CGCCAATGCA AATGTCCGCC GTTTGTGTGA CGATGAAGTC GGGAAAGGGG
251  ATTTTTCCTG GCGGAATGG CAGGATTTT TCGACAAAGC GGCTTACAAG
301  GCGGACATCG TCAAGATTAT GCACCGCCCC TCACATCGC GTCCGTGGTA
351  TGTGTTCCGC ACGGGAAT TCGGCAAGG GAAATTCGC GCGCGCGGCC
401  GGTTTTATGC GGAAAACCGC GCGCTTATCG ATGATGTGCG GCAAAAATAC
451  GGCGTGCCTG CCGAATTAT CGTGGCGGTT ATCGGGATTG AAACGAATTA
501  CCGCAAAAT ACGGGCAGTT TCCGTGTGCG GGACGCATTG GCGACCTTAG
551  GCTTTGATTA CCCCCGCCG GCCGGGTTT TCAAAAAGA ATTGGTCGAG

```

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```

601 CTTTAAAGC TGGCAAAGA AGAAGGCGGC GATGTTTTCG CCTTAAAGG
651 CAGCTATGCG GCGCAATGG GGATGCCGCA ATTTATGCCT TCGAGCTACC
701 GGAATGGGC GGTGGATTAT GACGGGGACG GACATCGGGA CATATGGGGC
751 AACGTCGGCG ATGTCGCGGC ATCGGTTGCC AATTATATGA AGCAGCACGG
801 TTGGCGCACG GCGGGGAAAA TGCTGGTGTC TGCAACATTG GCGCCGGGTG
851 CGGATGTTCA GGCAATCATT GGCGAAAAA CCGCCCTGAC GCGGACGGTG
901 GCGGATTGTA AGCGGTACGG CATCATCCCC GGCGAAGAGC TTGCAGATGA
951 TGAAGAGGCG GTTTTGTTC AACTGGAAAC CGCACCAGGC GTGTTTGAAT
1001 ATTATTTGGG CTTGAACAAT TTTTATACGG TATGGCAGTA CAACCACAGC
1051 CGGATGTATG TAACGGCGGT CAGGGACATT GCCAATTTCG TTGGCGGCCC
1101 GGGATTGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2816; ORF 922>:

m922.pep

```

1 MKKRKILPLA ICLAALSACT AMEARPPRAN EAQAPRAVEM KKERPAFDA
51 AAVFDAAAVP VSDSGFAANA NVRRFVDEV GKGDfsRAEW QDFFDKAAYK
101 ADIVKIMHRP STSRPWVFR TNGSGKAKFR GARRFYAENR ALIDDDVAQKY
151 GVPaelIVAV IGIETNYGKN TGSFRVADAL ATLGFDYPRR AGFFQKELVE
201 LLKLAKKEGG DVFAFKGSYA GAMGMPQFMP SSYRKWAVDY DGDGHRDIWG
251 NVGDVAASVA NYMKQHGWR TGGKMLVSATL APGADVQAI GEKTALTRTV
301 ADLKAYGIIP GEELADDEKA VLFKLETAPG VFEYLLGLNN FYTVWQYNHS
351 RMYVTAVRDI ANSLGGPGL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 922 shows 95.9% identity over a 369 aa overlap with a predicted ORF (ORF 922.ng) from *N. gonorrhoeae*:

m922/g922

m922.pep	10	20	30	40	50	60
	MKKRKILPLAICLAALSACTAMEARPPRANEAQAPRAVEMKKESRPAFDAAAVFDAAAVP					
g922	MEKRKILPLAICLAALSACTAMEARTPRANEAQAPRADEMKKESRPAFDAA-----AVP					
	10	20	30	40	50	
m922.pep	70	80	90	100	110	120
	VSDSGFAANANVRRFVDEVGKGDFSRAEWQDFFDKAAYKADIVKIMHRPSTSRPWVFR					
g922	VSDSGFAANANVRRFVDEVGKGDFSQAEWQDFFDKAAYKADIVKIMHRPSTSRPWVFR					
	60	70	80	90	100	110
m922.pep	130	140	150	160	170	180
	TNGSGKAKFRGARRFYAENRALIDDDVAQKYGVPaelIVAVIGIETNYGKNTGSFRVADAL					
g922	TNGSGRAKFHARRFYAENRAVIDDDVAQKYGVPaelIVAIIGIETNYGKNTGSFRVADAL					
	120	130	140	150	160	170
m922.pep	190	200	210	220	230	240
	ATLGFDYPRRAGFFQKELVELLKLAKKEGGDVFAFKGSYAGAMGMPQFMPSSYRKWAVDY					
g922	ATLGFDYPRRAGFFQKELVELLKLAKKEGGDVFAFKGSYAGAMGMPQFMPSSYRKWAVDY					
	180	190	200	210	220	230
m922.pep	250	260	270	280	290	300
	DGDGHRDIWGNVGDVAASVANVMKQHGWR TGGKMLVSATLAPGADVQAI IGEKTALTRTV					
g922	DGDGHRDIWGNVGDVAASVANVMKQHGWR TGGKMLVSATLAPGADVQAI IGEKTALTRTV					
	240	250	260	270	280	290
m922.pep	310	320	330	340	350	360
	ADLKAYGIIPGEELADDEKAVLFLKLETAPGVFEYLLGLNNFYTVWQYNHSRMYVTAVRDI					
g922	ADLKAYGIIPGETLADDEKAVLFLKLETAPGVFEYLLGLNNFYTVWQYNHSRMYVTAVRDI					

300 310 320 330 340 350

m922.pwp

g922

a922.seq

1	ATGAAAAACA	GAAAAATACT	GCCGCTGGCA	ATTTGTTTGG	CGCCTTTGTC
51	TGCCTGTACG	GCGATGGAGG	CACGCCCGCC	CCGGGCAAAT	GAAGCCCAAG
101	CCCCCGCGC	GGATGAAATT	AAAAAAGAAA	GCCGCCCCGC	GTTTGACGCG
151	GCAGCCGTAT	TTGACGCGCG	AGCCGTACCG	GATATCCAGCA	CGGGGTTTG
201	GCCTAATGCA	AATGTCGCGC	GTTTTGTGGA	CGATGGAATC	GCGAAAGGGG
251	ATTTTTCCTG	GGCGGAATGG	CAGGATTTTT	TTGACAAAGC	GGCTTACAAG
301	GCGGACATCG	TCAAGATTAT	GCACCGCCCC	TCCACATCGC	CTCCGTGGTA
351	TGTGTTCCCG	ACGGGAATTT	CGGGCAAGGC	GAAATTTCCG	GGCGCGCGCC
401	GCTTTTATGC	GGAAACCGCG	CGCTTATCG	ATGATGTGGC	GCAAAAATAC
451	GGCGTGCCTG	CCGAACTTAT	CGTGGCGGTT	ATCGGGATTG	AACCAATTA
501	CGGCAAAAAT	ACGGGCAGTT	TCCGTGTGGC	GGACGCATTG	GCGACCTTAG
551	GCTTTGATTA	CCCCCGCGCG	GCCGGGTTTT	TCCAAAAAGA	ATTGGTCGAG
601	CTTTTAAAGC	TGGCAAAAAG	AGAAGCGCGC	GATGTTTTCC	CCTTTAAAGG
651	CAGCTATCGG	GGCGCAATGG	GACGTCCGCA	ATTTATGCCT	TCGAGCTACC
701	GGAAATGGGC	GGTGGATTAT	GACGGGGACG	GACATCGGGA	CATATGGGGC
751	AATGTTGGCG	ATGTCGCGGC	ATCGATTGCC	AATTATATGA	AGCAGCACGG
801	TTGGCGCCAC	GCGGGGAAAT	TACTGGTGTC	TGCAACATTG	GCGCCGGGTG
851	CGGATGTTCA	GGCAATCAAT	GGCAAAAAAT	CGGCCCTGAC	GCGGACGGTG
901	GCGGATTTGA	AGCGCTACGG	CATCATCCCC	GCGGAAGAGC	TGTCGGATGA
951	TGAAAAGGCG	GTITTGTTC A	AACTGGAAC	CGCACCCGGC	GTGTTTGAAT
1001	ATTATTGGG	CTTGAACAAT	TTTTATACGG	TATGGCAGTA	CAATCACAGT
1051	CGGATGTATG	TAACGGCGGT	CAGGGACATT	GCCAATTCCG	TTGGCGGCC
1101	GGGATTGTAA				

a922.ppt

```

2. pep
1  MKNRKILPLA ICLAALSACT AMEARPPRAN EAQAPRADEM KXESRPAFDA
51  AAVFDAAAVP VSDSGFAANA NVRRFVDDEV GKGFDSRAEW QDFFDKAAAYK
101 ADIVKIMHRP STSRPWYVFR TGNSGKAKFR GARRFYAENR ALIDDDVAQKY
151 GVPaelIVAV IGIETNYGKN TGSFRVADAL ATLGFDPYPRR AGFFQKELVE
201 LLKLAKKEEGG DVFAFKGSYA GAMGMPQFMP SSKRWAVDY DGDGHRDIWG
251 NVGDVAASIA NYMKQHGWRT GKKILVSATL APGADVQAI I GERTALTRTV
301 ADLKAYGIIP GEELADDEKA VLFKLETAPG VFEEYLLGLNN FYTVWQYNHS
351 RMYVTAVRDI ANSLGGVPL*

```

11/11/11, 09:58 PM

	10	20	30	40	50	60
m922.pep	MKKRKILPLAICLAALSACTAMEARPPRANEQAQAPRAVEMKKESRPAFDAAAVFDAAAVP					
a922						
	10	20	30	40	50	60
	MKNRKILPLAICLAALSACTAMEARPPRANEQAQAPRADEMCKESRPAFDAAAVFDAAAVP					
	70	80	90	100	110	120
m922.pep	VSDSGFAANANVRREFVDDEVGKGDFSRAEWQDDFKAAKYKADIVKIMHRPSTSRPWYVFR					
a922						
	70	80	90	100	110	120
	VSDSGFAANANVRREFVDDEVGKGDFSRAEWQDDFKAAKYKADIVKIMHRPSTSRPWYVFR					
	130	140	150	160	170	180
m922.pep	TGNSGKAKFRGARRFYAENRALIDDVAQKYGVPAELIVAVIGIETNYGKNTGSFRVADAL					
a922						
	130	140	150	160	170	180
	TGNSGKAKFRGARRFYAENRALIDDVAQKYGVPAELIVAVIGIETNYGKNTGSFRVADAL					
	190	200	210	220	230	240

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```

m922.pep  ATLGFDYPRRAGFFQKELVELLKLAKKEGGDVFAFKGSYAGAMGMPQFMPSSYRKWAVDY
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a922      ATLGFDYPRRAGFFQKELVELLKLAKKEGGDVFAFKGSYAGAMGMPQFMPSSYRKWAVDY
          190      200      210      220      230      240

          250      260      270      280      290      300
m922.pep  DGDGHRDIWGNVGDVAASVANYMKQHGWRGTGGKMLVSATLAPGADVQAIIGEKALTRTV
          ||||||||||||| ||:|||||||||||:||||||||||||||||||
a922      DGDGHRDIWGNVGDVAASIANYMKQHGWRGTGGKILVSATLAPGADVQAIIGEKALTRTV
          250      260      270      280      290      300

          310      320      330      340      350      360
m922.pep  ADLKAYGIIIPGEELADDEKAVLFKLETAPGVFEYYLGLNNFYTVWQYNHSRMYVTAVRDI
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a922      ADLKAYGIIIPGEELADDEKAVLFKLETAPGVFEYYLGLNNFYTVWQYNHSRMYVTAVRDI
          310      320      330      340      350      360

          370
m922.pep  ANSLGGPGLX
          |||||||||
a922      ANSLGGPGLX
          370

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2819>:

```

g923.seq
1  ATGAAGCGGC AGGCTTTCTT CAAACCGATG GCGTGTGCGG CATTTCTGTC
51  CGCCGTTTCG CTGCGCCTCC CCGTATTGGG CGCGTGTAC GCAATATTGT
101 CCCTCTATGC GTTTGCACTT TACGGCATCG ACAAACGGCG TGCCGTGCGG
151 GGAAAACGCC GCATTCCCGA ACACCGCCTG CTCCTGCCTG CCTTGTTCCG
201 CGGTTGGACG GCGGCATACT TGGGTAGTAG GATGTTTCAGG CATAAAACGG
251 CGAAAAGCG TTTTGTGTG CTGTTCCGTC TGACTGTTTC GGGCAATGTC
301 CTGGCGACCT GCATCCTGAT TGATTATTTT GTTCCGCCCG AACTTTTGTG
351 AAAACTCGGG CAACATCTCT GA

```

This corresponds to the amino acid sequence <SEQ ID 2820; ORF 923.ng>:

```

g923.pep
1  MKRQAFKPM ACAAFLSAVS LRLPVLGACY AILSLYAFAL YGIDKRRAVR
51  GKRRIPRHRL LLPALPGGWT GAYLGSRMFR HKTAKKRFV LFRLTVSGNV
101 LATCILIDYF VPPELFVKLG QHL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2821>:

```

m923.seq
1  ATGAAGCGGC AGGCTTTCTT CAAACTGATG GCGTGTGCGG CATTTCTGTC
51  TGCCGTTTCG CTGCGCCTCC CCGTATTGGG CGCGTGTAC GCAATATTGT
101 CCCTCTATGC GTTTGCACTT TACGGCATCG ACAAACGGTG CGCCATACGG
151 GGGCAACGCC GCATTCCCGA ACACCGCCTG CTGCTGCCTG CATTGCTCGG
201 CGGCTGGGTG GCGCGGTATT TCGGCAGCAT GACATTCAAA CATAAGACAG
251 CGAAAAGCG TTTTGTGTG CTGTTCCGTC TGACTGTTTC AGGTAATGTC
301 TTGGCGACCC TCATCCTGAT TTATAGTGA TTAAATTTAA ACCAGTACGG
351 CGTTGCCTCG CCTTGCCGTA CTATTGTAC TGTCTGCGGC TTCGTGCGCT
401 TGTCTGATT TTTGTTAATC CACTATAT.T ATTTTGTCCC GCCTGAATT
451 TTCGTAAAC TCGGCAGAA TACCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2822; ORF 923>:

```

m923.pep
1  MKRQAFKLM ACAAFLSAVS LRLPVLGACY AILSLYAFAL YGIDKRCRIR
51  GQRRIPRHRL LLPALLGGWV GAYFGSMTEK HKTAKKRFV LFRLTVSGNV
101 LATLILYSG LNLNOYGVAS PCRTICTVCG FVALS*FLLI HXYFVPPPEF
151 FVKLGQNT*

```

Computer analysis of this amino acid sequence gave the following results:

1330

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 923 shows 68.8% identity over a 157 aa overlap with a predicted ORF (ORF 923.ng) from *N. gonorrhoeae*:

g923/m923

	10	20	30	40	50	60
g923.pep	MKRQAFFKPMACAAFLSAVSLRPLVGLGACYAILSLYAFALYGIDKRRRAVRGKRRIPEHRL					
m923	MKRQAFFKLMACAAFLSAVSLRPLVGLGACYAILSLYAFALYGIDKRCAIRGQRRRIPEHRL					
	10	20	30	40	50	60
	70	80	90	100		
g923.pep	LLPALFGGWTGAYLGSRMFRHKHTAKKRFVVLFRLLTVSGNVLATCILID-----					
m923	LLPALLGGWVGAYFGSMTFKHKHTAKKRFVVLFRLLTVSGNVLATLILYISGLNQLNQYGVAS					
	70	80	90	100	110	120
			110	120		
g923.pep	-----YFVPPELFFVKLGQHLX					
m923	PCRTICTVCGFVALSXFLLIHYIYFVPPEFFVKLGQNTX					
	130	140	150			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2823>:

a923.seq

```

1  ATGAAGCGGC AGGCTTTCTT CAAACTGATG GCGTGTGCGG CATTCTGTGC
51  TGCCGTTTCG CTGCGCCTCC CCGTATTGGG CGCGTGTAC GCAATATTGT
101 CCCTCTATGC GTTTCGACTT TACGGCATCG ACAACGCGCG TGCCGTGCGG
151 GGAAAACGCC GCATTCCCGA ACACCGCCTG CTGCTGCCTG CCTTGTTCCG
201 CGGTTGGGCG GGCGCATACT TGGGCAGCAG GATATTCAGG CATAAACCGG
251 CGAAAAAGCG TTTTGTGTG CTGTTCCGTC TGAAGTTTC GGGCAATGTC
301 CTGGCGACCC TCATCCTGAT TTATAGTGGA TTAAATTTAA ACCAGTACGG
351 CGTTGCCTCG CCTTA.GCTC AAAGAGAACG ATTCTCTAAG GTGCTGAAGC
401 ACCAAGTGAA TCGGTTCCGT ACTATTGTA CTGTCTGCGG CTTGCTCGCC
451 TTGTCCTGAT TTTTGTTAAT CCACTAT.AT TATTTGTGCC CGCCTGAATT
501 TTTCGTAAAA CTCGGGCAGA ATACCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2824; ORF 923.a>:

a923.pep

```

1  MKRQAFFKLM ACAAFLSAVS LRLPVLGACY AILSLYAFAL YGIDKRAVR
51  GKRRRIPEHRL LLPALFGGWA GAYLGSRIFR HKTAKKRFV LFRLLTVSGNV
101 LATLILYISG LNLNQYGVAS PXAQRERFSK VLKHQVNRFR TICTVCGFVA
151 LS*FLLIHYX YFVPPEFFVK LGQNT*

```

m923/a923 84.6% identity in 175 aa overlap

	10	20	30	40	50	60
m923.pep	MKRQAFFKLMACAAFLSAVSLRPLVGLGACYAILSLYAFALYGIDKRCAIRGQRRRIPEHRL					
a923	MKRQAFFKLMACAAFLSAVSLRPLVGLGACYAILSLYAFALYGIDKRRRAVRGKRRIPEHRL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m923.pep	LLPALLGGWVGAYFGSMTFKHKHTAKKRFVVLFRLLTVSGNVLATLILYISGLNQLNQYGVAS					
a923	LLPALFGGWAGAYLGSRIFRHKHTAKKRFVVLFRLLTVSGNVLATLILYISGLNQLNQYGVAS					
	70	80	90	100	110	120
			130	140	150	159
m923.pep	PC-----RTICTVCGFVALSXFLLIHYXYFVPPEFFVKLGQNTX					
a923	PXAQRERFSKVLKHQVNRFTICTVCGFVALSXFLLIHYXYFVPPEFFVKLGQNTX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2825>:

```
g925.seq
  1  ATGAAACAAA TGCTTTTGGC cgtcggcggtg ggcgcggtgt TGGCGGGCTG
 51  CGGCAaggat gcCGGCGGtt acgaggggta TTGGCGCGAA AAGTCGGACA
101  AAAAagaggG CGTGATTGCC GTCAAAAAAA AAGGCAATTA CTTCCTTAAT
151  AAAATCAACG TGTTTACAGG CAAGGAGGAG TCTTTGCTTT TGTCTGAAAA
201  AGACGGCGCG CTTTCGATAA ACACGGGGAT AGGGGAAATC CCGATCAAAC
251  TTTCCGACGA CGGGAAAGAG CTGTATGTCT AACGCAGGCG GTATGTGAAA
301  ACCGATGCGG CGATGAAGGA CAAAATCATC GCCCACCAGA AAAAGTGCGG
351  ACAACCGGCA CAGGCATACC TCGACGCGCG AAATGCGTTG CCGTCAAACC
401  AAACGTATCA GCAGCGTCAG GCGGCGATCG AGCAATTGAA ACGGCGGTTT
451  GAAGCCGAGT TTGACGAATT GGA AAAAGAA ATCAAATGCA ACGGCAAACC
501  GACATTGTTG TTTTAG
```

This corresponds to the amino acid sequence <SEQ ID 2826; ORF 925.ng>:

```
g925.pep
  1  MKQMLLAVGV GAVLAGCGKD AGGYEGYWRE KSDKKEGVIA VKKKGNVFLN
 51  KINVFTGKEE SLLSEKDGA LSINTGIGEI PIKLSDDGKE LYVERRRYVK
101  TDAAMKDKII AHQKKCGQT QAYLDARNAL PSNQTYQQRQ AAIEQLKRRF
151  EAFFDELEKE IKCNKPTLL F*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2827>:

```
m925.seq (partial)
  1  ATGAAACAAA TGCTTTTAGC CGTCGGCGTG GTGGCGGTGT TGGCGGGCTG
 51  CGGCAAGGAT GCCGGCGGTT ACGAGGGTTA TTGGCGCGAA AAGTCGGACA
101  AAAAAGAGGG TATGATTGCC GTCAAAAAG AAAAAGGCAA TTACTTCCTT
.....
```

This corresponds to the amino acid sequence <SEQ ID 2828; ORF 925>:

```
m925.pep (partial)
  1  MKQMLLAVGV VAVLAGCGKD AGGYEGYWRE KSDKKEGMIA VKKEKGNVFL..
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 925 shows 94.0% identity over a 50 aa overlap with a predicted ORF (ORF 925.ng) from *N. gonorrhoeae*:

m925/g925

	10	20	30	40	50
m925.pep	MKQMLLAVGVVAVLAGCGKDAGGYEGYWREKSDKKEGMIAVKKKEKGNVFL				
g925	MKQMLLAVGVGAVLAGCGKDAGGYEGYWREKSDKKEGVIAVKK-KGNVFLNKNINVFTGKE				
	10	20	30	40	50
g925	ESLLSEKDGALSINTGIGEIPKLSDDGKELYVERRRYVKTDAAAMKDKIIAHQKKCGQT				
	60	70	80	90	100
	110				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2829>:

```
g925-1.seq
  1  ATGAAACAAA TGCTTTTGGC CGTCGGCGTG CCGGCGGTGT TGGCGGGCTG
 51  CGGCAAGGAT GCCGGCGGTT ACGAGGGTTA TTGGCGCGAA AAGTCGGACA
101  AAAAAGAGGG CGTGATTGCC GTCAAAAAAA AAGGCAATTA CTTCCTTAAT
151  AAAATCAACG TGTTTACAGG CAAGGAGGAG TCTTTGCTTT TGTCTGAAAA
201  AGACGGCGCG CTTTCGATAA ACACGGGGAT AGGGGAAATC CCGATCAAAC
251  TTTCCGACGA CGGGAAAGAG CTGTATGTCT AACGCAGGCG GTATGTGAAA
301  ACCGATGCGG CGATGAAGGA CAAAATCATC GCCCACCAGA AAAAGTGCGG
351  ACAACCGGCA CAGGCATACC TCGACGCGCG AAATGCGTTG CCGTCAAACC
401  AAACGTATCA GCAGCGTCAG GCGGCGATCG AGCAATTGAA ACGGCGGTTT
451  GAAGCCGAGT TTGACGAATT GGA AAAAGAA ATCAAATGCA ACGGCAAACC
501  GACATTGTTG TTTTAG
```

This corresponds to the amino acid sequence <SEQ ID 2830; ORF 925-1.ng>:

g925-1.pep

1332

```

1  MKOMLLAVGV AAVLAGCGKD AGGYEGYWRE KSDKKEGVIA VKKKGNYFLN
51 KINVFTGKEE SLLSEKDG ALSINTGIGE IPIKLSDDGKE ELYVERRRYV
101 TDAAMKDKII AHQKKCGQT AQAYLDARNA LPSNQTYYQQRQ AAIEQLKRRR
151 EAEFDELEKE IKCNGKPTLL F*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2831>:

```

m925-1.seq
1  ATGAAACAAA TGCTTTTACG CGTCGGCGTG GTGGCGGTGT TGGCGGGCTG
51  CGGCAAGGAT GCCGGCGGTT ACGAGGGTTA TTGGCGCGAA AAGTCGGACA
101 AAAAAGAGGG TATGATTGCC GTCAAAAAAG AAAAAGGCAA TTACTTCCTT
151 AATAAAATCC ACGTGGTTAC AGGCAAGGAA GAGTCCTTGC TTTTGTCTGA
201 AAAAGACGGC GCGCTTTCGA TAAACACAGG GATAGGGGAA ATCCCGATCA
251 AACTTTCCGA CGACGGGAAA GAGCTGTATG TCGAACGTCG GCAGTATGTC
301 AAAACCGATG CGGCGATGAA GGACAAAATC ATCGCCCATC AGAAAAAGTG
351 CGGACAAACA GCACAGGCAT ACCGCGACGC GCGAAATGCG TTGCCGTCAA
401 ACCAGACGTA TCAGCAGCAT CTGGCGGCGA TCGAGCAATT GAAACGGCGG
451 TTTGAAGCCG AGTTTGACGA ATTGGAAGAA GAAATCAAT GCAACGGCAG
501 AAGCCCGCGA TTGTTGCTTT AS

```

This corresponds to the amino acid sequence <SEQ ID 2832; ORF 925-1>:

```

m925-1.pep..
1  MKOMLLAVGV VAVLAGCGKD AGGYEGYWRE KSDKKEGMIA VKKEKGYFLN
51 NKINVFTGKE ESLLSEKDG ALSINTGIGE IPIKLSDDGK ELYVERRQYV
101 KTDAMKDKII IAHQKKCGQT AQAYRDARNA LPSNQTYYQH LAIEQLKRR
151 FEAEFDELEK EIKCNGRSPA LLL*

```

m925/g925 92.5% identity in 173 aa overlap

	10	20	30	40	50	60
m925-1.pep	MKQMLLAGVVAVLAGCGKDAGGYEGYWREKSDKKEGMIAVKKEKGYFLNKHVVVTGKE					
g925-1	MKQMLLAGVAAVLAGCGKDAGGYEGYWREKSDKKEGVIAVKK-KGNYFLNKHVVVTGKE					
	10	20	30	40	50	
	70	80	90	100	110	120
m925-1.pep	ESLLSEKDGALSINTGIGEIPKLSDDGKELYVERRRYVKTDAAMKDKIIAHQKCGQT					
g925-1	ESLLSEKDGALSINTGIGEIPKLSDDGKELYVERRRYVKTDAAMKDKIIAHQKCGQT					
	60	70	80	90	100	110
	130	140	150	160	170	
m925-1.pep	AQAYRDARNALPSNQTYYQHLAAIEQLKRRFEAEFDELEKEIKCNGRSPALLLX					
g925-1	AQAYLDARNALPSNQTYYQQAIEQLKRRFEAEFDELEKEIKCNGK-PTLLFX					
	120	130	140	150	160	170

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2833>:

```

a925-1.seq
1  AATAAAATCA ACGTGTTTAC AGGTAAGGAA GAATCTATGC TTTTGTCTGA
51 AAAAGACGGC GCGCTTTCGA TAAACACGGG GATAGGGGAA ATCCCGATCA
101 AACTTTCCGA CGACGGGAAA GAGCTGTATG TCGAACGCAG GCAGTATGTC
151 AAAACCGATG CGGCGATGAA GGACAAAATC ATCGCCCATC AGAAAAAGTG
201 CGGACAAACG GCACAGGCAT ATCTCGACGC GCGAAATGCG TTGCCGTCAA
251 ACCAGACGTA TCAGCAGCAT CAGGCGGCGA TCGAGCAGTT GAAACGGCGG
301 TTTGAAGCCG AGTTTGACGA ATTGGAAGAA GAAATCAAT GCAACGGCAA
351 ACCGACATTG TTGTTTTAG

```

This corresponds to the amino acid sequence <SEQ ID 2834; ORF 925-1.a>:

```

a925-1.pep
1  NKINVFTGKE ESMLLSEKDG ALSINTGIGE IPIKLSDDGK ELYVERRQYV
51 KTDAMKDKII IAHQKKCGQT AQAYLDARNA LPSNQTYYQH QAAIEQLKRR
101 FEAEFDELEK EIKCNGKPTL LF*

```

a925-1/m925-1 92.7% identity in 123 aa overlap

	10	20	30
a925-1.pep	NKINVFTGKEESMLLSEKDGALSINTGIGE		
m925-1	AGGYEGYWREKSDKKEGMIAVKKEKGYFLNKHVVVTGKEESLLSEKDGALSINTGIGE		
	30	40	50
	60	70	80
	90		

1333

```

a925-1.pep  IPIKLSDDGKELYVERRQYVKTDAAMKDKIIAHQKKCGQTAQAYLDARNALPSNQTYYQH
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
m925-1      IPIKLSDDGKELYVERRQYVKTDAAMKDKIIAHQKKCGQTAQAYRDARNALPSNQTYYQH
              90      100      110      120      130      140

              100      110      120
a925-1.pep  QAAIEQLKRRFEAEFDELEKEIKCNGK-PTLLFX
              |||||||||||||||||||||:|:|:|
m925-1      LAATIEQLKRRFEAEFDELEKEIKCNGRSPALLLX
              150      160      170

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2835>:

```

g926.seq (partial)
1  ATGAAACACA CCGTATCCGC ATCGGTCATC CTGCTTTTGA CCGCTTGCGC
51  GCAATTACCT CAAAATAACG AAAACCTGTG GCAGCCGTCC GAACACATCA
101 GCAGTTTTCG AGCGGAAGGG CGGTTGGCAG TCAAAGCGGA AGGGAAGGT
151 TCGTATGCAA ATTTCGATTG GACATACCAA CCGCCCGTGG AAACCATCAA
201 TATCAACACC CCTTTGGGCA GTACGCTCGG ACAGTTGTGT CAAGAcAGGG
251 ACGGCGCATT GGCAGTGGAC GGCAAAGGAA ATGTCTATCA GGCAGAGGCT
301 ACGgaagact tGAGCAGGCA GCTGGTCGGT TTCAAACGTC CAATCCAATA
351 TCTGCATATC TGGGCGGAAG GCAGGCGTGT GCGGGGCGCG CCTtaccGCA
401 TCCGTTTCA GGCATATTG GAACAATAcg GttggACAAT cgggCagaac
451 tgcCGACAGT GGGGGGCaag tccgaacgtt gcaactGAa...

```

This corresponds to the amino acid sequence <SEQ ID 2836; ORF 926.ng>:

```

g926.pep (partial)
1  MKHTVSASVI LLLTACAQLP QNNENLWQPS EHISSFAAEG RLAVKAEGKG
51  SYANFDWTYQ PPVETININT PLGSTLGQLC QDRDGALAVD GKGNVYQAE
101 TEDLSRQLVG FKLPIQYLHI WAEGRRVAGA PYRIRSDGIL EQYGTWIGQN
151 CRQWGASPNV ATE...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2837>:

```

m926.seq
1  ATGAAACACA CCGTATCCGC ATCGGTCATC CTGCTTTTGA CCGCTTGCGC
51  GCAATTACCT CAAAATAACG AAAACCTGTG GCAGCCGTCC GAACACATCA
101 GCAGTTTTCG AGCAGAAGGG CGGTTGGCAG TGAAGCGGA AGGGAAGGT
151 TCGTATGCAA ATTTCGATTG GACATACCAA CCGCCCGTGG AAACCATCAA
201 TATCAATACC CCTTTGGGCA GTACGCTCGG GCAGTTGTGT CAAGACAGGG
251 ACGGCGCATT GGCAGTGGAC GGCAAAGGAA ATGTCTATCA GCGGAAAGT
301 GCGGAAGAAT TGAGCAGGCA GCTGGTCGGT TTCAAACGTC CAATCCAATA
351 TCTGCATATC TGGGCAGATG GCAGGCGTGT GCGGGGCGCG CCTTACCGCA
401 TCCTGCCGGA CGGCATATTG GAACAATACG GTTGGACTGT CGGCAGAACC
451 GCCGACAGTG GGGGGCAAGT CCGAACGTTG CAACTGAATA ACGGAAATTT
501 GAACATCAGG CTGGTTTTC CCGAAATCGG TATGCCGTCT GAAACCGAAA
551 CCCCAGAACG CTGTGCGGCG CCCACGAGAT AA

```

This corresponds to the amino acid sequence <SEQ ID 2838; ORF 926>:

```

m926.pep
1  MKHTVSASVI LLLTACAQLP QNNENLWQPS EHISSFAAEG RLAVKAEGKG
51  SYANFDWTYQ PPVETININT PLGSTLGQLC QDRDGALAVD GKGNVYQAE
101 AEELSRQLVG FKLPIQYLHI WADGRVAGA PYRILPDGIL EQYGTWVGR
151 ADSSGQVRTL QLNNGNLNIR LVFTEIGMPS ETETPERCAA RTR*

```

g926/m926 91.6% identity in 155 aa overlap

```

              10      20      30      40      50      60
g926.pep  MKHTVSASVILLTACAQLPQNNENLWQPSEHISSFAAEGRLAVKAEGKGSYANFDWTYQ
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
m926      MKHTVSASVILLTACAQLPQNNENLWQPSEHISSFAAEGRLAVKAEGKGSYANFDWTYQ
              10      20      30      40      50      60

              70      80      90      100     110     120
g926.pep  PPVETININTPLGSTLGQLCQDRDGALAVDGKGNVYQAEGETEDLSRQLVGFKLPIQYLHI
              |||||||||||||||||||||||||||||:|:|:|
m926      PPVETININTPLGSTLGQLCQDRDGALAVDGKGNVYQAEAEELSRQLVGFKLPIQYLHI
              70      80      90      100     110     120

              130     140     150     160
g926.pep  WAEGRRVAGAPYRIRSDGILEOYGTWIGQNCRWGASPNVATE

```

1334

```

|||||
m926  WADGRRVAGAPYRILPDGILEQYGWTVGRTADSGGQVRTLOLNNGNLNIRLVFTEIGMPS
      130      140      150      160      170      180

a926.seq
1  ATGAAACACA CTGTATCCGC ATCGGTCATC CTGCTTTTGA CCGCTTGCGC
51  GCAATTACCT CAAAATAACC AAAACCTGTG GCAGCCGTCC GAACACACCC
101 GCAGTTTCAC GCGGAAGGG CGGTTGGCAG TGAAAGCGGA AGGGAAAGGT
151 TCGTATGCAA ATTTCGATTG GACATACCAA CCGCCCGTGG AAACCATCAA
201 TATCAACACC CCTTTGGGCA GTACGCTCGG GCAGTTGTGT CAAGACAGGG
251 ACGGCGCATT GGCAGTGGAC GGCAAAGGAA ATGTCTATCA GSCGGAAAGT
301 GCGGAAGAAT TGAGCAGGCA GCTGGTCGGT TTCAAACTGC CAATCCAATA
351 TCTGCATATC TGGGCAGATG GCAGGCCTGT GGCGGGCGCG CTTACCGCA
401 TCCTGCCGGA CGGCATATTG GAACAATACG GTTGGACTGT CAGCAGAACCC
451 GCCGACAGTG GGGGGCAAGT CCGAACGTTG CAACTGAATA ACGGAAATTT
501 GAACATCAGG CTGCTTTTCA CCGAGATTGG TATGCCGTCT GAAACCGAAA
551 CCCAAGAACA ATGCGCGGCA CGCATACAGT AA

a926.pep
1  MKHTVSASVI LLLTACAQLP QNNENLWQPS EHTRSFTAEG RLAVKAEKGK
51  SYANFDWTYQ PPVETININT PLGSTLGQLC QDRDGALAVD GKGNVYQAES
101 AEELSRQLVG FKLPIQYLHI WADGRPVAGA PYRILPDGIL EQYGWTVGRT
151 ADSSGQVRTL QLNNGNLNIR LVFTEIGMPS ETETQECCAA RIQ*

```

m926/a926 96.9% identity in 191 aa overlap

```

      10      20      30      40      50      60
m926.pep  MKHTVSASVILLTACAQLPQNNENLWQPSSEHISFAAEGRLAVKAEKGKSYANFDWTYQ
      |||||
a926      MKHTVSASVILLTACAQLPQNNENLWQPSSEHTRSFTAEGRLAVKAEKGKSYANFDWTYQ
      10      20      30      40      50      60

      70      80      90      100     110     120
m926.pep  PPVETININTPLGSTLGQLCQDRDGALAVDGKGNVYQAESAEELSRQLVGFKLPIQYLHI
      |||||
a926      PPVETININTPLGSTLGQLCQDRDGALAVDGKGNVYQAESAEELSRQLVGFKLPIQYLHI
      70      80      90      100     110     120

      130     140     150     160     170     180
m926.pep  WADGRRVAGAPYRILPDGILEQYGWTVGRTADSGGQVRTLOLNNGNLNIRLVFTEIGMPS
      |||||
a926      WADGRPVAGAPYRILPDGILEQYGWTVGRTADSGGQVRTLOLNNGNLNIRLVFTEIGMPS
      130     140     150     160     170     180

      190
m926.pep  ETETPERCAARTRX
      |||| |:|||
a926      ETETQECCAAARIQX
      190

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2839>:

```

g927.seq
1  atgaaaacct acGCacAggC ACTCTATacc GCAGCCCTGC TCACCGCCTG
51  CAGCCCGcga GCcgatTcaa accaTCCGTC CGGAcAaAAT GCCCCGGCCA
101 ATACCGAATC cgacGgaaAA AACATtacc TGctcaatgc cTcgtacgat
151 gtGACACGGT ATTTttacaa agaatacgac cacTtggttg tcggaaCATA
201 CCAATCCGAA CACCCCGGCA CATCCGTcAG CATCCAACAA TCCCACGCGC
251 GCTTCAGCAA ACAGGCATTA TCCGTAGCCA ACGGCCTTCA AGCCGATGTC
301 GTAACCATGA ACCAATCTTC CGACATCGAC CTGCTCGAAA AAAA.GGACT
351 GGTAGAAAAA GGCTGGCAAC AAGCCCTCCC CGATCACGCC GCACCCCTACA

```

1335

```

401 CCAGCACTAT GGTTCCTT GTCCGAAAA ACAACCCaa ACAGAtccgC
451 GATTGGAACG ACCTTGCCAA AGACGGCGTT AACATCGTCA TCGCCAAGAC
501 CTCGGGCAAC GGACGCTACG CCTTCCTCGG CGCATACGGT TACGGTCTGA
551 AAGCCAACAA CGGcaaCGAG CA3GAAGCCC AAAAATCTGT CGCATCCATC
601 CTCAAAAACA CACCCGTTTT TGAAAACGGC GGACGCGc.C CGCCGCCACC
651 ACCTTCACAC AACGCAACAT CGGCGACGTA CTCATCACTT TTGAAAACga
701 agCcaactac gtCAGCAAAA AACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2840; ORF 927.ng>:

g927.pep

```

1 MKTYAQALYT AALLTACSPA ADSNHPSGQN APANTESDGK NITLLNASYD
51 VTRYFYKEYD HLFVGTYSQSE HPGTSVSIQQ SHGGFSKQAL SVANGLQADV
101 VTMNQSSDID LLEKXGLVEK GWQQALPDHA APYTSTMVFL VRKNNPKQIR
151 DWNDLAKDGV NIVIAKTSN GRYAFLGAYG YGLKANNGNE QEAQKLVASI
201 LKNTVPFENG GRXPPPPSH NATSATYSSL LKTKPTTSAK N*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2841>:

m927.seq

```

1 ATGAAAACCT ACGCACCAGC ACTCTATACC GCAGCCCTGC TCACCGCCTG
51 CAGCCCCGCA GCCGATTCAA ACCATCCGTC CGGACAAAT GCCCCGCCA
101 ATACCGAATC CGACGGAAAA AACATTACCC TGCTCAACGC CTCATACGAT
151 GTGGCAGCGG ATTTTACAA AGAATACAAC CCCTATTATTA TCAAAACATA
201 CCAATCCGAA CACCCCGGCA CATCCGTCAG CATCCAACAG TCCACCGGCG
251 GCTCCAGCAA ACAGGCATTA TCCGTAGCCA ACGGCCTTCA AGCCGATGTC
301 GTAACCATGA ACCAATCCTC CGACATCGAC CTGCTCGAAA AAAAAGGACT
351 GGTAGAAAAA GGCTGGCAAC AAGCCCTCCC CGACCACGCC GCGCCCTACA
401 CCAGCACTAT GGTTCCTT GTCCGAAAA ACAACCCAA ACAGATCCGC
451 GATTGGAACG ACCTTGCCAA AGACGGC3TT AACATCGTCA TCGCCAATCC
501 CAAACCTCG GGCAACGGAC GCTACGCCTT CCTCGGCGCA TACGGTTACG
551 GTCTGAAAAA CACCAACGGC AACGAACAGG AAGCCCAAAA ACTCGTCGCA
601 TCCATCTCA AAAACACCCC CGTTTGTGAA AACGGCGGAC GCKCgCCACC
651 ACCACCTTCA CACAACGCAA CATCGGCGAC GTACTCATCA CTTTGTAAAA
701 CGAAGCCAAC TACGTACGc AAAAActGA

```

This corresponds to the amino acid sequence <SEQ ID 2842; ORF 927>:

m927.pep

```

1 MKTYAPALYT AALLTACSPA ADSNHPSGQN APANTESDGK NITLLNASYD
51 VARDFYKEYN PLFIKTYQSE HPGTSVSIQQ SHGGSSKQAL SVANGLQADV
101 VTMNQSSDID LLEKGLVEK GWQQALPDHA APYTSTMVFL VRKNNPKQIR
151 DWNDLAKDGV NIVIANPKTS GNGRYAFLGA YGYGLKTTNG NEQEAQKLVA
201 SILKNTVPFE NGRXPPPPS HNATSATYSS LLKTKPTTSA KN*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 927 shows 94.2% identity over a 243 aa overlap with a predicted ORF (ORF 927.ng) from *N. gonorrhoeae*:

g927/m927

	10	20	30	40	50	60
g927.pep	MKTYAQALYTAALLTACSPAADSNDHPSGQNAPANTESDGKNITLLNASYDVTRYFYKEYD					
m927	MKTYAPALYTAALLTACSPAADSNDHPSGQNAPANTESDGKNITLLNASYDVARDFYKEYN					
	10	20	30	40	50	60
g927.pep	HLFVGTYSQSEHPGTSVSIQQSHGGFSKQALSVANGLQADVVTMNQSSDIDLLEKXGLVEK					
m927	PLFIKTYQSEHPGTSVSIQQSHGGSSKQALSVANGLQADVVTMNQSSDIDLLEKGLVEK					
	70	80	90	100	110	120
g927.pep	GWQQALPDHAAPYTSTMVFLVRKNNPKQIRDWNDLAKDGVNIVIA--KTSNGRYAFLGA					
m927	GWQQALPDHAAPYTSTMVFLVRKNNPKQIRDWNDLAKDGVNIVIANPKTSNGRYAFLGA					
	130	140	150	160	170	180

1336

```

      180      190      200      210      220      230
g927.pep  YGYGLKANNGNEQEAQKLVASILKNTPVFENGGRXPPPPPSHNATSATYSSLLKTKPTTS
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m927      YGYGLKTTNGNEQEAQKLVASILKNTPVFENGGRXPPPP-SHNATSATYSSLLKTKPTTS
          190      200      210      220      230

      240
g927.pep  AKNX
          ||||
m927      AKNX
          240

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2843>:

```

a927.seq
1  ATGAAAACCT  ACGCACCGGC  AACTCTATACC  GCAGCCCTGC  TCAGCGCCTG
51  CAGCCCCGCA  GCCGATTCAA  ACCATCCGTC  CGGACAAAAT  GCCCCGGCCA
101 ATACCGAATC  CGACGGAAAA  AACATTACCC  TGCTCAACGC  CTCATACGAT
151 GTGGCACGGG  ATTTTACAA  AGAATACAAC  CCCTTATTTA  TCAAAACATA
201 CCAATCCGAA  CACCCCGGCA  CATCCGTCAG  CATCCAACAG  TCCCACGGCG
251 GCTCCAGCAA  ACAGGCATTA  TCCGTAGCCA  ACGGCCTTCA  AGCCGATGTC
301 GTAACCATGA  ACCAATCCTC  CGACATCGAC  CTGCTCGAAA  AAAAAGGACT
351 GGTAGAAAAA  GGCTGGCAAC  AAGCCCTCCC  CGACCACGCC  GCGCCCTACA
401 CCAGCACTAT  GGTTTTCTT  GTCCGAAAAA  ACAACCCCAA  ACAGATCCCG
451 GATTGGAACG  ACCTTGCCAA  AGACGGCGTT  AACATCGTCA  TCGCCAATCC
501 CAAAACCTCG  GGCAACGGAC  GTACGCCTT  CCTCGGCGCA  TACGGTTACG
551 GTCTGAAAAC  CACCAACGGC  AACGAACAGG  AAGCCCAAAA  ACTCGTCGCA
601 TCCATCCTCA  AAAACACCCC  CGTTTTTGAA  AACGGCGGAC  GCGCGCCACC
651 ACCACCTTCA  CACAACGCAA  CATCGGCGAC  GTACTCATCA  CTTTGAAAA
701 CGAAGCCAAC  TACGTCAGCA  AAAAAGTGA

```

This corresponds to the amino acid sequence <SEQ ID 2844; ORF 927.a>:

```

a927.pep
1  MKTYAPALYT  AALLSACSPA  ADSNHPSGQN  APANTESDGK  NITLLNASYD
51  VARDFYKEYN  PLFIKTYQSE  HPGTSVSIQQ  SHGGSSKQAL  SVANGLQADV
101 VTMNQSSDID  LLEKKGLVEK  GWQALPDHA  APYTSTMVFL  VRKNNPKQIR
151 DWNDLAKDGV  NIVIANPKTS  GNGRYAFLGA  YGYGLKTTNG  NEQEAQKLVA
201 SILKNTPVFE  NNGRAPPPPS  HNATSATYSS  LLKTKPTTSA  KN*

```

m927/a927 99.2% identity in 242 aa overlap

```

      10      20      30      40      50      60
m927.pep  MKTYAPALYTAALLTACSPAADSNHPSGQNAPANTESDGKNITLLNASYDVARDFYKEYN
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a927      MKTYAPALYTAALLSACSPAADSNHPSGONAPANTESDGKNITLLNASYDVARDFYKEYN
          10      20      30      40      50      60

      70      80      90      100     110     120
m927.pep  PLFIKTYQSEHPGTSVSIQQSHGGSSKQALSVANGLQADVVTMNQSSDIDLLEKKGLVEK
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a927      PLFIKTYQSEHPGTSVSIQQSHGGSSKQALSVANGLQADVVTMNQSSDIDLLEKKGLVEK
          70      80      90      100     110     120

      130     140     150     160     170     180
m927.pep  GWQALPDHAAPYTSTMVFLVRKNNPKQIRDWNDLAKDGVNIVIANPKTSGNGRYAFLGA
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a927      GWQALPDHAAPYTSTMVFLVRKNNPKQIRDWNDLAKDGVNIVIANPKTSGNGRYAFLGA
          130     140     150     160     170     180

      190     200     210     220     230     240
m927.pep  YGYGLKTTNGNEQEAQKLVASILKNTPVFENGGRXPPPPSHNATSATYSSLLKTKPTTSA
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a927      YGYGLKTTNGNEQEAQKLVASILKNTPVFENGGRAPPPPSHNATSATYSSLLKTKPTTSA
          190     200     210     220     230     240

```

m927.pep KNX
 |||
 a927 KNX

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2845>:

g929.seq
 1 ATGAAATTGG GTTCAAACC GATACCCCTC GCCATTGCCG CAGTATTGTG
 51 CGCCTTGGTT TTGGCACTGC CCGTACcga CGGGGTCAAG CCTCAGGCTT
 101 GGACGCTGCT GGCTATGTTT GTCGGTGTGA TTGCCGCCAT TATCGGCAAG
 151 GTTATGCCGT TGGGCGCGCT GTCGATTATT GCCGTCGGGT TGGTCGCAGT
 201 AACCGGCGTA ACCGCCGACA AACCGGGCGC GGCGATGAGC GATGCGTTGA
 251 GTGCGTTCGC CAATCCGTTG ATTTGGCTGA TTGCCATCGC AGTTATGATT
 301 TCGCGCGGTT TGCTCAAAAC AGGCTGCGG ATGCGTATCG GATATTGTGTT
 351 TATCGCCGTT TTTGGAAGAA AAacgctggg CATCGGTTAC AGTCTCGCTC
 401 TTCCGAACT GCTGCTGGCT CCCGTTACCC CTTCCAATAC CGCGCGCGGC
 451 GGCGGCATTA TACATCcgat TATGCagtcg attgCcgCA GttacggctC
 501 caatCCCGCA AAAGGCACag aaggcaagat gggtaAATAT TtggcTTtgg
 551 tcaattaTCA TTCcaaTCCC atttcgctcg ctAtggctat taCTGcaact
 601 gCCCCcaaCC CTTTAATcgt caacttgatt gccGaaaaTt taggcagtag
 651 tttccgctCTT Tcttgggggg cgTGGGcgtg ggcaaTGGCT Gttcccggeg
 701 ttatcgctctt TtctgTTATG CTTTGTATTT TATATTTTTT GTATCGGCCT
 751 GAAATTAAAG AAACGCCCAA TGCTGttcAA TTTGCCAAAG ACCGCTGAG
 801 CGAGATGGGT AAAATGtcgg CAGACGAAAT CATTATGGCG GTCATTTTCG
 851 GTATCTTGCT GCTGTTGTGG GCAGATGTTT CCGCCCTTAT TACCGGCAAT
 901 CACGCTTTTA GTATCAacgc caccGCCACC GCATTATCG GATTAAGCCT
 951 GCTTTTGCTT TCCGGTGTAT TGACTTGGGA CGATGTTTTT AAAGAAAAAA
 1001 GCGCGTGGGA TACGATTATT TGGTTTGGCG CATTGATTAT GATGCGCGCA
 1051 TTTTtaATA Aactcggact gattaaatGG TTCTCCGAG TGTGGCGGA
 1101 Aagtgtcggc GGTTTGGCGC TTAGCGGCAC GGCTGCGGGC GTAATCCTCG
 1151 TGCTTGCTta TATGTATGCG CATTATATGT TTGCCAGTAC TACTGCACAT
 1201 ATTACCGCTA TGTTCGGCGC ATTTCTCGCT GCTGCCGTTT CACTGAATGC
 1251 CCCGGCGATG CCGACTGCGC TGATGATGGC GGCCGCATCC AACATTATGA
 1301 TGACCCTTCA TCATTATGCG ACCGGTACTT CACCTGTGAT TTTCCGGCTCG
 1351 GGCTACACCA CAATGGGAGA ATGGTGAAG GCGGTTTTTA TCATGAGCGT
 1401 AGTCAATTTT CTGATTTTTT CCGTTATCGG CAGCATTTGG TGGAAAGTTC
 1451 TGGGATATTG GTAA

This corresponds to the amino acid sequence <SEQ ID 2846; ORF 929.ng>:

g929.pep
 1 MKLGFKPIPL AIAAVLCALV LALPVPDGVK PQAWTLLAMF VGVIAAIIGK
 51 VMPLGALSII AVGLVAVTGV TADKPGAAMS DALSAFANPL IWLIAIAVMI
 101 SRGLLKTGLG MRIGYLFIAV FGRKTLGIGY SLALSELLLA PVTSPNTARG
 151 GGIHHPIMQS IAGSYGSNPA KGTGKMGKY LALVNYHNSP ISSAMAITAT
 201 APNPLIVNLI AENLGSSFRL SWGAWAWAMA VPGVIAFFVM PLILYFLYPP
 251 EIKETPNAVQ FAKDRLSEMG KMSADEIIMA VIFGILLLLW ADVPALITGN
 301 HAFSINATAT AFIGLSLLLL SGVLTWDJVL KERSAWDII WFGALIMMAA
 351 FLNKLGLIKW FSGVLAESVG GLGVSGTAAG VILVLAYMYA HYMFASSTAH
 401 ITAMFGAFLA AAVSLNAPAM PTALMMAAAS NIMTLTHYA TGTSPVIFGS
 451 GYTTMGEWWK AGFIMSVVNF LIFSVIGSIW WKVLGYW*

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2847>:

m929.seq
 1 ATGAAATTGG GTTCAAACC GATACCCCTC GCCATTGCCG CAGTATTGTG
 51 CGCCTTGGTT TTGGCACTGC CCGTACCCGA CGGGGTCAAG CCTCAGGCTT
 101 GGACGCTGCT GGCCATGTTT GTCGGTGTGA TTGCCGCCAT TATCGGCAAG
 151 GCCATGCCGT TGGGCGCGCT GTCGATTATT GCCGTCGGGT TGGTCGCAGT
 201 AACCGGCGTA ACCGCCGACA AACCGGGCGC GGCGATGAGC GATGCGTTGA
 251 GTGCGTTCGC CAATCCGTTG ATTTGGCTGA TTGCCATCGC AGTTATGATT
 301 TCGCGCGGTT TGCTCAAAAC AGGCTGCGG ATGCGTATCG GATATTGTGTT
 351 TATCGCCGTT TTTGGAAGAA AAACGCTGGG CATCGGTTAC AGTCTCGCTC
 401 TTTCCGAACT GCTGCTGGCT CCCGTTACCC CTTCCAATAC CGCGCGCGGC

```

451 GCGCGCATTA TACATCCGAT TATGCAGTCG ATTGCCGGCA GTTACGGCTC
501 CAATCCGCGA AAAGGCACAG AAGGCAAGAT GGGTAAATAT TTGGCTTTGG
551 TCAACTATCA TTCCAATCCC ATTTCTGTCG CTATGTTTAT TACTGCAACT
601 GCCCCCAACC CTTTAATCGT CAACTTGATT GCCGAAAATT TAGGCAGTAG
651 TTTCCGCTCT TCTTGGGGGG CGTGGGCGTG GGCAATGGCT GTTCCCGGCG
701 TTATCGCCTT TTTCTTATG CCTTTGATT TATATTWYT GIATCCGCCT
751 GAAATTAAAG AAACGCCCAA TGCCGTTCAA TTTGCCAAAG ACCGTCTGAG
801 GGAGATGGGT AAAATGTCGG CAGACGAAAT CATTATGGCG GTCATTTTCG
851 GTATCTTGCT GCTGTTGTGG GCAGATGTTT CCGCCCTTAT TACCGGCAAT
901 CACGCTTTTA GTATCAACGC CACCGCCACC GCATTATCG GATTAAGCCT
951 GCTTTTGCTT TCCGGTGTAT TGAATTGGGA CGATGTTTTG AAAGAAAAAA
1001 GCGCGTGGGA TACGATTATT TGTTTTCGCG CATTGATTAT GATGGCCGCA
1051 TTTTAAATA AACTCGGACT GATTAAATGG TTCTCCGGAG TGTGGCGGA
1101 AAGTGTCCGC GGTTTGGGCG TTAGCGGCAQ GGCTGCGGGC GTAATCCTCG
1151 TGCTTGCTTA TATGTATGCG CATTATATGT TTGCCAGTAC TACTGCACAT
1201 ATTACGCTTA GTTTCGGCGC ATTTTTCGCT GCTGCCGTTT CACTGAATGC
1251 CCCGGCGATG CCGACCGCGC TGATGATGGC GgCCGCATCC AACATTATGA
1301 TGACCCTCAC TCATTATGCG ACCGGTACTT CGCCTGTGAT TTTCCGTTCC
1351 GGCTACACCA CAATGGGAGA ATGGTGGAAG GCGGGTTTTA TCATGAGCGT
1401 AGTCAATTTT CTGATTTTTT TCGTTATCGG CAGCATTGGG TGGAAAGTTC
1451 TGGGTATTG GTAA

```

This corresponds to the amino acid sequence <SEQ ID 2848; ORF 929>:

m929.pep

```

1  MKLGFKPIPL AIAAVLCALV LALPVPDGVK PQAWTLLAME VGVIAAIIGK
51  AMPLGALSII AVGLVAVTGV TADKPGAAMS DALSAFANPL IWLIAIAVMI
101 SRGLLKTGLG MRIGYLFIAV FGRKTLGIGY SLALSELLA PVTSPNTARG
151 GGIIHPIMQS IAGSYGSNPA KGTGKMGKY LALVNYHNSP ISSAMFITAT
201 APNPLIVNLI AENLGSSFRL SWGAWAWAMA VPGVIAFFVM PLILYXLYPP
251 EIKETPNAVQ FAKDRLREMG KMSADEIIMA VIFGILLLLW ADVPALITGN
301 HAFSINATAT AFIGLSLLLL SGVLTWDDVL KEKSAWDTII WFGALIMMAA
351 FLNKLGLIKW FSGVLAESVG GLGVSGETAG VILVLAYMYA HYMFASSTAH
401 ITAMFGAFFA AAVSLNAPAM PTALMMAAAS NIMMTLTHYA TGTSPVIFGS
451 GYTTMGEWWK AGFIMSVVNF LIFFVIGSIW WKVLGYW*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 929 shows 98.8% identity over a 487 aa overlap with a predicted ORF (ORF 929.ng) from *N. gonorrhoeae*:

g929/m929

	10	20	30	40	50	60
g929 .pep	MKLGFKPIPLAIAAVLCALVLALPVPDGVKPKQAWTLLAMFVGVIAAIIGKVMPLGALSII					
m929	MKLGFKPIPLAIAAVLCALVLALPVPDGVKPKQAWTLLAMFVGVIAAIIGKAMPLGALSII					
	10	20	30	40	50	60
g929 .pep	AVGLVAVTGV TADKPGAAMS DALSAFANPLIWLIAIAVMI SRGLLKTGLGMRIGYLFIAV					
m929	AVGLVAVTGV TADKPGAAMS DALSAFANPLIWLIAIAVMI SRGLLKTGLGMRIGYLFIAV					
	70	80	90	100	110	120
g929 .pep	FGRKTLGIGYSLALSELLAPVTPSNTARGGGIIHPIMQSIAGSYGSNPAKGTGKMGKY					
m929	FGRKTLGIGYSLALSELLAPVTPSNTARGGGIIHPIMQSIAGSYGSNPAKGTGKMGKY					
	130	140	150	160	170	180
g929 .pep	LALVNYHNSNPISSAMAITATAPNPLIVNIAENLGSSFRLSWGAWAWAMAVPGVIAFFVM					
m929	LALVNYHNSNPISSAMFITATAPNPLIVNLIENLGSSFRLSWGAWAWAMAVPGVIAFFVM					
	190	200	210	220	230	240

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	190	200	210	220	230	240
	250	260	270	280	290	300
g929.pep	PLILYFLYPPEIKETPNVQFAKDRLEMGKMSADEIIMAVIFGILLLLWADVLPALITGN					
m929	PLILYXLYPPEIKETPNVQFAKDRLEMGKMSADEIIMAVIFGILLLLWADVLPALITGN					
	250	260	270	280	290	300
	310	320	330	340	350	360
g929.pep	HAFSINATATAFIGLSLLLLSGVLTWDDVLKEKSAWDTIIWFGALIMMAAFLNKLGLIKW					
m929	HAFSINATATAFIGLSLLLLSGVLTWDDVLKEKSAWDTIIWFGALIMMAAFLNKLGLIKW					
	310	320	330	340	350	360
	370	380	390	400	410	420
g929.pep	FSGVLAESVGGGLGVSGTAAGVILVLAIFYAHYMFASSTTAHITAMFGAFLAAVSLNAPAM					
m929	FSGVLAESVGGGLGVSGTAAGVILVLAIFYAHYMFASSTTAHITAMFGAFAAAVSLNAPAM					
	370	380	390	400	410	420
	430	440	450	460	470	480
g929.pep	PTALMMAAASNIMMTLTHYATGTSPVIFGSGYTTMGEWWKAGFIMSVVNFLIFSVIGSIW					
m929	PTALMMAAASNIMMTLTHYATGTSPVIFGSGYTTMGEWWKAGFIMSVVNFLIFFVIGSIW					
	430	440	450	460	470	480
g929.pep	WKVLGYWX					
m929	WKVLGYWX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2849>:

```

a929.seq
1  ATGAAATTGG GTTCAAACC GATACCCCTC GCCATTGCCG CAGTATTGTG
51  CGCCTTGGTT TTGGCACTGC CCGTACCCGA CGGGGTCAAG CCTCAGGCTT
101 GGACGCTGCT GGCCATGTTT ATCGGTGTGA TTGCCGCCAT TATCGGCAAG
151 GCCATGCCGT TGGTGCCGCT GTCGATTATT GCCGTCGGGT TGGTCGCAGT
201 AACCGGCGTA ACCGCCGACA AACCGGGTGC GCGCATGAGC GATGCGTTGA
251 GTGCGTTTCG CAATCCGTTG ATTTGGCTGA TTGCCATCGC AGTTATGATT
301 TCGCGCGGTT TGCTCAAAC AGGGCTGGGG ATGCGTATCG GATATTTGTT
351 TATCGCCGTT TTTGGAAGAA AAACGCTGGG CATCGGTTAC AGTCTCGCTC
401 TTTCCGAAC TCTGCTGGCT CCCGTTACCC CTTCCAATAC CGCGCGCGGC
451 GCGGCGATTA TACATCCGAT TATGCAGTCG ATTGCCGCGA GTTACGCTC
501 CAATCCCGCA AAAGGCACAG AAGGCAAGAT GGGTAAATAT TTGGCTTTGG
551 TCAACTATCA TTCCAATCCC ATTTCGTCGG CTATGTTTAT TACTGCAACT
601 GCCCCAACCC CTTTAATCGT CAACTTGATT GCCGAAATTT TAGGCAGTAG
651 TTTCCGTCCT TCTTGGGGGG CGTGGGCGTG GGCAATGGCT GTTCCCGCGC
701 TTATCGCCTT TTTCGTTATG CCTTTGATTT TATATTTTAT GTATCCGCTT
751 GAAATTAAAG AAACGCCCAA TGCCGTTCAA TTGCCAAAG ACCGTCTGAG
801 GGAGATGGGT AAAATGTCGG CAGACGAAAT CATTATGGCG GTCATTTTCG
851 GTATCTTGTT GCTGTTGTGG GCAGATGTTT CCGCCCTTAT TACCGGCAAT
901 CACGCTTTTA GTATCAACGC CACCGCCACC GCATTTATCG GATTAAGCCT
951 GCTTTTGCTT TCCSGTGTAT TGACTTGGGA CGATGTTTTC AAAGAAAAAA
1001 GCGCGTGGGA TACSATTATT TGGTTTGGCG CATTGATTAT GATGGCGCA
1051 TTTTAAATA AACTCGGACT GATTAAATGG TTCTCCGAG TGTTGGCGGA
1101 AAGTGTGCGC GGTTTGGCGC TTAGCGGCAC GGCTGCGGGC GTAATCCTCG
1151 TGCTTGCTTA TATGATGCGC CATTATATGT TTGCCAGTAC TACTGCACAT
1201 ATTACCGCTA TGTTCCGCGC ATTTTTCGCT GCTGCGGTTT CACTGAATGC
1251 CCCGGCGATG CCGACCGCGC TGATGATGGC GGCCGCATCT AACATTATGA
1301 TGACCTCAC TCATTATGCG ACCGGTACTT CGCCTGTGAT TTTCCGTTCC
1351 GGCTACACCA CAATGGGAGA ATGGTGGAAG GCGGGTTTTC TCATGAGCGT
1401 AGTCAATTTT CTGATTTTTC TCGTTATCGG CAGCATTTGG TGGAAGTTC
1451 TGGGGTATTG GTAA

```

This corresponds to the amino acid sequence <SEQ ID 2850; ORF 929.a>:

```

a929.pep
  1  MKLGFKPIPL AIAAVLCALV LALPVPDGVK PQAWTLLAMF IGVIAAIIGK
51  AMPLGALSII AVGLVAVTGV TADKPGAAMS DALSAFANPL IWLIAIAVMI
101 SRGLLKTGLG MRIGYLFIAV FGRKTLGIGY SLALSELLA PVTPSNTARG
151 GGIIHPIMQS IAGSYGSNPA KGTEGKMGKY LALVNYHNSP ISSAMFITAT
201 APNPLIVNLI AENLGSSFRL SWGAWAWAMA VPGVIAFFVM PLILYFLYPP
251 EIKETPNAVQ FAKDRLREMG KMSADEITMA VIFGILLLLW ADVPALITGN
301 HAFSINATAT AFIGLSLLLL SGVLTWDDVL KEKSAWDTII WFGALIMMAA
351 FLNKLGLIKW FSGVLAESVG GLGVSGTAAG VILVLAYMYA HYMFASHTAH
401 ITAMFGAFFA AAVSLNAPAM PTALMMAAAS NIMMTLTHYA TGTSPVIFGS
451 GYTTMGEWWK AGFIMSVVNF LIFFVIGSIW WKVLGYW*

```

m929/a929 99.6% identity in 487 aa overlap

m929.pep	10	20	30	40	50	60
	MKLGFKPIPLAIAAVLCALVLALPVPDGVKQAWTLLAMFVGVIAAIIGKAMPLGALSII					
a929	MKLGFKPIPLAIAAVLCALVLALPVPDGVKQAWTLLAMFVGVIAAIIGKAMPLGALSII					
	10	20	30	40	50	60
m929.pep	70	80	90	100	110	120
	AVGLVAVTGV TADKPGAAMSDALSAFANPLIWLIAIAVMISRGLLKTGLGMRIGYLFIAV					
a929	AVGLVAVTGV TADKPGAAMSDALSAFANPLIWLIAIAVMISRGLLKTGLGMRIGYLFIAV					
	70	80	90	100	110	120
m929.pep	130	140	150	160	170	180
	FGRKTLGIGYSLALSELLAPVTPSNTARGGGIIHPIMQSIAGSYGSNPAKGTEGKMGKY					
a929	FGRKTLGIGYSLALSELLAEVTPSNTARGGGIIHPIMQSIAGSYGSNPAKGTEGKMGKY					
	130	140	150	160	170	180
m929.pep	190	200	210	220	230	240
	LALVNYHNSPISSAMFITATAPNPLIVNLI AENLGSSFRLSWGAWAWAMAVPGVIAFFVM					
a929	LALVNYHNSPISSAMFITATAPNPLIVNLI AENLGSSFRLSWGAWAWAMAVPGVIAFFVM					
	190	200	210	220	230	240
m929.pep	250	260	270	280	290	300
	PLILYXLYPPEIKETPNAVQFAKDRLREMGKMSADEIIMAVIFGILLLLWADV PALITGN					
a929	PLILYFLYPPEIKETPNAVQFAKDRLREMGKMSADEIIMAVIFGILLLLWADV PALITGN					
	250	260	270	280	290	300
m929.pep	310	320	330	340	350	360
	HAFSINATATAF IGLSLLLLSGVLTWDDVLKEKSAWDTIIWFGALIMMAAFLNKLGLIKW					
a929	HAFSINATATAF IGLSLLLLSGVLTWDDVLKEKSAWDTIIWFGALIMMAAFLNKLGLIKW					
	310	320	330	340	350	360
m929.pep	370	380	390	400	410	420
	FSGVLAESVGG LGVSGTAAGVILVLAYMYAHYMFASHTAHITAMFGAFFAAAVSLNAPAM					
a929	FSGVLAESVGG LGVSGTAAGVILVLAYMYAHYMFASHTAHITAMFGAFFAAAVSLNAPAM					
	370	380	390	400	410	420
m929.pep	430	440	450	460	470	480
	PTALMMAAASNIMMTLTHYATGTSPVIFGSGYTTMGEWWKAGFIMSVVNF LIFFVIGSIW					
a929	PTALMMAAASNIMMTLTHYATGTSPVIFGSGYTTMGEWWKAGFIMSVVNF LIFFVIGSIW					
	430	440	450	460	470	480
m929.pep	WKVLGYWX					

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a929 WKVLGYWX

g930.seq not found yet

g930.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2851>:

m930.seq

```

1  ATGAAACTTC CTTTATCCTA TTTGCCTAAT ATTCGCTTTT TGTCTTGGTG
51  CTGCTTATTG GCAGGTATCA TTGCTCCTGC TACTTTGTTG GCCTCCCCCA
101 ACCCTGCCGA AATCCGTATG CAGCAAGATA TTCAGCAACG CCAACGCGAA
151 GAGCAGTTGC GCCAAACCAT GCAGCCTGAA AGCGATGTGC GTTTGCATCA
201 AAAAAACACG GGGGAAACGG TTAATCAGTT GATGGGCGAT GACAGCAGCC
251 AACCGTGTTC TGCCATTAAAC GAATGGGTGT TGGAAGGCGA ACACCATGCT
301 CGGTTTCAGT TTGCCCTAAA ACGTGCCTTG CGCGAAACGG GTTTTCAGGC
351 TGGCAAGTGT CTGCATGCGG GCAACATTAA TCAAATCATG TCCTTAGCAC
401 AAAATGCTTT GATCGGCAGG GGATATACCA CGACCCGTAT CTTGGCTGCG
451 CCACAGGATT TGAATAgTGG aAGCTTCAAT TAA

```

This corresponds to the amino acid sequence <SEQ ID 2852; ORF 930>:

m930.pep

```

1  MKLPLSYLPN IRFLSWCCLL AGIIPATLL ASPNPAEIRM QODIQORORE
51  EQLRQTMQPE SDVRLHQKNT GETVNQIMGD DSSQPCFAIN EWLVEGEHHA
101 RFQFALKRAL RETGFQAGKC LHAGNINQIM SLAQNALIGR GYTTTRILAA
151 PQDLNSGSFN *

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2853>:

g930-1.seq (partial)

```

1  GGCAAGTGTC TGCATGCGGG CGACATTAAT CAAATCATGT CCTAGCACAC
51  AAATSCTTTG ATCGGCAGGG GATATACCAC GACCCGTATC TTGGCTGCGC
101 CACAGGATTT GAATAGTGGC AAGCTTCAAT TAACCTGAT GCCGGGCTAT
151 CTGCGCTCCA TACGAATCGA TCGGTCCAAC GATGATCAAA CCCATGCAGG
201 ACGTATTGCA GCATTCCAAC ACAAAATTCC CACCCGCTCG AACGATCTGT
251 TGAATCTGCG TGATTTGGAA CAAGGACTGG AAAATCTCAA ATGTCTCCCG
301 ACTGCGGAAG CCGATCTCCA AATCGTTCCC GTAGAGAGAG AACCAAAACCA
351 AAGTGATGTC GTGGTGCAAT GCCGGTAACG TCTGCTGCCC TACTGTGTGA
401 GTGTGGGGAT GGATAATTCG GGTAGTGAGG CGACAGGAAA ATACCAAGGA
451 AATATCACTT TCTCTGCCGA CAATCCTTTT GGAAGTGTG ATATGTTCTA
501 TGTAAATTAT GGACGTTCAA TTGGCGGTAC GCCCGATGAG GAAAATTTTG
551 ACGGCCATCG CAAAGAAGGC GGATCAACAC ATTACGCCGT ACATTATTCA
601 GCCCCTTTTC GTAAATGGAC ATGGGCATTC AATCACAATG GCTACCGTTA
651 CCATCAGGCG GTTTCGGGAT TATCGGAAGT CTATGACTAT AATGGAAAAA
701 GTTACAACAC TGATTTGGGC TTCAACCGCC TGTGTATCG TGATGCCAAA
751 CGCAAAACCT ATCTCAGTGT AAAACTGTGG ACGAGGGAAA CAAAAAGTTA
801 CATTGATGAT GCCGAAGTGA CTGTACAACG GCGTAAACCC ACAGGTTGGT
851 TGGCAGAACT TTCCCACAAA GGATATATCG GTCGCAGTAC GGCAGATTTT
901 AAGTTGAAAT ATAAACACCG CACCGGCATG AAAGATGCTC TCGCGCGGCC
951 TGAAGAAGCC TTTGGCGAAG GCACGTCACG TATGAAAATT TGGACGGCAT
1001 CGGCTGATGT AAATACTCCT TTTCAAATCG GTAAACAGCT ATTTGCCTAT
1051 GACACATCCG TTCATGCACA ATGGAACAAA ACCCCGCTAA CATCGCAAGA
1101 CAAACTGGCT ATCGGCGGAC ACCACACCGT ACGTGGCTTC GACGGTGAAA
1151 TGAGTTTGCC TGCCGAGCGG GGATGGTATT GCGGCAACGA TTTGAGCTGG
1201 CAATTTAAAC CAGGCCATCA GCTTTATCTT GGGGCTGATG TAGGACATGT
1251 TTCAGGACAA TCCGCCAAAT GGTATTCGGG CCAAACCTTA GCCGGCACAG
1301 CAATTGGGAT ACGCGGGCAG ATAAAGCTTG GCGGCAACCT GCATTACGAT
1351 ATATTACCG GCGGTGCATT GAAAAAGCCC GAATATTTTC AGACGAAGAA
1401 ATGGGTAACG GGGTTTCAGG TGGTTATTTC GTTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2854; ORF 930-1.ng>:

g930-1.pep (partial)

```

1  GKCLHAGDIN QIMSLAQNAL IGRGYTTTRI LAAPQDLNSG KLQLTLMPGY
51  LRSIRIDRSN DDQTHAGRIA AFQNKFPTRS NDLLNLRDLE QGLENLKLCP
101 TAEADLQIVP VEREPNQSDV VVQWR*RLLP YCVSVGMDNS GSEATGKYQG
151 NITFSADNPF GLSDMFYVNY GRSIGGTPDE ENFDGHRKEG GSNNYAVHYS
201 APFGKWTWAF NHNGYRYHOA VSLGSEVYDY NGKSYNTDFG FNRLLYRDAK
251 RKTYLSVKLW TRETKSYIDD AELTVQRRKT TGWLAELSHK GYIGRSTADF
301 KLKYKHGTGM KDALRAPEEA FEGGTSRMKI WTASADVNTF FOIGKOLFAY
351 DTSVHAQWNK TPLTSQDKLA IGGHHTVRGF DGEMSLPAER GWYWRNDLSK
401 QFKPGHQLYL GADVGHVSGO SAKWLSGQTL AGTAIGIRGQ IKLGGNLHYD

```

1342

451 IFTGRALKKP EYFQTKKVVV GFQVGYSF*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2855>:

m930-1.seq

```

1  ATGAACTTC CTTATCCTA TTTGCCTAAT ATTGCTTTT TGTCTGGTG
51  CTGCTTATTG GCAGGTATCA TTGCTCCTGC TACTTGTGTG GCCTCCCCCA
101 ACCCTGCCGA AATCCGTATG CAGCAAGATA TTCAGCAACG CCAACGCCGA
151 GAGCAGTTGC GCCAAACCAT GCAGCCTGAA AGCGATGTGC GTTTGCATCA
201 AAAAAACACG GGGGAAACGG TTAATCAGTT GATGGGCGAT GACAGCAGCC
251 AACCGTGTTC TGCCATTAAAC GAAGTGGTGT TGGGAAGCGA ACACCATGCT
301 CGGTTTCAGT TTGCCCTAAA ACGTGCCTTG CGCGAAACGG GTTTTCAGGC
351 TGGCAAGTGT CTGCATGCGG GCAACATTAA TCAATCATG TCCTTAGCAC
401 AAAATGCTTT GATCGGCAGG GGATATACCA GCACCCGTAT CTTGGCTGCG
451 CCACAGGATT TGAATAGTGG CAAGCTTCAA TTAACCTGTA TACCGAGCTA
501 TCTGCCCTCC ATACGAATCG ATCGGTCTAA CGATGATCAA ACCCATGCAG
551 GACGTATTGC AGCATTCAG AACAAATTTT CCACCCGCTC GAACGATCTG
601 TTGAATCTGC GTGATTGGA ACAAGGACTG GAAAATCTCA AACGTCTCCC
651 GACTGCGGAA GCCGATCTCC AAATCGTTCC CGTAGAGGGA GAACCAAACC
701 AAAGTGATGT CGTGGTGCAA TGGCGGCAAC GTCTGCTGCC CTACCGTGTG
751 AGTGTGGGGA TGGATAATTC GGGTAGTGAG GCGACAGGAA AATACCAAGG
801 AAATATCACT TTCTCTGCCG ACAATCCTTT GGGACTGAGT GATATGTTCT
851 ATGTAATTA TGGACGTTTC ATTGGCGGTA CGCCCGATGA GGAAAGTTT
901 GACGGCCATC GCAAAGAAGG CGGATCAAAC AATTACGCCG TACATTATTC
951 AGCCCTTTTC GGTAAATGGA CATGGGCATT CAATCACAAT GGCTACCGTT
1001 ACCATCAGGC AGTTTCCGGA TTATCGGAAG TCTATGACTA TAATGGAAAA
1051 AGTTACAATA CTGATTTCGG CTCAACCGC CTGTTGTATC GTGATGCCAA
1101 ACGCAAAACC TATCTCGGTG TAAACTGTG GATGAGGGAA ACAAAAGTTT
1151 ACATTGATGA TGCCGAACAT ACTGTACAAC GGCCTAAAC TGCGGGTTGG
1201 TTGCCAGAAC TTTCCACAA AGAATATATC GGTCGCAGTA CGGCAGATTT
1251 TAAGTTGAAA TATAACGCG GCACCGGCAT GAAAGATGCT CTGCGCGCGC
1301 CTGAAGAAAC CTTTGGCGAA GGCACGTCAC GTATGAAAT TTGGACGGCA
1351 TCGGCTGATG TAAATACTCC TTTTCAATC GGTAAACAGC TATTGCTCTA
1401 TGACACATCC GTTCATGCAC AATGGAACAA AACCCCGCTA ACATCGCAAG
1451 ACAACTGGC TATCGGCGGA CACCACCCG TACGTGGCTT CGACGGTGAA
1501 ATGAGTTTGT CTGCCGAGCG GGGATGGTAT TGGCGCAACG ATTTGAGCTG
1551 GCAATTTTAA CCAGGCCATC AGCTTTATCT TGGGGCTGAT GTAGGACATG
1601 TTTCAGGACA ATCCGCCAAA TGGTTATCGG GCCAACTCT AGTCGGCACA
1651 GCAATTGGGA TACCGGGGCA GATAAAGCTT GGCGGCAACC TGCATTACGA
1701 TATATTACG GCGCGCGCAT TGAAAAAGCC CGAATTTTTC CAATCAAGGA
1751 AATGGCAAG CGGTTTTCAG GTAGCTATA CGTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2856; ORF 930-1>:

m930-1.pep

```

1  MKLFLSYLPN IRFLSWCCLL AGIIAPATLL ASPNPAEIRM QQDIQQRQRE
51  EQLRQTMQPE SDVRLHQKNT GETVNQLMGD DSSQPCFAIN EVVLEGEHHA
101 RFQFALKRAL RETGFQAGKC LHAGNINQIM SLAQNALIGR GYTTTRILAA
151 PQDLNSGKLQ LTLIPSYLRS IRIDRSNDDQ THAGRIAAFQ NKFPTRSNDL
201 LNLRLDLEQL ENLKRLLPTAE ADLQIVPVEG EPNQSDVVQV WRQRLLPYRV
251 SVGMNDSGSE ATGKYQGNIT FSADNPLGLS DMFYVNYGRS IGGTPDEESF
301 DGHREKGSY NYAVHYSAPF GKWTWAFNHN GYRYHQAVSG LSEVYDYNKG
351 SYNTDFGFNR LLYRDAKRKT YLGVKLWMRE TKSIIIDAEI TVQRRKTAGW
401 LAELSHKEYI GRSTADFKLK YKRGTMKDA LRAPEEAFGE GTSRMKIWTA
451 SADVNTPFQI GKQLFAYDTS VHAQWNKTPL TSQDKLAIGG HHTVRGFDGE
501 MSLSAERGWY WRNDLSWQFK PGHQLYLGLD VGHVSGQSAK WLSGQTLVGT
551 AIGIRGQIKL GGNLHYDIFT GRALKKPEFF QSRKWASGFQ VGYTF*

```

m930-1/g930-1 95.4% identity in 478 aa overlap

	90	100	110	120	130	140
m930-1.pep	AINEVVLEGEHHRFQFALKRALRETGFQACKCLHAGNINQIMSLAQNALIGR	GYTTTRI				
g930-1.pep				:		
				10	20	30
	150	160	170	180	190	200
m930-1.pep	LAAPQDLNSGKLQLTLIPSYLRSIRIDRSNDDQTHAGRIAAFQNKFPTRSNDDLNLRLDLE					
g930-1.pep	LAAPQDLNSGKLQLTLMPGYLRSIRIDRSNDDQTHAGRIAAFQNKFPTRSNDDLNLRLDLE					
	40	50	60	70	80	90
	210	220	230	240	250	260
m930-1.pep	QGLNLKRLPTAEADLQIVPVEGEPNOSDVVQWRQRLLPYRVSVGMNDSGSEATGKYQG					

[illegible]

a930-1.pep not yet found

g931.seq

This corresponds to the amino acid sequence <SEQ ID 2858; ORF 931.ng>:

q931.ppt

1 MKPKFKTVLT ALLLAVSLPS MAATRVLMET DMGNIRLVLD ESASKTVAN
51 FVRYARKGFY DNTIFHRVIG GFVIQGDGLT EDLVQKATDK AVANESGNGL
101 KNTVGTIAMA RTAAPDSAAA OFFINLADNG SLDYKNGQYG YTVFGRVESG
151 MDTVSKIARV KTATRGFYQN VPVQPKIRR VVIGO*

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2859>:

m931.seq

```

1  ATGAAACCCA AATTCAAAC CGTTTAAACC GCGCTGCTTT TGGCGGTTTC
51  CCTGCCGTCT ATGGCGGCAA CCCATGTTTT GATGGAAACC GATATGGGCA
101 ATATCCGTTT GGTTTTGGAC GAATCCAAAG CCCCCAAAAC CGTTGCTAAT
151 TTCGTGCGCT ATGCCCGAAA AGGCTTTTAC GACGACACCG TTTTTCACCG
201 CGTTATCGAC GGTTTTGTTA TCCAGGCGCG TGGATTGACC GAGGACTTGG
251 CACAAAAGGC AAGCGATAAG GCCGTTGCCA ACGAATCCGG CAACGGCTTG
301 AAAAACACCG CCGGCACCAT CGCCATGGCG CGGACGACAG CCCCCGATTG
351 CGCCACCAGC CAATTCTTTA TCAATCTGGC GGACCA.kCT TCGCTCGACT
401 ACAAAAACGG ACAATACGGC TATACCGTTT TCGGCAGGGT CGAAAGCGGC
451 ATGAACACCG TTTCCAAAAT CGCCCGCGTC AAAACCGCCA CGCGCGGCTT
501 TTATCAAACG GTACCCGTAC AGCCCGTCAA AATCCGTCGC GTTGTTGTCT
551 GGCAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2860; ORF 931>:

m931.pep..

```

1  MKPKFKTVLT ALLLAVSLPS MAATHVIMET DMGNIRLVLD ESKAPKTVAN
51  FVRYARKGFY DDTVFHRVID GFVIQGGGLT EDLAQKASDK AVANESGNGL
101 KNTAGTIAMA RTTAPDSATS QFFINLADXX SLDYKNGQYG YTVFGRVESG
151 MNTVSKIARV KTATRGFYQN VPVQPVKIRR VVVGQ*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 931 shows 91.9% identity over a 185 aa overlap with a predicted ORF (ORF 931.ng) from *N. gonorrhoeae*:

g931/m931

	10	20	30	40	50	60
g931.pep	MKPKFKTVLTALLLAVSLPSMAATRVLMDGNIRLVLD ESKAPKTVANFVRYARKGFY					
m931	MKPKFKTVLTALLLAVSLPSMAATHVLMETDMGNIRLVLD ESKAPKTVANFVRYARKGFY					
	10	20	30	40	50	60
g931.pep	DNTIFHRVIGGFVIQGGGLTEDLVQKATDKAVANESGNGLKNTVGTIAMARTAAPDSAAA					
m931	DDTVFHRVIDGFVIQGGGLTEDLAQKASDKAVANESGNGLKNTAGTIAMARTTAPDSATS					
	70	80	90	100	110	120
g931.pep	DNTIFHRVIGGFVIQGGGLTEDLVQKATDKAVANESGNGLKNTVGTIAMARTAAPDSAAA					
m931	DDTVFHRVIDGFVIQGGGLTEDLAQKASDKAVANESGNGLKNTAGTIAMARTTAPDSATS					
	70	80	90	100	110	120
g931.pep	QFFINLADNGSLDYKNGQYGYTVFGRVESGMDTVSKIARVKTATRGFYQNPVQPVKIRR					
m931	QFFINLADXXSLDYKNGQYGYTVFGRVESGMNTVSKIARVKTATRGFYQNPVQPVKIRR					
	130	140	150	160	170	180
g931.pep	QFFINLADNGSLDYKNGQYGYTVFGRVESGMDTVSKIARVKTATRGFYQNPVQPVKIRR					
m931	QFFINLADXXSLDYKNGQYGYTVFGRVESGMNTVSKIARVKTATRGFYQNPVQPVKIRR					
	130	140	150	160	170	180
g931.pep	VVVGQX					
m931	VVVGQX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2861>:

a931.seq

```

1  ATGAAACCCA AATTCAAAC CGTTTAAACC GCGCTGCTTT TGGCGGTTTC
51  CCTGCCGTCT ATGGCGGCAA CCCATGTTTT GATGGAAACC GATATGGGCA
101 ATATCCGTTT GGTTTTGGAC GAATCCAAAG CACCCAAAAC CGTTGCCAAT
151 TTCGTGCGCT ATGCCCGAAA AGGCTTTTAC GACAATACGA TTTTTCACCG
201 CGTCATCGGC GGCTTCGTTA TCCAAGGCGG CGGATTGACC GASGACTTGG
251 CACAAAAGGC AAGCGATAAG GCCGTTGCCA ACGAATCCGG CAACGGCTTG
301 AAAAACACTG TCGGCACCAT CGCCATGGCG CGGACGGCCG ATCCGGATTG
351 CGCCACCAGC CAATTCTTTA TCAATCTGGT GGACAATGAT TCGCTCAACT
401 ACAAAAACGG ACAATACGGC TATACCGTTT TCGGCAGGGT CGAAAGCGGC

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1345

451 ATGAACACCG TTTCCAAAT CGCCCGCGTC AAAACCGCCA CGCGCGGCTT
 501 TTATCAAAC GTACCCGTAC AGCCCGTCAA AATCCGTCGC GTTGTCTCG
 551 GGCAGTAA

This corresponds to the amino acid sequence <SEQ ID 2862; ORF 931.a>:

a931.pep
 1 MKPKFKTVLT ALLAVSLPS MAATHVIMET DMGNIRLVLD ESKAPKTVAN
 51 FVRYARKGFY DNTIFHRVIG GFVIQGGGLT EDLAQKASDK AVANESGNGL
 101 KNTVGTIAMA RTADPDSATS QFFINLVDND SLNYKNGQYG YTVFGRVESG
 151 MNTVSKIARV KTATRGFYQN VPVQPKIRR VVVGQ*

m931/a931 94.6% identity in 185 aa overlap

	10	20	30	40	50	60
m931.pep	MKPKFKTVLTALLAVSLPSMAATHVIMETDMGNIRLVLD	ESKAPKTVANFVRYARKGFY				
a931	MKPKFKTVLTALLAVSLPSMAATHVIMETDMGNIRLVLD	ESKAPKTVANFVRYARKGFY				
	10	20	30	40	50	60
	70	80	90	100	110	120
m931.pep	DDTVFHRVIDGFVIQGGGLTEDLAQKASDKAVANESGNGLKNTAGTIAMARTTAPDSATS					
a931	DNTIFHRVIGGFVIQGGGLTEDLAQKASDKAVANESGNGLKNTVGTIAMARTADPDSATS					
	70	80	90	100	110	120
	130	140	150	160	170	180
m931.pep	QFFINLADXXSLDYKNGQYGYTVFGRVESGMNTVSKIARVKTATRGFYQNV	VPVQPKIRR				
a931	QFFINLVDNDSLNYKNGQYGYTVFGRVESGMNTVSKIARVKTATRGFYQNV	VPVQPKIRR				
	130	140	150	160	170	180
m931.pep	VVVGQX					
a931	VVVGQX					

g932.seq not found yet

g932.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2863>:

m932.seq
 1 ATGAAATATA TCGTATCAAT CTCTCTGGCT ATGGGATTGG CTGCCTGTTC
 51 GTTTGGGGGA TTAAACCAA ATCCGTGGGA CGCCGCGTCA TTTTGGGAAT
 101 TGAATAATTA CGCCAATCCC TATCCGGGAT CAGCCTCGGC GGCACCTGAC
 151 CAATATCCAT CGAAAGCAA ACGAAGGCAA CTGAAAGACA TGCAAGAGTG
 201 CGGCTATGAC CCAATAGACG GCGGAAAGTC TGAAGCAGAT GCCTGCCTGA
 251 GGAAAAAAGG CTGGTGTCTG AAGGGTTTCG ACCCTTATCC CGAAAAACAA
 301 AAATACGAAT GGCCTCGAGA AGAAGGAAAA ACAAATGA

This corresponds to the amino acid sequence <SEQ ID 2864; ORF 932>:

m932.pep
 1 MKYIVSISLA MGLAACSFEGG FKPNPWAAS FWELKNYANP YPGSASAALD
 51 QYPSKARRRQ LKDMQECGYD PIDGKSBAD ACLRKKGWCR KGFDYPYENK
 101 KYEWPREEGK TK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 932 shows ___% identity over a ___ aa overlap with a predicted ORF (ORF 932.ng) from *N. gonorrhoeae*:

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2865>:

g934.seq
 1 ATGAAAAAAA TCATCGCCTC CGCGCTTATC GCAACATTCG CACTCACC GC

g934.pep

1	<u>MKKI</u>	<u>IASALI</u>	ATFALTACQD	DTQARLERQQ	KQIEALQQQL	AQQADDTVYQ
51	LTPEAVKDTI	PAQAQANGNN	GQPVTKRRA	AVYLRPIDRK	LAAAKPDWRG	
101	GRRVYQRQAG	KOIHDTGNAPR	QPRPSRACF	LPSTVTPQCA	HQQGFEHAQP	
151	PCKTTGGAGA	ALPPDNGAPR	QLPPSRYARF	RQKAVNPARQ	CRLKGFQTAF	
201	LYLLGALLCC	RLIFRRHFVS	KRLMSGWOF*			

m934.seq (partial)

1	CGGCTCGAAC	AGCAGCAGAA	ACAGATTGAA	GCCCTGCAAC	AGCAGCTCGC
51	ACAGCAGGAC	GACGATACGG	TTTACCAACT	GACTCCCGAA	GCAGTCAAAG
101	ACACCATTC	TGCCGAAGCA	CAGGCAAACG	GCAACAACGg	GCACCCGTT
151	ACCGGTAA.A	CAGGGCAGC	AGTATATTTA	CGACCAATCG	ACAGGAAGCT
201	3CGTCTGCA	AAGCTTGGT	GGCGCGCGCG	GAGCGCGTT	TATCGCAAC
251	3CGCTGGCAA	ACAAATTCAC	ACGGGCAGCG	AACCAAGACA	GTCCCGTCGC
301	CCGGCGCGCG	CGTGAGCCT	ACCATCAGTC	CGCAGCCTCC	AATGCGCGCA
351	yCAGCAGGGA	TTTGAACAGC	CGCAGCCTCC	GTGCAAAAAC	ACAGGCGCGCG
401	CAGKCGCAGC	GTTACCGCCC	GACAAACGCG	CCGsCGsCA	ATTACCGCCG
451	CCCCGCTATG	CGCGGTTTCG	GCAGGAGGCG	GTAAACCCGG	CGCGCCAATG
501	CGTCTGAAG	AGTTTTCAGA	CGGCATTnT	GCATTGTGTA	GGGACATTGT
551	TATGTTGCCG	TTTGATTTC	AGACGGCATT	TTGTTTCCAA	GCCTTGTATG
601	TCGGGATGGC	AATTCTGA			

m934.pep (partial)

```

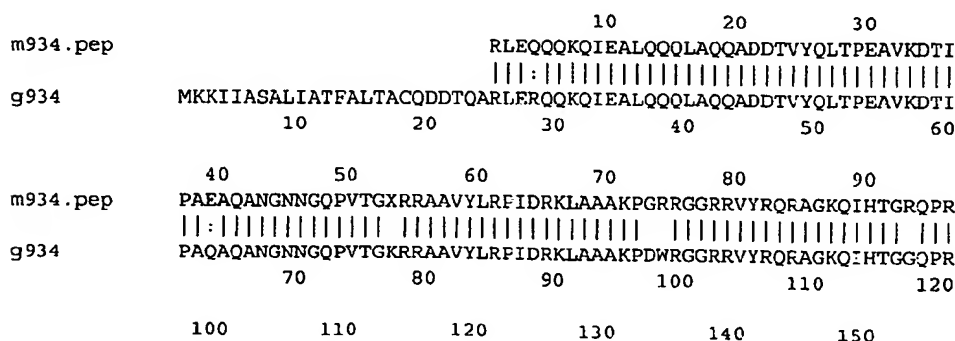
1  ..RLEQQQKQIE ALQQLAQQA DDTVYQLTPE AVKDTIPAEA QANGNNGQPV
51  TGXRRAAVYL RPIDRKLAAA KPGRGGRRV YRQRAGKQIH TGRQPRQSR
101 PARACSLPSV RTPQCAHQG FEHAQPCKT TGGAXAALPP DNAPXROLPP
151 PRYARLFQEA VNPAROCLK SFOTAFXHLL GTLCCRLIF RRHFVSKRLM
201 SGWOF*

```

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 934 shows 91.7% identity over a 205 aa overlap with a predicted ORF (ORF 934.ng) from *N. gonorrhoeae*:

m934/g934



```

m934.pep      QSRRLPARACSLPSVRTPQCAHQQGFQFEHAQPPCKTTGGAXAALPPDNAPXROLPPPRYARF
|  |||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g934          QPRRPSRACCLPSVRTPQCAHQQGFQFEHAQPPCKTTGGAGAALPPDNAPARQLPPSRYARF
              130      140      150      160      170      180

              160      170      180      190      200
m934.pep      RQEAVNPARQCRLKSFQTAFXHLGLTLLCCRLIFRRHFVSKRLMSGWQFX
| |:||||| |:||||| |:||||| |:||||| |:||||| |:||||| |:||||| |:|||||
g934          RQKAVNPARQCRLKGFQTAFLLYLLGALLCCRLIFRRHFVSKRLMSGWQFX
              190      200      210      220      230

```

```
a934.seq
1  ATGAAAAAAA TCATCGCCTC CGCGCTTATC GCAACATTCT CACTCGCCGC
51  CTGCCAAGAC GACGCGCAGG CGCGGCTCGA ACAGCAGCAG AACACAGATTG
101 AAGCCCTGCA ACAGCAGCTC GCACAGCAGG GACAGCATAC GGTTTACCAA
151 CTGACTCCCG AAGCAGTCAA AGACACCAAT CTGCGCGAAG CACAGGCAAA
201 CGGCAACAAC GGGCAACCGG TTACCGG.TA AAGACGGGCA GCAGTATATT
251 TACGACCAAT CGACAAGAA GCTGCTGCTG CAAAGCTTGG TCGGCGCGGG
301 GGCAGGCGCG TTTATCGGCA ACGCGCTGCG AACACAAATT ACACGGGCAG
351 GCAACCAAGA CAGTCCCGTC GCCCGGCGCG CGCGTGCCGC CTACCATCTG
401 TCCGCACATC CCAATGCGCG CACCAGCAGG GATTTGAACA CGCGCAGCTT
451 CCGTGCAAAA CAACAGGCGG CGCAGGCGCA CGGTTACCGC CGGACAACGC
501 GCCCGCCCGC CAATTACCGC CGCCCGGCCA TCGCGGTTT CCGCAGAAGG
551 CGGTAAATCT GCGTGCCAA TGCCTCTGCA AGGGCTTTCA GACGGCATTT
601 TTGTATTGTG TAGGGACATT GTTATGTTGC CGTTTGAATT TTAGCGGCA
651 TTTTGTTTCC AAGAGTTTGA TGTCCGGATG CCAATCTCGA
```

a934.pep

1	<u>MKKIIASALI</u>	<u>ATFALAACQD</u>	DAQARLEQQQ	KQIEALQQQL	AQQADDTVYQ
51	LTPEAVKDTI	PAEAQANGNN	GQVPTX*RR	AVYLRPIDRK	LAAAKPGRRG
101	GRVRVQRAG	KQIHTRGRPR	QSRPARACR	LPSVRTSQCA	HQQGFHAQP
151	PCKTTGGAGA	ALPPDNAPAR	QLPPPHARF	RQKAVNPACQ	CRLKGQ TAF
201	LYLLGTLLCC	RLIFRRHFS	KSLMSGWQF*		

```

m934.pep      10      20      30
                RLEQQQKQIEALQQQLAQQADDTVYQLTPEAVKDTI
                |||||
a934          MKKIIASALIATFALAACQDDAQARLEQQQKQIEALQQQLAQQADDTVYQLTPEAVKDTI
                10      20      30      40      50      60

m934.pep      40      50      60      70      80      90
                PAEAQANGNNGQPVTCXRRRAAVYLRPIDRKLAAPGRRGGRVYRQAGKQIHTGRQPR
                |||||
a934          PAEAQANGNNGQPVTXRRRAAVYLRPIDRKLAAPGRRGGRVYRQAGKQIHTGRQPR
                70      80      90      100     110     120

m934.pep      100     110     120     130     140     150
                QSRRPARACSLPSVRTPQCAHQGQFEHAQPPCKTTGGAXAALPPDNAPXRQLPPPRYARF
                |||||
a934          QSRRPARACRLPSVRTSQCAHQGQFEHAQPPCKTTGGAGAALPPDNAPARQLPPPRHARF
                130     140     150     160     170     180

m934.pep      160     170     180     190     200
                RQEAVNPARQCRLKSFQTAFXHLGLTLLCCRLIFRRHFVSKRLMSGWQFX
                ||:|||||
a934          RQKAVNPACQCRLKGFQTAFYLLGLTLLCCRLIFRRHFVSKSLMSGWQFX
                190     200     210     220     230

```

g935.sec not found yet

1349

```

601 AATAGAAATG CCAATAATGC CGCGCCGCAG TATTGCCGGC AAAACGGAGG
651 CCGGCAGATA TGCAGTGTCA GCCGGGCGGA GCGGGCGGCA GGCTTGAATT
701 ATGAAATCGA GCGGAAAAA CTGACGGCGT TGGCAGATAA TCATTATTG
751 TTGTTCCGTT CCAATATCGG CGGCACGAGC TATTATTTC AAAAAAATC
801 AGCTTATGAC GACGGGTTCG GCAGAGCGTA TTTGGGTTGG CAGTATAAAA
851 ATGCACGGCA GACGGCGGGG ATTTTGCCGT TTTATCAGGT SCAGTTGTCG
901 GGCAGCGACG GCTTTGATGC GAAAACAAA CGGGTAAACA ACCGCCGCCT
951 GCCGCCGTAT ATGCTGGCGC ACGGAGTCGG CGTGCACTTG TCCCATACTT
1001 ACCGCCCAAA CCCGGGATGG CAATTTTCGG TCGCGCTGGA ACATTACCGC
1051 CAACGCTACC GCGAACAGGA TAGGGCGGAA TACAATAACG STCGGCAGGA
1101 CCGGTTTTAT GTTTCGTCGG CAAAACGTTT GGGCGAATCG SCAACTGTGT
1151 TCGGCGGCTG GCAGTTTGTG CGGTTTGTGC CGAAACGCGA AACCGTGGGC
1201 GGCAGCGTCA ATAATGCCGC CTACCGGCGC AACCGTGTTT ATGCCGGCTG
1251 GCGCGCAGAG TGGCGGCGAG TGGGCGGTTT GAACAGTCGG STTTCCGCGT
1301 CTTATGCCCG CCGCAACTAT AAGGGCGTTG CGGCTTCTC SACAGAGGCG
1351 CAACGCAACC GCGAATGGA TGTCTCGCTG GCTTTGAGCC ACGACAAGTT
1401 GTCGTACAAA GGTATCGTGC CCGCGTTGAA TTATCGTTTC GGCAGGACGG
1451 AAAGTAATGT GCCGTATGCG AAACGCCGCA ACAGCGAGGT STTTGTGTCTG
1501 GCGGATTGGC GGTTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2874; ORF 935.a>:

```

a935.pep
1  MLYFRYGFV VWCAAGVSAA YGADAPAILD DKALLQVQRS VSDKWAESDW
51  KVDNDAPRVV DGDFLLAHPK MLEHSLRDVL NGNQADLIAS LADLYAKLPD
101 YDAVLYGRAR ALLAKLAGRP AEAVARYREL HGENAADERI LLDLAAEFDD
151 DFRKLSAERH FAEAEKLDLP APVLENVGRF RKAEGLTGW QFSGGISPAV
201 NRRNANNAAPQ YCRQNGGRQI CSVSRAERAA GLNYEIEAEK LTALADNHYL
251 LFRSNIGGTS YYFSKKSAYD DGFGRAYLGW QYKNARQTAG ILPFYQVQLS
301 GSDGFDAKTK RVNNRRLPPY MLAGVGVQQL SHTYRPNPGW QFSVALEHYR
351 QRYREQDRAE YNNGRQDGFY VSSAKRLGES ATVFGGWQFV REVVPKRETVG
401 GAVNNAAYRR NGVYAGWAE WRQLGLNSR VSASYARNY KGVAAFSTEA
451 QRNREWNVSL ALSHDKLSYK GIVPALNYRF GRTESNVPYA KRRNSEVFVS
501 ADWRF*

```

m935/a935 98.8% identity in 505 aa overlap

m935.pep	10	20	30	40	50	60
	MLYFRYGFV VWCAAGVSAA YGADAPAILD DKALLQVQRS VSDKWAESDW KVDNDAPRVV					
a935	MLYFRYGFV VWCAAGVSAA YGADAPAILD DKALLQVQRS VSDKWAESDW KVDNDAPRVV					
	10	20	30	40	50	60
m935.pep	70	80	90	100	110	120
	DGDFLLAHPK MLEHSLRDALNGNQADLIAS LADLYAKLPD YDAVLYGRAR ALLAKLAGRP					
a935	DGDFLLAHPK MLEHSLRDALNGNQADLIAS LADLYAKLPD YDAVLYGRAR ALLAKLAGRP					
	70	80	90	100	110	120
m935.pep	130	140	150	160	170	180
	AEAVARYREL HGENAADERI LLDLAAEFDD FRKLSAERHFAEAEKLDLPAPVLENVGRF					
a935	AEAVARYREL HGENAADERI LLDLAAEFDD FRKLSAERHFAEAEKLDLPAPVLENVGRF					
	130	140	150	160	170	180
m935.pep	190	200	210	220	230	240
	RKKTEGLTGW RFSGGISPAV NRRNANNAAPQ YCRQNGGRQICSVSRAERAAGLNYEIEAEK					
a935	RKAEGLTGW RFSGGISPAV NRRNANNAAPQ YCRQNGGRQICSVSRAERAAGLNYEIEAEK					
	190	200	210	220	230	240
m935.pep	250	260	270	280	290	300
	LTPLADNHYLLFRSNIGGTSYYFSKKSAYDDGFGRAYLGWQYKNARQTAGILPFYQVQLS					
a935	LTALADNHYLLFRSNIGGTSYYFSKKSAYDDGFGRAYLGWQYKNARQTAGILPFYQVQLS					
	250	260	270	280	290	300

g935.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2871>:

m935.seq

```

1  ATGTTGTATT TCAGATACGG CTTTTTGGTT GTTTGGTGTG CGGCAGGTGT
51  TTCTGCCGCC TATGGGGCGG ATGCGCCCGC GATTTTGGAT GACAAGGCAT
101 TGTTCAGGT GCAGCGGTCG GTGTCGGATA AGTGGGCGGA ATCAGATTGG
151 AAAGTTGAAA ATGATGCCCC GCGCGTGGTT GACGGGGATT TTTGTTGGC
201 GCATCCGAAA ATGTTGGAAC ATAGTTTGGC CGACGCGCTC AACGGCAATC
251 AGGCGGATTT AATCGCTTCG TTGGCGGATT TGTATGCCAA GCTGCCGGAT
301 TATGACGCGG TTTTGTACGG CAGGGCGCGG GCTTTGCTGG CGAAATTGGC
351 GGAAGGCCG GCGGAGGCGG TGGCGCGGTA TCGGGAACG CACGGGGAAA
401 ATGCGGCAGA CGAGCGGATT TTGCTGGATT TGGCGGCGGC GGAGTTTGAC
451 GATTTCCGGC TGAAGTCGGC AGAAAGGCAT TTTGCGGAGG CGGCAAAATT
501 GGATTTGCCG GCACCGGTTT TGGAAAATGT GGGGCGTTT CGGAAAAAAT
551 CCGAGGGGCT GACGGGCTGG CGTTTTTCGG GCGGCATCAG TCCGGCGGTC
601 AATAGAAATG CCAATAATGC CGCGCCGCAA TATGCGCGC AAAACGGAGG
651 CCGGCAGATA TGCAGTGTCA GCCGGGCGGA GCGGGCGCA GGTTTGAATT
701 ATGAAATCGA GCGGAAAAAG CTGACGCCGT TGGCAGATAA TCATTATTG
751 TTGTTCCGTT CCAATATCGG CGGCACGAGC TATTATTTCG GTAAAAAATC
801 AGCTTATGAT GACGGGTTCC GCAGGGCGTA TTTGGGTTGG CAGTATAAAA
851 ATGCACGGCA GACGGCGGGG ATTTGCGGT TTTATCAGGT GCAGTTGTGC
901 GGCAGCGACG GCTTTGATGC GAAAAAATAA CCGGTAAACA ACCGCCGCTT
951 GCCGCCGTAT ATGCTGGCGC ACGGAGTCGG CGTGACGCTG TCCCATACTT
1001 ACCGCCAAA CCCGGGATGG CAATTTTCGG TCGCGCTGGA ACATTACCGC
1051 CAACGCTACC GCGAACAGGA TAGGGCGGAA TACAATAACG GCAGGCAGGA
1101 CCGGTTTTAT GTTTCGTCCG CAAAACGTTT GGGCGAATCG GCAACTGTGT
1151 TCGGCGGCTG GCAGTTTGTG CGGTTTGTGC CGAAACGCGA AACGGTGGGC
1201 GGCGCGGTCA ATAATGCCGC CTACCGGCGC AACGGTGTTT ATGCCGGTTG
1251 GGCGCAGGAG TGGCGGCAGT TGGGCGGTTT GAACAGTCGG GTTTCGCGT
1301 CTTATGCCCG CCGCAACTAT AAGGGCATG CGGCTTTCTC GACAGAGGCG
1351 CAACGCAACC GCGAATGGAA TGTCTCGCTG GCTTTGAGCC ACGACAAGTT
1401 CTCGTACAAA GGTATCGTGC CGGCGTTGAA TTATCGTTTC GGCAGGACGG
1451 AAAGTAATGT GCCGTATGCG AACGCCGCA ACAGCGAGGT GTTGTGTCTG
1501 GCGATTGGC GGTTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2872; ORF 935>:

m935.pep

```

1  MLYFRYGLV VWCAAGVSAA YGADAPAILD DKALLQVORS VSDKWAESDW
51  KVENDAPRVV DGDFLLAHPK MLEHSLRDAL NGNQADLIAS LADLYAKLPD
101 YDAVLYGRAR ALLAKLAGRP AEAVARYREL HGENAADERI LLDLAAAEFD
151 DFRKLSAERH FAEAAKLDP APVLENVGRF RKKTEGLTGW RFSGGISPAV
201 NNRNANNAPO YCRQNGGRQI CSVSRAERAA GLNYEIEAEK LTPLADNHYL
251 LFRSNIGGTS YYFSKKSAYD DGFGRAYLGW QYKNARQTAG ILPFYQVOLS
301 GSDGFDAKTK RVNRRRLPPY MLAGVGVQL SHYRPNPGW QFSVALEHYR
351 QRYREQDRAE YNNGRQDGFY VSSAKRLGES ATVFQGWQFV RFVPKRETVG
401 GAVNNAAYRR NGVIAGWAE WRQLGGLNSR VSASYARRNY KGIAAPSTEA
451 QRNREWNVSL ALSHDKLSYK GIVPALNYRF GRTESNVPYA KRNSEVFVS
501 ADWRF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2873>:

a935.seq

```

1  ATGTTGTATT TCAGATACGG TTTTTTGGTT GTTTGGTGTG CGGCAGGTGT
51  TTCTGCCGCC TATGGGGCGG ATGCGCCCGC GATTTTGGAT GACAAGGCAT
101 TGTTCAGGT GCAGCGGTCG GTGTCGGATA AGTGGGCGGA ATCGGATTGG
151 AAAGTTGACA ATGATGCCCC GCGCGTGGTT GACGGGGATT TTTGTTGGC
201 GCATCCGAAA ATGTTGGAAC ATAGTTTGGC CGACGTGCTC AACGGCAATC
251 AGGCGGATTT GATCGCTTCG TTGGCGGATT TGTATGCCAA GCTGCCGGAT
301 TATGACGCGG TTTTGTACGG CAGGGCGCGG GCTTTGCTGG CGAAATTGGC
351 GGAAGGCCG GCGGAGGCGG TGGCGCGGTA TCGGGAACG CACGGGGAAA
401 ATGCGGCAGA CGAGCGGATT TTGCTGGATT TGGCGGCGGC GGAGTTTGAC
451 GATTTCCGGC TGAAGTCGGC AGAAAGGCAT TTTGCCGAGG CGGAAAAAAT
501 GGATTTGCCG GCGCGGTTT TGGAAAATGT GGGGCGTTT CGGAAAAAAT
551 CCGAGGGGCT GACGGGCTGG CGTTTTTCGG GCGGCATCAG TCCGGCGGTC

```

1350

	310	320	330	340	350	360
m935.pep	GSDGFDATKRVNNRRLPPYNLAHGVGVQLSHTYRPNPGWQFSVALEHYRQRYREQDRAE					
a935	GSDGFDATKRVNNRRLPPYNLAHGVGVQLSHTYRPNPGWQFSVALEHYRQRYREQDRAE					
	310	320	330	340	350	360
	370	380	390	400	410	420
m935.pep	YNNGRQDGFYVSSAKRLGESATVFGGWQFVRFPKRETVGGAVNNAAYRRNGVYAGWAQE					
a935	YNNGRQDGFYVSSAKRLGESATVFGGWQFVRFPKRETVGGAVNNAAYRRNGVYAGWAQE					
	370	380	390	400	410	420
	430	440	450	460	470	480
m935.pep	WRQLGGLNSRVASAYARRNYKGIAAFSTEAQRNREWNVSLALSHDKLSYKGIVPALNYRF					
a935	WRQLGGLNSRVASAYARRNYKGIAAFSTEAQRNREWNVSLALSHDKLSYKGIVPALNYRF					
	430	440	450	460	470	480
	490	500				
m935.pep	GRTESNVPIAKRRNSEVFVSADWRF					
a935	GRTESNVPIAKRRNSEVFVSADWRF					
	490	500				

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2875>:

g936.seq

```

1  ATGAAACCCA  AACCACACAC  CGTCCGCACC  CTGATTGCCG  CCGTCCTCAG
51  CCTTGCCCTC  GCGGGCTGCT  TCAGCGCAGT  CGTCGGCGGG  GCCGCCGTCG
101 GCGCAAAATC  CGTCATCGAC  CGcgcgAACCA  CCGgcgcgca  AACCGATGac
151 aACGTTATGG  CGTTGCGTAT  CGAAACCACC  GCCCGTTCCT  ACCTGCGCCA
201 AAACAACCAA  ACCAAAGGCT  ACACGCCCCA  AATCTCCGTC  GTCGGCTACA
251 ACCGCCACCT  GCTGCTGCTC  GGACAAGTCG  CCACCGAAGG  CGAAAAACAG
301 TTCGTCGGTC  AGATTGCACG  TTCCGAACAG  GCCGCCGAAG  GCGTATACAA
351 CTACATTACC  GTCGCCTCCC  TGCCGCGCAC  TGCGGGCGAC  ATCGCCGGCG
401 ACACCTGGAA  CACGTCCAAA  GTCCGCGCca  cgCTGCTGGG  CATCAGCCCC
451 GCTACACAGG  CGCGCGTCAA  AATCATTACC  TACGGCAATG  TAACCTACGT
501 TATGGGCATC  CTCACCCCG  AAGAACAGGC  GCAGATTACC  CAAAAAGTCA
551 GCACCACcgT  CGGCGTACAA  AAAGTCATTA  CCCTTACCA  AAACCTACGTC
601 CAACGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2876; ORF 936.ng>:

g936.pep

```

1  MKPKPHTVRT  LIAAVLSLAL  GGCFSAVVGG  AAVGAKSVID  RRTTGAQTDD
51  NVMALRIETT  ARSYLRQNNQ  TKGYTPQISV  VGYNRHLLLL  GOVATEGEKQ
101 FVGQIARSEQ  AAEGVYNYIT  VASLPRTAGD  IAGDTWNTSK  VRATLLGISP
151 ATQARVKIIT  YGNVTYVMGI  LTPEEQAQIT  QKVSTTVGVQ  KVITLYQNYV
201 QR*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2877>:

m936.seq (partial)

```

1  ATGAAACCCA  AACCGCACAC  CGTCCGCACC  CTGATTGCCG  CCATTTCAG
51  CCTTGCCCTT  AGCGGCTGCG  TCAGCGCAGT  AATCGGAAGC  GCCGCCGTCG
101 GCGCGAAATC  CGCCGTCGAC  CGCCGAACCA  CCGCGCGCA  AACCGACGAC
151 AACGTTATGG  CGTTGCGTAT  CGAAACCACC  GCCCGTTCCT  ATCTGCGCCA
201 AAACAACCAA  ACCAAAGGCT  ACACGCCCCA  AATCTCCGTC  GTCGGCTACA
251 ACCGCCACCT  GCTGCTGCTC  GGACAAGTCG  CCACCGAAGG  CGAAAAACAG
301 TTCGTCGGTC  AGATTGCACG  TTCCGAACAG  GCCGCCGAAG  GCGTGTACAA
351 CTATATTACC  GTCGCCTCCC  TGCCGCGCAC  TGCC...

```

This corresponds to the amino acid sequence <SEQ ID 2878; ORF 936>:

m936.pep (partial)

```

1  MKPKPHTVRT  LIAAIFSLAL  SGCVSIVIGS  AAVGAKSAVD  RRTTGAQTDD
51  NVMALRIETT  ARSYLRQNNQ  TKGYTPQISV  VGYNRHLLLL  GOVATEGEKQ
101 FVGQIARSEQ  AAEGVYNYIT  VASLPRTA...

```

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 936 shows 93.8% identity over a 128 aa overlap with a predicted ORF (ORF 936.ng) from *N. gonorrhoeae*:

m936/g936

	10	20	30	40	50	60
m936.pep	MKPKPHTVRTLIAAIFSLALSGCVSAVIGSAAVGAKSAVD	RRRTTGAQTDDNV	MALRIETT			
g936	MKPKPHTVRTLIAAVLSLALGGCFSAVVGGAAVGAKSV	VIDRRTTGAQTDDNV	MALRIETT			
	10	20	30	40	50	60
	70	80	90	100	110	120
m936.pep	ARSYL	RQN	NOTKGYTPQIS	VVGYNRHLL	LLGQVATEGEKQFVG	QIARSEQAAEGVNYIT
g936	ARSYL	RQN	NOTKGYTPQIS	VVGYNRHLL	LLGQVATEGEKQFVG	QIARSEQAAEGVNYIT
	70	80	90	100	110	120
	130					
m936.pep	VASLPRTAXXX					
g936	VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIITYGNVTYVMGILTPEEQAQIT					
	130	140	150	160	170	180

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 2879>:

a936.seq

1	ATGAAACCCA	AACCGCACAC	CGTCCGCACC	CTGACTGCCG	CGGTCTCTAG
51	CCTTGCCCTC	GGCGGCTGCG	TCAGCGCAGT	CGTCGGCGGC	CGGGCGGTTCG
101	CGCGGAATC	CGCCGTCGAC	CGCGCAACCA	CCGGCGGACCA	AACCGACGAC
151	AACGTAATGG	CGCTGCGTAT	CGAAACCACC	GCCCGCTCCT	ATCTGCGCCA
201	AAACAACCAA	ACCAAAGGCT	ACACGCCCCA	AATCTCCGTT	GTCGGGTACA
251	ACCGCGACCT	GCTGCTGCTC	GGACAAGTCG	CCACCGAAGG	CGAGAACACG
301	TTCGTCGGTC	AGATTGCACG	TTCGGAACAG	GCCGCGGAAG	CGGTGTACAA
351	CTACATTACC	GTCGCCTCC	TGCCCGGCAC	TGCCGCGGAC	ATCGCCGGCG
401	ACACTTGGAA	CACATCCAAA	GTCGCGGCCA	CGCTGTTGGG	CATCAGCCCC
451	CGCACACAGG	CGCGCGTCAA	ATTCGTTACC	TACGGCAACG	TAACTACGTC
501	TATGGGCATC	CTCACCCCCG	AAGAACAGGC	GCAGATTACC	CAAAAAGTCA
551	GCACCAACCGT	CGGCGTACAA	AAAGTCATCA	CCCTCTAGCA	AAACTACGTC
601	CAACGCTGA				

This corresponds to the amino acid sequence <SEQ ID 2880; ORF 936.a>:

a936.pep

1	MKPKPHTVRT	LTAAVLSLAL	GGCVSAVVGG	AAVGAKSVD	RRTTGAQTD
51	NVMALRIETT	ARSYLRQNNQ	TKGYTPQISV	VGYNRHLLLL	QGVATEGEKQ
101	FVGQIARSEQ	AAEGVYNYIT	VASLPRTAGD	IAGDTWNTSK	VRATLLGISP
151	ATQARVKIVT	YGNVTYVMGI	LTPEEQAQIT	QKVSTTVGVQ	KVITLYQNYV
201	OR*				

m936/a936 95.3% identity in 128 aa overlap

	10	20	30	40	50	60
m936.pep	MKPKPHTVRTLIAAIFSLALSGCVSAVIGSAVGA	SAVD	RRTTGAQTDDNV	MALRIETT		
a936	MKPKPHTVRTLTA	AVLSLALGGCVSAVVGGA	AVGA	SAVD	RRTTGAQTDDNV	MALRIETT
	10	20	30	40	50	60
	70	80	90	100	110	120
m936.pep	ARSYL	RQN	NQTKGYT	POISVVGYNRHL	LLLLQVATEGEKQFV	GQIARSEQAAEGVNYIT
a936	ARSYL	RQN	NQTKGYT	POISVVGYNRHL	LLLLQVATEGEKQFV	GQIARSEQAAEGVNYIT
	70	80	90	100	110	120
m936.pep	VASL	PRTA				

1352

```

          |||||
a936      VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIVTYGNVTYVMGILTPEEQAQIT
          130      140      150      160      170      180

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2881>:

```

g936-1.seq
1  ATGAAACCCA AACCACACAC CGTCCGCACC CTGATTGCCG CCGTCCTCAG
51 CCTTSCCCTC GGCGGCTGCT TCAGCGCAGT CGTCGGCGGG GCCGCCGTCG
101 GCGCAAAATC CGTCATCGAC CGccgAACCA CCgcgcgca AACCgATGac
151 aACGTTATGG CGTTGCGTAT CGAAACCACC GCCCGTTCCT ACCTGCGCCA
201 AAACAACCAA ACCAAAGGCT ACACGCCCCA AATCTCCGTC GTCGGCTACA
251 ACCGCCACCT GCTGCTGCTC GGACAAGTCG CCACCGAAGG CGAAAAACAG
301 TTCGTCGGTC AGATTGCACG TTCCGAACAG GCCGCCGAAG GCGTATACAA
351 CTACATTACC GTCGCCCTCC TGCCGCGCAC TCGGGCGGAC ATCGCCGGCG
401 ACACTTGGAa CACGTCCAAa GTCCGCGCca cgCTGCTGGG CATCAGCCCC
451 GCTACACAGG CGCGCGTCAA AATCATTACC TACGGCAATG TAACCTACGT
501 TATGGGCATC CTCACCCCGG AAGAACAGGC GCAGATTACC CAAAAAGTCA
551 GCACCACcgT CGGCGTACAA AAAGTCATTA CCCTCTACCA AAACCTACGTC
601 CAACGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2882; ORF 936-1.ng>:

```

g936-1.pep
1  MKPKPHTVRT LIAAVLSLAL GGCFSAVVGG AAVGAKSVID RRTTGAQTDD
51 NVMALRIETT ARSYLRONNQ TKGYTPQISV VGYNRHLLLL GQVATEGEKQ
101 FVGQIARSEQ AAEGVYNYIT VASLPRTAGD IAGDTWNTSK VRATLLGISP
151 ATQARVKIIT YGNVTYVMGI LTPEEQAQIT QKVSTTVGVQ KVITLYQNYV
201 QR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2883>:

```

m936-1.seq
1  ATGAAACCCA AACCACACAC CGTCCGCACC CTGATTGCCG CCATTTTCAG
51 CCTTGCCTTT AGCGGCTGCG TCAGCGCAGT AATCGGAAGC GCCGCCGTCG
101 GCGCAAAATC CGCGCTCGAC CGCCGAACCA CCGCGCGCA AACCgACGAC
151 AACGTTATGG CGTTGCGTAT CGAAACCACC GCCGTTTCCT ATCTGCGCCA
201 AAACAACCAA ACCAAAGGCT ACACGCCCCA AATCTCCGTC GTCGGCTACA
251 ACCGCCACCT GCTGCTGCTC GGACAAGTCG CCACCGAAGG CGAAAAACAG
301 TTCGTCGGTC AGATTGCACG TTCCGAACAG GCCGCCGAAG GCGTGTACAA
351 CTATATTACC GTCGCCCTCC TGCCGCGCAC TCGGGCGGAC ATCGCCGGCG
401 ACACTTGGAa CACATCCAAa GTCCGCGCCA CGCTGTTGGG CATCAGCCCC
451 GCCACACAGG CGCGCGTCAA AATCGTTACC TACGGCAACG TAACCTACGT
501 TATGGGCATC CTCACCCCGG AAGAACAGGC GCAGATTACC CAAAAAGTCA
551 GCACCACCGT CGGCGTACAA AAAGTCATCA CCCTCTACCA AAACCTACGTC
601 CAACGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2884; ORF 936-1>:

```

m936-1.pep
1  MKPKPHTVRT LIAAIFSLAL SGCVSAVIGS AAVGAKSAVD RRTTGAQTDD
51 NVMALRIETT ARSYLRONNQ TKGYTPQISV VGYNRHLLLL GQVATEGEKQ
101 FVGQIARSEQ AAEGVYNYIT VASLPRTAGD IAGDTWNTSK VRATLLGISP
151 ATQARVKIIV YGNVTYVMGI LTPEEQAQIT QKVSTTVGVQ KVITLYQNYV
201 QR*

```

m936-1/g936-1 95.5% identity in 202 aa overlap

```

          10      20      30      40      50      60
m936-1.pep  MKPKPHTVRTLIAAIFSLALSGCVSAVIGSAAVGAKSAVDRRTTGAQTDDNVMALRIETT
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g936-1      MKPKPHTVRTLIAAVLSLALGGCFSAVVGGAAVGAASVIDRRTTGAQTDDNVMALRIETT
          10      20      30      40      50      60

          70      80      90      100     110     120
m936-1.pep  ARSYLRONNQTKGYTPQISVVGYNRHLLLLGQVATEGEKQFVGQIARSEQAAEGVYNYIT
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g936-1      ARSYLRONNQTKGYTPQISVVGYNRHLLLLGQVATEGEKQFVGQIARSEQAAEGVYNYIT
          70      80      90      100     110     120

          130     140     150     160     170     180
m936-1.pep  VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIVTYGNVTYVMGILTPEEQAQIT
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

1353

```

g936-1      VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIITYGNVTYVMGILTPEEQAOIT
              130      140      150      160      170      180

              190      200
m936-1.pep  QKVSTTVGVQKVITLYQNYVQRX
              |||||
g936-1      QKVSTTVGVQKVITLYQNYVQRX
              190      200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2885>:

```

a936-1.seq
1  ATGAAACCCA AACCGCACAC CGTCCGCACC CTGACTGCCG CCGTCCTCAG
51 CCTTGCCCTC GCGGCTGCG TCAGCGCAGT CGTCGGCGGC GCGGCGGTCTG
101 GCGCGAAATC CGCGCTCGAC CGCGGAACCA CCGGCGCGCA AACCGACGAC
151 AACCTAATGG CGCTGCGTAT CGAAACCACC GCCCGCTCCT ATCTGCGCCA
201 AAACAACCAA ACCAARAGCT ACACGCCCCA AATCTCCGTT GTCGGCTACA
251 ACCGCCACCT GCTGCTGCTC GGACAAGTCG CCACCGAAGG CGAGAAACAG
301 TTCGTCGGTC AGATTGCACG TTCCGAACAG GCCGCCAAG GCGTGTACAA
351 CTACATTACC GTCGCCCTCC TGCCGCGCAC TGCCGCGCAC ATCGCCGGCG
401 ACACCTTGGA CACATCCAAA GTCCGCGCCA CGCTGTTGGG CATCAGCCCC
451 GCCACACAGG CGCGCGTCAA AATCGTTACC TACGGCAACG TAACCTACGT
501 TATGGGCATC CTCACCCCGG AAGAACAGGC GCAGATTACC CAAAAAGTCA
551 GCACCACCGT CGCGGTACAA AAAGTCATCA CCTCTACCA AACTACGTC
601 CAACGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2886; ORF 936-1.a>:

```

a936-1.pep
1  MKPKPHTVRT LTAAVLSLAL GGCVS AVVGG AAVGAKSAVD RRTTGAQTDD
51 NVMALRIETT ARSYLRQNNQ TKGYTPQISV VGYNRHL LLL GQVATEGEKQ
101 FVGQIARSEQ AAEGVYNYIT VASLPRTAGD IAGDTWNTSK VRATLLGISP
151 ATQARVKIVT YGNVTYVMGI LTPPEEQAOIT QKVSTTVGVQ KVITLYQNYV
201 QR*

```

a936-1/m936-1 97.0% identity in 202 aa overlap

```

              10      20      30      40      50      60
m936-1.pep  MKPKPHTVRTLIAAIFSLALSGCVSAVIGSAAVGAASAVDRRTTGAQTDDNVMLRIETT
              |||||
a936-1      MKPKPHTVRTLTAAVLSLALGGCVSAVVGGAASAVDRRTTGAQTDDNVMLRIETT
              10      20      30      40      50      60

              70      80      90      100     110     120
m936-1.pep  ARSYLRQNNQTKGYTPQISVVGYNRHL LLL GQVATEGEKQFVGQIARSEQAAEGVYNYIT
              |||||
a936-1      ARSYLRQNNQTKGYTPQISVVGYNRHL LLL GQVATEGEKQFVGQIARSEQAAEGVYNYIT
              70      80      90      100     110     120

              130     140     150     160     170     180
m936-1.pep  VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIITYGNVTYVMGILTPEEQAOIT
              |||||
a936-1      VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIITYGNVTYVMGILTPEEQAOIT
              130     140     150     160     170     180

              190     200
m936-1.pep  QKVSTTVGVQKVITLYQNYVQRX
              |||||
a936-1      QKVSTTVGVQKVITLYQNYVQRX
              190     200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2887>:

```

g937.seq
1  atGAAAAATA TTCTCTTAgT ATTTGTTAGC TTTGTGCCAT TATGTGTCCG
51 CACTGATCTG CCGCTGAaTa tCGAAGACAT AATGaccgAC AAGGGAAAAT
101 GGAAaactGA AACTTccctt acctacctgA acaGCGAAAA cagCCGCGCC
151 GCACTTGCCT CACCGGTTTA CATTcAGACC GGCTCCGCTT CCTTTATCCC
201 CGTCCCGACC GAAATTCAGG AAAACGGCAG CAATACCGAT ATGCTCGCGG
251 GCACGCTCGG TTTGCGCTAC GGACTGAcCG GCAataccgA CATTTACGGC
301 AGCGGCAGCT ATCTGTGGCA CGAAGAACGC AAACTCGacg GCAACGGCAA

```

g937.pep

1	MKNILLVFVS	FVPLCVRTDL	PLNIEDIMTD	KGKWKLETSL	TYLNSNSRA
51	<u>ALASPVYIQT</u>	GSASPIPVPT	EIQENGSTDI	MLAGTLGLRY	GLTGNTDIYG
101	SGSYLWHEER	KLDGNGKTRN	KRMSDISAGI	SH7FLKDGKN	PALIAFLEST
151	VYEKSRNKAS	SGKSWLIGAT	TYKAIDPIVL	SLTAAARYNG	SKTLSDDVKY
201	KAGNYWMLNP	NISFAANDRI	SLTGQIOWLG	KQPRIDGKK	ESARNTSTYA
251	HFGAGFGFTK	TAALNASARF	NVSGQSSSEL	KLGVOHTF*	

m937.seq

1	ATGAAGCGCA	TCTTTTGGCC	CGCTTGCCC	GCCATCTGCG	CTTTATCCAC
51	TTATGCCGAC	CTGCCCTTGA	CGATTGAAGA	CATAATGACC	GACAAGGGAA
101	AATGGAAACT	GGAACTTCC	CTTACCTTAC	TGAAACAGCGA	AAAAACCCGC
151	GCGCAACTTG	GCAACCGGT	TTACATTCAA	ACCGCGCGAA	CCTCGTTTAT
201	CCCCATTCCG	ACCGAAATCC	AaGAAAaCGG	CAGCAATACC	GATATGCTCG
251	TCGGCAGCCT	CGGTTTGCCT	TACGGACTGA	CCGGGAATAC	CGACATTTAC
301	GGCAGCGGCA	GCTATCTGTG	GCACAGAGTA	CGCAAACTCG	ACGGCAACAG
351	CAAAACCCGC	AACAAACGGA	TGTCCGAGGT	ATCCCTCGCG	ATCAGCCACA
401	CTTTCTTTAA	AGACGACAAA	AACCCCGCCC	TAATCAGCTT	CTTTGAAGC
451	ACGGTTTACG	AAAAATCGCG	CAACAAAGCC	TCGTGCGGAA	AATCCTGGCT
501	CATCGCGGCC	CCCGCTTACA	AAGCCATAGA	TCCGATTGTC	CTTTCCCTCA
551	CCGCGCGCTA	ACGCATCAAC	GGCAGCAAAA	CCCTTTTCAG	CGGCATCCGC
601	TACAAATCGG	GCAACTACCT	GCTGCTCAAC	CCCAACATCT	CATTTGCTCG
651	CAACGACAGA	ATCAGCCTGA	CCGGAGGCAT	CCAATTGGCTG	CGAGGCAGC
701	CCGACCGGAC	GGACGGCAAA	CGGAATCCTT	CCAGAAACAC	ATCCACCTAC
751	GCCCATTTTC	GCGCAGGTTT	CGGTTTCACC	AAAACCAACG	CTTTAAACGC
801	ATCCGCACGT	TTCAACGTTT	CAGGGCAAAG	CAGTTCCGAA	CTGAAATTTC
851	CGGTACAGCA	TACATTTTAA			

m937.pcp..

1	MKRIFLPAL	AILPLSTYAD	LPLTIEDINT	DKGKWKLETS	LTYLNSENNRR
51	AELAAVPVYIQ	TGATSFIPIP	TEIQENGDSMT	DMLVFLTKLGR	YGLTGNLTDIY
101	GSQSYLWHEE	RKLDGNSKTR	NKRMDSVSLG	ISHTFLKDDK	NPALISFLES
151	TVYEKSRNKA	SSGKSWLIGA	TTYKAIIDPIR	LSLTAAYRIN	GSKTLDSEGIR
201	YKSGNYLLN	PNISFAANDR	ILVTGGIQWL	GRQPDRTDGH	RESSRNTSTY
251	AHFGAGFGFT	KTALNASAR	FNVSQGSSE	LKFGVHTFP*	

Homology with a predicted ORF from *N.gonorrhoeae*

q937/m937

	10	20	30	40	50	59
g937.pep	MKNILL-VFVSFVPLCVRTLPLNIEDIMTDKGKWKLETSLTYLNSENSRAALASPVYIQ					
	} :: :: : : : : : : : : :					
m937	MKRIFLPAIPAILPLSTYADLPLTIEDIMTDKGKWKLETSLTYLNSENNRAELAAPVYIQ					
	10	20	30	40	50	60
	60	70	80	90	100	119
g937.pep	TGSASFIPVPTEIQENGSTNDMLAGTLGLRYGLTGNTDIYGSGSYLWHEERKLDGNGKKT					

[illegible]

```

a937.seq
1  ATGAAGCGCA TCTTTTGGCC CGCCTTGCCC GGCATCCTGC CTTTATCCGC
51  TTATGCCGCA CTGCCCTTGA CGATTGAAGA CATATATACC GACAAGGGCA
101 ATAGGAAACT GGAAACTTCC CTTACTTACC TGAACAGCGA AAACAACCTG
151 GCCGAACCTG CCGCACCGBT TTACATCCAA ACCGCGCGAA CCTCGTTTAT
201 CCCCATTTCC ACCGAAATCC AAGAAAACGG CAGCAATACC GATATGCTCG
251 TTGGCACGCT CGGTTTGGCC TACGGACTGA CCGGGAATAC CGACATTTAC
301 GGCAGCGGCA GCTATCTGTG GCACGAAGAA CGGAAACTCG AGCGCAACGG
351 CAAAACCCGA AACAAACGGA TGTCCGACGT ATCCCTCGGC ATCAGGCCA
401 CCTTCTTTAA AGACGACAAA AACCCCGCCC TAATCAGCTT TCTTTAAAGC
451 ACGGTTTACG AAAAATCGCG CAACAAGGCC TCGTCGGGAA ARTCCTGGCT
501 CATCGCGGCC ACCACTACA AAGCATCGA CCCCCTGTCT CTCTATTGA
551 CCGCTGCCTA CCGTATCAAC GGCAGCAAAA CCTTTCAAG CAACACCAAA
601 TACAAGCAG GCAATTACTG GATCTGTAAT CCCAATATAT CCTTCGCGC
651 CAACGACAGA ATCAGCTCA CGGGCGGCAT CCAATGGCTG GGCAAGCAGC
701 CCGACCGTCT GGACGGCAAA AAAGAATCG CAAGAAACAC ATCCACCTAT
751 GCCCATTTCC GCGCAGGTTT CGGTTTCACC AAAACCACSG CTTTAAACGC
801 ATCCGCACGT TTCACGTTT CAGGGCAAAG CAGTTCGGAA CTGAAATTG
851 CGGTACGCA TACGTTTAA

```

```
a937.pap
1 MKRIFLPALP AILPLSAYAD LPLTIEDIMT DKGKWKLETS LTYLNSNNR
51 AELAAPVYIQ TGATSFIPIP TEIQENGST DMLVGLTLGLR YGLTGNTDIY
101 GSGSYLWHEE RKLDGNGKTR NKRMSDVSLG ISHTFLKDDK NPLAISFLES
151 TVYEKSRNKA SSGKSWLIGA TTYKADIPVV LSLTAAYRIN GSKTLLSNTK
201 YKAGNYWMLN PNISFAANDR ISLTGGIQWL GKQPPRDLGK KESARNSTSY
251 AHFGAGFGFT KTTALNASAR FNVSGQSSE LKFGVOHTF*
```

	10	20	30	40	50	60
m937.pep	MKRIFLPALPAILPLSTYADLPLTIEDIMTDKGKWKLETSLTYLNSENNAELAAPVYIQ					
a937		:				
	10	20	30	40	50	60
	MKRIFLPALPAILPLSAYADLPLTIEDIMTDKGKWKLETSLTYLNSENNAELAAPVYIQ					
	70	80	90	100	110	120
m937.pep	TGATSFIPITPEIQENGSNTDMLVGTLGLRYGLTGNTDIYGSGSYLWHEERKLDGNSKTR					
a937						
	70	80	90	100	110	120
	TGATSFIPITPEIQENGSNTDMLVGTLGLRYGLTGNTDIYGSGSYLWHEERKLDGNGKTR					

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	130	140	150	160	170	190
m937.pep	NKRMSDVS LGISHTFLKDDKNPALISFLESTVYEXSRNKASSGKSWLIGATTYKAIDPIV					
a937	NKRMSDVS LGISHTFLKDDKNPALISFLESTVYEXSRNKASSGKSWLIGATTYKAIDPVV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m937.pep	LSLTAAYRINGSKTLSDGIRYKSGNYLLNPNISFAANDRISLTGGIQWLGRQPDRTDGK					
a937	LSLTAAYRINGSKTLSSNTKYKAGNYWMLNPNISFAANDRISLTGGIQWLGRQPDRLDGK					
	190	200	210	220	230	240
	250	260	270	280	290	
m937.pep	RESSRNTSTYAHFGAGFGFTKTTALNASARFNVSGSSSELKFGVQHTFX					
a937	KESARNTSTYAHFGAGFGFTKTTALNASARFNVSGSSSELKFGVQHTFX					
	250	260	270	280	290	

g939.seq not found yet

g939.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2893>:

m939.seq (partial)

```

1  ATGAAACGAT TGACTTTATT GGCCTTTGTT TTGGCTGCCG GTGCGGTTTC
51  CGCATCTCCC AAAGCAGACG TGGAAAAAGG CAAACAGGTT GCCGCAACGG
101 TTTGTGCGGC TTGCCATGCA GCAGACGGTA ACAGCGGCAT TGCGATGTAT
151 CCGCGTTTGG CGGCACAGCA TACTGCTTAC ATCTATCATC AAACATATCGG
201 CATCCGCGAC GTAAACGCAC CC...
```

This corresponds to the amino acid sequence <SEQ ID 2894; ORF 939>:

m939.pep (partial)

```

1  MKRLTLLAFV LAAGAVSASP KADVEKGKQV AATVCAACHA ADGNSGIAMY
51  PRLAAQHTAY IYHQTIGIRD VNAP...
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2895>:

a939.seq

```

1  ATGAAACGAT TGACTTTATT GGCCTTTGTT TTGGCTGCCG GTGCGGTTTC
51  CGCATCTCCC AAAGCAGACG TGGAAAAAGG CAAACAGGTT GCCGCAACGG
101 TTTGTGCGGC TTGCCATGCA GCAGACGGTA ACAGCGGCAT TGCGATGTAT
151 CCGCGTTTGG CGGCACAGCA TACTGCTTAC ATCTATCATC AAACATATCGG
201 CATCCGCGAC GGTAAACGCA CCCACGGTTC GGCAGCTGTG ATGAAACCGG
251 TGGTAATGAA TTTGAGCGAT CAGGATATTT TGAACGTATC CGCATTTCTAT
301 GCCAAACAGC AGCCAAATC CGGTGAAGCC AATCCTAAGG AAAATCCCGA
351 ATTGGGTGCG AAAATCTATC GCGGCGGTTT GAGCGATAAA AAAGTGCCGG
401 CGTGATATGC CTGCCACGGT CCGAGCGGTG CCGGTATGCC GGGGGGCGGA
451 AGCGAAATTC AGGCTTATCC GCGTTTGGGC GGTGAGCATC AGGCATATAT
501 TGTGTAACAG ATGAATGCCT ACAAGTCCGG TCAGCGTAAA AATACCATCA
551 TGGGAAGATAT TGCAAACCGT ATGTCTGAAG AAGATTTGAA AGCGGTCGCC
601 AACTTTATCC AAGTTTTCG TTA
```

This corresponds to the amino acid sequence <SEQ ID 2896; ORF 939.a>:

a939.pep

```

1  MKRLTLLAFV LAAGAVSASP KADVEKGKQV AATVCAACHA ADGNSGIAMY
51  PRLAAQHTAY IYHQTIGIRD GKRTHGSAV MKPVVMNLSQ QDILNVSAFY
101 AKQPKSGEA NPKNPELGA KIYRGGLSDK KVPACMSCHG PSAGMPGGG
151 SEIQAYPRLG GQHQAIVEQ MNAYKSGQRK NTIMEDIANR MSEEDLKAVA
201 NFIQGLR*
```

m939/a939 100.0% identity in 70 aa overlap

	10	20	30	40	50	60
m939.pep	MKRLTLLAFVLAAGAVSASP KADVEKGKQVAATVCAACHAADGNSGIAMY PRLAAQHTAY					
a939	MKRLTLLAFVLAAGAVSASP KADVEKGKQVAATVCAACHAADGNSGIAMY PRLAAQHTAY					

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	10	20	30	40	50	60
	70					
m939.pep	IYHQTIGIRDVNAP					
a939	IYHQTIGIRDGKRTHGSAAVMKPVVMNLSDDQILNVSAFYAKQPKSGEANPKENPELGA					
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2897>:

g950.seq

1	ATGAACAAAA	ATATTGCTGC	CGCACTCGCC	GGTGCTTTAT	CCCTGTCTCT
51	GGCCGCCGCG	GCCGTTGCCG	CCCACAAACC	GGCAAGCAAC	GCAACAGGCG
101	TTCAAAAATC	CGCCCAAGGC	TCTTGCGGCG	CATCCAAATC	TGCCGAAGGT
151	TCGTGCGGCG	CATCCAAATC	TGCCGAAGGT	TCGTGCGGCG	CGGCTGCTTC
201	TAAAGCAGGC	GAAGGCAAAAT	GCGGCGAGGG	CAAAATGCGGT	GCAACTGTAA
251	AAAAAGCCCA	CAACACACC	AAAGCATCTA	AAGCCAAAGC	CAAACTGTCC
301	GAAGCAAAAT	GCGGCGAAGG	CAAAATGCGGT	TCTAAATAA	

This corresponds to the amino acid sequence <SEQ ID 2898; ORF 950.ng>:

g950.pep

1	MNKNIAAALA	GALSLSLAAG	AVAANKPASN	ATGVOKSAQG	SCGASKSAEG
51	SCGASKSAEG	SCGAAASKAG	EGKCGEGKCG	ATVKKAHKHT	KASKAKAKSA
101	EGKCGEGKCG	SK*			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2899>:

m950.seq

1	ATGAACAAAA	ACATTGCTGC	CGCTCTCGCC	GGTGCTTTAT	CCCTGTCTTT
51	GGCCGCCGCG	GCAGTTGCTG	CCAACAAACC	GGCAAGCAAC	GCAACAGGCG
101	TTCAATAATC	CGCCCATGGC	TCTTGCGGCG	CGTCCAAATC	TGCCGAAGGT
151	TCGTGCGGCG	CGGCTGGTTC	TAAAGCAGGC	GAAGGCAAAAT	GCGGCGAGGG
201	CAAATGCGGT	GCGACCGTAA	AAAAAACCCA	CAACACACC	AAAGCATCTA
251	AAGCCAAGGC	CAAATCTGCC	GAAGGCAAAAT	GCGGCGAAGG	CAAATGCGGT
301	TCTAAATAA				

This corresponds to the amino acid sequence <SEQ ID 2900; ORF 950>:

m950.pep

1	MNKNIAAALA	GALSLSLAAG	AVAANKPASN	ATGVHKSAGH	SCGASKSAEG
51	SCGAAGSKAG	EGKCGEGKCG	ATVKKTHKHT	KASKAKAKSA	EGKCGEGKCG
101	SK				

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 950 shows 86.6% identity over a 112 aa overlap with a predicted ORF (ORF 950) from *N. gonorrhoeae*

m950/g950 86.6% identity in 112 aa overlap

	10	20	30	40	50
m950.pep	MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHKSAGHSCGASKSAEGSCGA-----				
g950	MNKNIAAALAGALSLSLAAGAVAANKPASNATGVOKSAOGSCGASKSAEGSCGASKSAEG				
	10	20	30	40	50
	60	70	80	90	100
m950.pep	-----AGSKAGEGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSK				
g950	SCGAAASKAGEGKCGEGKCGATVKKAHKHTKASKAKAKSAEGKCGEGKCGSKX				
	70	80	90	100	110

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2901>:

a950.seq

1	ATGAACAAAA	ACATTGCTGC	CGCACTCGCC	GGTGCTTTAT	CCCTGTCTTT
51	GGCCGCCGCG	GCAGTTGCTG	CCAACAAACC	GGCAAGCAAC	GCAACAGGCG
101	TTCAATAATC	CGCCCATGGC	TCTTGCGGCG	CGTCCAAATC	TGCCGAAGGT
151	TCGTGCGGCG	CGGCTGGTTC	TAAAGCAGGC	GAAGGCAAAAT	GCGGCGAGGG
201	CAAATGCGGT	GCGACCGTAA	AAAAAACCCA	CAACACACC	AAAGCATCTA
251	AAGCCAAGGC	CAAATCTGCC	GAAGGCAAAAT	GCGGCGAAGG	CAAATGCGGT
301	TCTAAATAA				

This corresponds to the amino acid sequence <SEQ ID 2902; ORF 950.a>:

```
a950.pep
1  MNKNIAAALA GALSLSLAAG AVAANKPASN ATGVHKS AHG SCGASKSAEG
51  SCGAAGSKAG EGKCGEGKCG ATVKKTHKHT KASKAKAKSA EGKCGEGKCG
101 SK*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 950 shows 100.0% identity over a 102 aa overlap with a predicted ORF (ORF 950) from *N. meningitidis*

a950/m950 100.0% identity in 102 aa overlap

```

          10      20      30      40      50      60
a950.pep  MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHKS AHG SCGASKSAEGSCGAAGSKAG
          |||||
m950      MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHKS AHG SCGASKSAEGSCGAAGSKAG
          10      20      30      40      50      60

          70      80      90      100
a950.pep  EGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSKX
          |||||
m950      EGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSK
          70      80      90      100
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2903>:

```
g951.seq
1  ATGATTATGT TACCCGCCCG TTCACTATT TTATCTGTCC TCGCAGCAGC
51  CCTGCTTGCC GGACAGGCGT ATGCTGCCGG CGCGGCGGAT GTGGAGCTGC
101  CGAAGGAACT CGGAAGGTT TTAAGGAAAC ATCGGCGTTA CAGCGAGGAA
151  GAAATCAAAA ACGAACGCGC ACGGCTTGCG GCAGTGGGCG AACGGGTCAA
201  CAGGGTGTTC ACGCTGTTGG GCGGTGAAAC GGCTTTGCAG AAAGGCGCAG
251  CGGGAACGGC TCTGGCAACC TATATGCTGA TGTGGAACG CACAAATCC
301  CCCGAAGTCG CCGAACGCGC CTTGGAATG GCCGTGTCGC TGAACGCGTT
351  TGAACAGGCG GAAATGATT ATCAGAAATG CCGGCAGATC GAGCCTATAC
401  CGGGTGAGGC GCAAAAACGG CGGGGTGGC TCGGGAACGT ATTGAGGGAA
451  GGGGSAATC AGCATCTGGA CGGGTTGGAA GAGGTGCTGG CGCAATCGGA
501  CGATSTGCAA AAACGCAGGA TATTTTGCT GCTGGTGCAA GCCGCCGTGC
551  AGCAGGGTGG GGTGGCTCAA AAAGCATCGA AAGCGGTTGC CCGTGGGCGC
601  TTGAAGTATG AACATCTGCC CGAAGCGGCG GTTGCCGATG CCGTGTTCGG
651  CGTACAGGCA CCGGAAAGG AAAAGGCAAT CGAAGCTTTG CAGCGTTTGG
701  CGAAGCTCGA TACGGAAATA TTGCCCCCA CTTAATGAC GTTGCGTCTG
751  ACTGCACGCA AATATCCCGA AATACTCGAC GGCTTTTTCG AGCAGACAGA
801  CACCCAAAAC CTTTCGGCCG TCTGGCAGGA AATGGAAAT ATGAATCTGG
851  TTTCCTGCG TAAGCCGAT GATGCCTATG CGCGTTGAA CGTGTGTTG
901  GAACACAACC CGAATGCAA CCTGTATATT CAGGCGCGCA TATTGCGGCG
951  AAACCGAAAA GAAGTGCCT CCGTTATCGA CGGCTACGCC GAAAAGGCAT
1001  ACGGCGGGG GACGGGGGAA CAGCGGGGCA GGGCGGCAAT GACGGCGGCG
1051  ATGATATATG CCGACCGCAG GGATTACGCC AAAGTCAGGC AGTGGTTGAA
1101  AAAAGTGTC GCGCCGGAAT ACCTGTTCGA CAAAGGCGTG CTGGCGGCTG
1151  CGGCGGCTGC CGAATTGGAC GGAGGCCGGG CGGCTTTGCG GCAGATCGGC
1201  AGGGTGCAGA AACTTCCCGA ACAGCAGGGG CCGTATTTTA CGGCAGACAA
1251  TTGTCCAAA ATACAGATGC TCGCCCTGTC GAAGTGCCCC GACAAACGGG
1301  AAGCCCTGAT CCGGCTGAAC AACATCATCG CCAAACTTTC GGCGGCGGGA
1351  AGCAGCGAAC CTTTGGCGGA AGCATTGGCA CAGCGTTCCA TTATTACGA
1401  ACAGTTCCGC AAACGGGGAA AATGATTGCG CAGCTTGAA ACCGCGCTCA
1451  AACCTACGCC CGATAATGCA CAAATTATGA ATAATCTGGG CTACAGCCTG
1501  CTTTCGATT CCAAACGTTT GGACGAGGGT TTCGCCCTGC TTCACACGGC
1551  ATACCAATC AACCCGAGC ATACCGCCGT TAACGACAGC ATAGGCTGGG
1601  CGTATTACCT GAAAGGCGAC GCGGAAAGCG CGCTGCCGTA TCTGCGGTAT
1651  TCGTTTGAAA ACGACCCCGA GCCCGAAGTT GCCGCCCAT TGGGCGAAGT
1701  GTTGTGGGCA TTGGGCGAAC CCGATCAGGC GGTGACGTA TGGACGAGG
1751  CGGCACACCT TAGGGGAGAC AAGAAAATAT GCGGGGAGAC GCTCAACGC
1801  TACGGAATCG CCTTGCCCGA GCCTTCCCGA AAACCCCGGA AATAA
```

This corresponds to the amino acid sequence <SEQ ID 2904; ORF 951.ng>:

```
g951.pep
1  MINLPAREFT LSVLAAALLA GQAYAGAAD VELPKEVGKV LRKHRRYSEE
```

```

51 EIKNERARLA AVGERVNRVF TLLGGETALQ KGQAGTALAT YNMLLERTKS
101 PEVAERALEM AVSLNAFEQA EMYQKWRQI EPIPGEAQKR AGWLRNVLRE
151 GGNCHLDGLE EVLAQSDDVQ KRRIFLLLVQ AAVQGGVAVQ KASKAVRRRA
201 LKYEHLPEAA VADAVFGVQG REKEKAIEAL QRLAKLDTEI LPPTLMTLRL
251 TARKYPEILD GFFEQDTQON LSAVWQEMEI MNLVSLRKP DAYARLNVLII
301 EHNPNANLYI QAAILAANRK EGASVIDGYA EKAYGRGTGF QRGRAAMTAA
351 MIYADRRDYA KVRQWLKVS APEYLFDKGV LAAAAAELD GGRAALROIG
401 RVRKLPEQQG RYFTADNLSK IOMLALSCLK DKREALIGLN NIIAKLSAAG
451 STEPLAEALA QRSIIYEQFG KRGKMIADLE TALKLTPDNA QIMNNLGYSL
501 LSDSKRLDEG FALLQYAYQI NPDDTAVNDS IGWAYYLGKD AESALPYLRY
551 SFENDPEPEV AAHLGEVLWA LGERDQAVDV WTQAAHLRGD KKIWRETLKR
601 YGIALPEPSR KPRK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2905>:

```

m951.seq
1 ATGATTATGT TACCTAACCG TTTCAAAATG ITAACTGTGT TGACGGCAAC
51 CTTGATTGCC GGACAGGTAT CTGCCGCCGG AGCGGGTGGC GGGGATATGA
101 AACAGCCGAA GGAAGTCGGA AAGGTTTCA GAAAGCAGCA GCGTTACAGC
151 GAGGAAGAAA TCAAAAACGA ACGCGCACGG CTTCGCCGAG TGGCGCAGCG
201 GGTTAATCAG ATATTTACGT TGCTGGGAGG GGAACCGGCC TTGCAAAAGG
251 GGCAGGCGGG AACGGCTCTG GCAACCTATA TGCTGATGTT GGAACGCACA
301 AAATCCCCCG AAGTCGCCGA ACGCGCCTTG GAAATGGCCG TGTCGCTGAA
351 CGCGTTTGA CAGGCGGAAA TGATTATCA GAAATGGCCG CAGATTGAGC
401 CTATACCGGG TAAGGCGCAA AAACGGGCGG GGTGGCTGCG GAACGTGCTG
451 AGGGAAGACG GAAATCAGCA TCTGGACGGA CTGGAAGAAG TGCTGGCTCA
501 GCGGACCGAA GGACAGAACC GCAGGGTGT TTTATTGTTG GCACAAGCCG
551 CCGTGCAACA GGACGGGTTG GCGCAAAAG CATCGAAAGC GGTTCGCCGC
601 GCGGCGTTGA AATATGAACA TCTGCCGAAA GCGCGGTTG CCGATGTGGT
651 GTTCAGCGTA CAGGACGCG AAAAGGAAAA GGCAATCGGA GCTTTGCAGC
701 GTTTGGCGAA GCTCGATACG GAAATATTGC CCCCCACTTT AATGACGTTG
751 CGTCTGACTG CACGCAATA TCCGAAATA CTCGACGGCT TTTTCGAGCA
801 GACAGACACC CAAAACCTTT CGGCCGTCTG GCAGGAAATG GAAATTATGA
851 ATCTGGTTTC CCTGCACAGG CTGGATGATG CCTATGCGCG TTTGAACGTG
901 CTGTGGAAAC GCAATCCGAA TGACAGCTGT TATATTGAG CAGCGATATT
951 GCGGCAAAAC CGAAAAGAAG GTGCTTCCGT TATCGACGGC TAGCCGGA
1001 AGGCATACGG CAGGGGACG GAGGAACAGC GGAGCAGGGC GGCCTAACG
1051 GCGGCGATGA TGTATGCCGA CCGCAGGGAT TACGCCAAAG TCAGGCAGTG
1101 GCTGAAAAAA GTATCCGCGC CGGAATACCT GTTCGACAAA GGTGTGCTGG
1151 CGCTGCGCGG GGCTGTCGAG TTGGACGGCG GCAGGGCGCG TTTGCGCGAG
1201 ATCGGCAGGG TCGGAAACT TCCGAACAG CAGGGCGGCT ATTTACGGC
1251 AGACAATTTG TCCAAAATAC AGATGCTCGC CCTGTCGAAG CTGCCGATA
1301 AATCGGAGGC TTTGAGGGG TTGGACAAGA TTATCGAAAA ACCGCTGCC
1351 GGCAGTAATA CAGAGTTACA GGCAGAGGCA TTGGTACAGC GGTGAGTTGT
1401 TTACGATCGG CTTCGCAAGC GGAATAAAT GATTTCAGAT CTGAAAGGG
1451 CGTTACAGGT TGCACCGGAT AACGCTCAGA TTATGAATAA TCTGGGCTAC
1501 AGCCTGCTGA CCGATTCCAA ACGTTTGGAC GAAGGTTTCG CCCTGCTTCA
1551 GACGGCATAC CAATCAACC CGGACGATAC CGCTGTCAAC GACAGCATAG
1601 GCTGGGCGTA TTACCTGAAA GCGGACGCGG AAAGCGGCT GCGGTATCTG
1651 CCGTATTCTG TTGAAAACGA CCCCAGCCCC GAAGTTGCCG CCCATTGGG
1701 CGAAGTGTG TGGGCATTGG GCGAACGCGA TCAGGCGGTT GACGTATGGA
1751 GCGAGGCGGC ACACCTTACG GGAGACAAGA AATATGGCG GGAACGCTC
1801 AAACGTCACG GCATCGCATT GCCCCAACCT TCCGAAAC CTCGGAATA
1851 A

```

This corresponds to the amino acid sequence <SEQ ID 2906; ORF 791>:

```

m951.pep
1 MIMLPNRFKM LTVLTATLIA GOVSAAGGGA GDMKQKEVG KVERKQORYS
51 EEEIKNERAR LAAVGERVNO IFTLLGGETA LQKQAGTAL ATYMLMLERT
101 KSEVAERAL EMAVSLNAFE OAEMIIYOKWR QIEPIPKAQ KRAGWLRNVL
151 RERNQHLDG LEEVLAQADE GQNRVFLLL AQAAVQDGL AQKASKAVRR
201 AALKYELPE AAVADVVSFV QGREKEKAIG ALQRLAKLDT EILPPTLMTL
251 LRTARKYPEI LDGFFEQTDT QNLSAVWQEM EIMNLVSLHR LDDAYARLNV
301 LLERNPNADL YIQAAAILAN RKEGASVIDG YAEKAYGRGT EEQSRRAALT
351 AAMMYADRRD YAKVRQWLKK VSAPEYLFDK GVLA AAAAVE LDGGRALRQ
401 IGRVRKLPEQ QGRYFTADNL SKIQMLALSK LPDKREALRG LDKIIEKPPA
451 GSNTLQAEA LVQSRVVYDR LGKRKKMISD LERAFRLAPD NAQIMNNLGY
501 SLLTCSKRLD EGFALLQYAY QINPDDTAVN DSIWAYYLLK GDAESALPYL
551 RYSFENDPEP EVAHLGEVL WALGEREQAV DVWTQAAHLT GDKKIWRETL
601 KRHGIALPQP SRKPRK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 951 shows 88.6% identity over a 616 aa overlap with a predicted ORF (ORF 951) from *N. gonorrhoeae*

m951/g951 88.6% identity in 616 aa overlap

m951.pep	10	20	30	40	50	60
	MIMLPNRFKMLTVLTATLIAGQVSAAGGGAGDMKQPKVEGKVFRRKQQRYSSEEEIKNERAR					
g951	10	20	30	40	50	
	MIMLPAREFTILSVLAAALLAGQAYAA--GAADVLPKEVGKVLRRKHRRYSSEEEIKNERAR					
m951.pep	70	80	90	100	110	120
	LAAVGERVNIQIFTLGGETALQKGQAGTALATYMLMLERTKSPVAERALEMAVSLNAFE					
g951	60	70	80	90	100	110
	LAAVGERVNRVFTLLGGETALQKGQAGTALATYMLMLERTKSPVAERALEMAVSLNAFE					
m951.pep	130	140	150	160	170	180
	QAEMIYQKWRQIEPIPGKAQKRAGWLRNVLREGNQHLQGLLEEVLAQADEGQNRVFLLL					
g951	120	130	140	150	160	170
	QAEMIYQKWRQIEPIPGKAQKRAGWLRNVLREGNQHLQGLLEEVLAQSDVQKRRIFLL					
m951.pep	190	200	210	220	230	240
	AQAAVQDGLAQKASKAVRRAALKYEHLPAAVADVVFVQGREKEKAIGALQRLAKLDT					
g951	180	190	200	210	220	230
	VQAAVQCGVAQKASKAVRRAALKYEHLPAAVADVVFVQGREKEKAIGALQRLAKLDT					
m951.pep	250	260	270	280	290	300
	EILPPTLMTLRLTARKYPEILDGFFEQTDTQNLQSAVWQEMEIMNLVSLHRLDDAYARLNV					
g951	240	250	260	270	280	290
	EILPPTLMTLRLTARKYPEILDGFFEQTDTQNLQSAVWQEMEIMNLVSLRKPDDAYARLNV					
m951.pep	310	320	330	340	350	360
	LLERNPNADLYIQAAAILAANRKEGASVIDGYAEKAYGRGTGEQSRRAALTAAMMYADRRD					
g951	300	310	320	330	340	350
	LLERNPNANLYIQAAAILAANRKEGASVIDGYAEKAYGRGTGEQSRRAALTAAMMYADRRD					
m951.pep	370	380	390	400	410	420
	YAKVRQWLKKVSAPEYLFDKGVLAATAAELDGGRAALRQIGRVRKLPEQGRYFTADNL					
g951	360	370	380	390	400	410
	YAKVRQWLKKVSAPEYLFDKGVLAATAAELDGGRAALRQIGRVRKLPEQGRYFTADNL					
m951.pep	430	440	450	460	470	480
	SKIOMLALSKLPDKREALRGLDKIIEKPFAGSNTLQAEALVQSRVYDRLGKRKKMISD					
g951	420	430	440	450	460	470
	SKIOMLALSKLPDKREALRGLNNIAXLSAAGSTEPLAALQRSIIYEQFCKRGKMIAD					
m951.pep	490	500	510	520	530	540
	LERAFRLAPDNAQIMNNLGYSLTDSKRLDEGFALLQTAYQINPDDTAVNESIGWAYYLK					
g951	480	490	500	510	520	530
	LETALKLTPDNAQIMNNLGYSLTDSKRLDEGFALLQTAYQINPDDTAVNDSIGWAYYLK					
m951.pep	550	560	570	580	590	600
	GDAESALPYLRYSFENDPEPEVAHLGEVLWALGERDQAVDVNTQAHLTGDKKIWRRTL					
g951	540	550	560	570	580	590
	GDAESALPYLRYSFENDPEPEVAHLGEVLWALGERDQAVDVNTQAHLRGDKKIWRRTL					
m951.pep	610					
	KRHGIALPQPSRKPRK					
g951	600	610				
	KRYGIALPEPSRKPRKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2907>:

```
a951.seq
1  ATGTTACCCG CCCGTTTCAC CATTTTATCT GTGCTCGCGG CAGCCCTGCT
51  TGCCGGGCAG GCGTATGCCG CCGGCGCGGC GGATGCGAAG CCGCCGAAGG
101 AAGTCGGAAG GGTTCACAGA AAGCAGCAGC GTTACAGCGA GGAAGAAATC
151 AAAAACGAAC CGCACGCGCT TCGGCGAGTG GCGGAGCGGG TTAATCAGAT
201 ATTTACGTTG CTGGGAGGGG AAACCGCCTT GCAAAGGGG CAGGCGGGAA
251 CGGCTCTGGC AACCTATATG CTGATCTTGG AACGCACAAA ATCCCCCGAA
301 GTCGCCGAAC GCGCCTTGGA AATGGCCGTG TCGCTGAACG CGTTTGAACA
351 GCGCGAAATG ATTTATCAGA AATGGCGGCA GATTGAGCCT ATACCGGGTA
401 AGGCGCAAAA ACGGGCGGGG TGGCTGCGGA ACGTGTCTAG GGAAGAGGA
451 AATCAGCATC TAGACGGACT GGAAGAAGTG CTGGCTCAGG CGGACGAAGG
501 ACAGAACCGC AGGGTGTITT TATTGTTGGC ACAAGCCGCC GTGCAACAGG
551 ACGGGTTGGC GCAAAAAGCA TCGAAAGCGG TTCGCCGCGC GCGGTTGAGA
601 TATGAACATC TGCCCCGAAG GCGCGTTGCC GATGTGGTGT TCAGCGTACA
651 GGGACGCGAA AAGGAAAAGG CAATCGGAGC TTTGCAGCGT TTGGCGAAGC
701 TCGATACGGA AATATTGCCC CCCACTTTAA TGACGTTGCG TCTGACTGCA
751 CGCAAAATAT CCGAAATACT CGACGCTTTT TTCGAGCAGA CAGACACCCA
801 AAACCTTTCC GCCGCTCTGC AGGAAATGGA AATTATGAAT CTGGTTTCCC
851 TGCACAGGCT GGATGATGCC TATGCCGCTT TGAACGTGCT GTTGGAACGC
901 AATCCGAATG CAGACCTGTA TATTAGGCA GCGATATTGG CGGCAAACCG
951 AAAAGAAGGT GCTTCCGTTA TCGACGCTA CGCCGAAAG GCATACGGCA
1001 GGGGACGGG GGAACAGCGG GGCAGGCGCG CAATGACGCG GCGGATGATA
1051 TATGCCGACC GAAGGGATTA CACCAAAGTC AGGCAGTGGT TGAAAAAAGT
1101 GTCCGCGCCG GAATACCTGT TCGACAAAGG TGTGCTGGCG GCTGCGCGCG
1151 CTGTGAGATT GGACGCGCGC AGGGCGGCTT TGCGGCAGAT CGGCAGGGTG
1201 CGGAAACTTC CGAACAGCA GGGCGGCTAT TTTACGGCAG ACAATTGTTC
1251 CAAATACAG ATGTTCCGCC TGTGCAAGCT CCCCACAAA CGGGAGGCTT
1301 TGAGGGGTTT GGACAAGATT ATCGAAAAC CGCCTCCCGC CAGTAATACA
1351 GAGTTACAGG CAGAGGCATT GGTACAGCGG TCAGTTGTTT ACGATCGGCT
1401 TGGCAAGCGG AAAAAATGA TTTAGATCT TGAAAGGGCG TTCAGGCTTG
1451 CACCCGATAA CGCTCAGATT ATGAATAATC TGGGTACAG CCTGCTTTCC
1501 GATTCCAAAC GTTTCACGA AGGCTTCGCC CTGCTTCAGA CGGCATACCA
1551 AATCAACCCG GACGATACCG CTGTCAACGA CAGCATAGGC TGGGCGTATT
1601 ACCTGAAAGG CGACGCGGAA AGCGCGCTGC CGTATCTGCG GTATTCTGTT
1651 GAAACGACC CCGAGCCCGA AGTTGCCGCC CATTGGGCGG AAGTGTGTG
1701 GGCATTGGGG GAACGCGATC AGGCGGTGTA CGTATGGCA CAGGCGGCAC
1751 ACCTTACGGG AGACAAGAAA ATATGGCGGG AACGCTCAA ACGTCACGGC
1801 ATCGCATTCG CCCAACCTTC CCGAAACCT CGGAAATAA
```

This corresponds to the amino acid sequence <SEQ ID 2908; ORF 951.a>:

```
a951.pep
1  MLPARFTILS VLAAALLAQO AYAAGAADAK FPKEVGKVF R KQORYSEEEI
51  KNERARLAAR GERNQIFTL LGGETALQKG CAGTALATYM LMLERTKSPE
101 VAERALEMAV SLNAFEQAEI IYQKWRQIEP IPGKAQKRAG WLRNVLRERG
151 NQHLGLEEV LAQADEGQNR RVFLLLAQAA VQDGLAQKA SKAVRRRAALR
201 YEHLEPAAVA DVVFSVQGRE KEKAIGALQR LAKLDTEILP PTLMTLRLLTA
251 RKYPEILDGF FEQTDTONLS AVWQEMEIMN LVSLHRLDDA YARLNVLLER
301 NPNADLIYQA AILAA NRKEG ASVIDGYAEK AYGRGTGEQR GRAAMTAAMI
351 YADRRDYTKV RQWLKVSAP EYLFDKCVLA AAAAVELDGG RAALRQIGRV
401 RKLPEQQQRY FTADNLSKIQ MFALSKLPDK REALRGLDKI IEKPPAGSNT
451 ELQAEALVQR SVVYDRLGKR KKMISDLERA FRLAPDNAQI MNNLGYSLLS
501 DSKRLDEGFA LLQYAYQINP DDTAVNDSIG WAYYLGDAE SALPYLRYSF
551 ENDEPEVEAA HLGVLWALG ERDQAVDVWT QAAHLTGDKK IWRETLKRHK
600 IALPQPSRKP RK*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 951 shows 96.4% identity over a 614 aa overlap with a predicted ORF (ORF 951) from *N. meningitidis*

a951/m951 96.4% identity in 614 aa overlap

```

          10      20      30      40      50
a951.pep  MLPARFTILSVLAAALLAQAYAAAG--AAAKPPKEVGKVFRRKQORYSEEEIKNERAR
          ||| || :||:|:|:|:| ||| | :| | ||||| ||||| |||||
m951      MIMLPNRFKMLTTLTATLIAGQVSAAGGAGDNKQPKVEGKVFRRKQORYSEEEIKNERAR
          10      20      30      40      50      60

          60      70      80      90     100     110
a951.pep  LAAGGERVNQIFTLGGETALQKGQAGTALATYMLMLERTKSPEVAERALEMAVSLNAFE
```

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```

|||||
m951  LAAVGERVNIQIFTLGGETALQKGQAGTALATYMLMLERTKSPEVAERALEMAVSLNAFF
      70      80      90      100     110     120

      120     130     140     150     160     170
a951.pep OAEMIYQKWROIPIPGKACKRAGWLRNVI.RERGNQHLDGLEEVLAQADEGQNRVFLLL
|||||
m951  QAEMIYQKWROIPIPGKACKRAGWLRNVI.RERGNQHLDGLEEVLAQADEGQNRVFLLL
      130     140     150     160     170     180

      180     190     200     210     220     230
a951.pep AQAAVQODGLAQKASKAVRRAALRYEHLPEAAVADVVSQGREKEKAI GALQRLAKLDT
|||||
m951  AQAAVQODGLAQKASKAVRRAALRYEHLPEAAVADVVSQGREKEKAI GALQRLAKLDT
      190     200     210     220     230     240

      240     250     260     270     280     290
a951.pep EILPPTLMTLRLTARKYPEILDGFFEQTDTQNLSAVWQEMEIMNLVSLHRLDDAYARLNV
|||||
m951  EILPPTLMTLRLTARKYPEILDGFFEQTDTQNLSAVWQEMEIMNLVSLHRLDDAYARLNV
      250     260     270     280     290     300

      300     310     320     330     340     350
a951.pep LLERNPNADLYIQAAAILAANRKEGASVIDGYAEKAYGRGTGEQGRAAMTAAMIYADRRD
|||||
m951  LLERNPNADLYIQAAAILAANRKEGASVIDGYAEKAYGRGTGEQGRAAMTAAMIYADRRD
      310     320     330     340     350     360

      360     370     380     390     400     410
a951.pep YTKVRQWLKKVSAPEYLFDKGVLA AAAA VELDGGRAALRQIGRVKRLPEQCGRYFTADNL
|||||
m951  YAKVRQWLKKVSAPEYLFDKGVLA AAAA VELDGGRAALRQIGRVKRLPEQCGRYFTADNL
      370     380     390     400     410     420

      420     430     440     450     460     470
a951.pep SKIQMFALSKLPDKREALRGLDKII EKPPAGSNTLQAEALVQRSVVYDRLGKRKKMISD
|||||
m951  SKIQMLALSKLPDKREALRGLDKII EKPPAGSNTLQAEALVQRSVVYDRLGKRKKMISD
      430     440     450     460     470     480

      480     490     500     510     520     530
a951.pep LERAFRLAEDNAQIMNNLGYSLLSDSKRLDEGFALLQTAYQINPDDTAVNDSIGWAYYLYK
|||||
m951  LERAFRLAEDNAQIMNNLGYSLLSDSKRLDEGFALLQTAYQINPDDTAVNDSIGWAYYLYK
      490     500     510     520     530     540

      540     550     560     570     580     590
a951.pep GDAESALPYLRYSFENDPEPEVA AHLGEVLWALGERDQAVDVWTQAAHLTGDKKIWRETL
|||||
m951  GDAESALPYLRYSFENDPEPEVA AHLGEVLWALGERDQAVDVWTQAAHLTGDKKIWRETL
      550     560     570     580     590     600

      600     610
a951.pep KRHGIALPQPSRKPRK
|||||
m951  KRHGIALPQPSRKPRK
      610

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2909>:

```

g952.seq (partial)
1  ..TTGCTTTATC GTTTGAATGC TGCACCGATG TTAAACGATA ATCCTGTTGT
51  TTACGGAAAA ATCAAATTGC AGAGTTGGAA AGCGCGGCGG GATTTCAATA
101 TTGTAAAGCA GGATTGGAT TTTCCTGCG GGGCGGCTTC GGTGGCGACG
151 CTTTTGAACA ATTTTACGG GCAAAAGCTG ACGGAAGAAG AACTGTTGGA
201 AAAACTGGGT AAGGAACAGA TCGCGCGGTC GTTTGAGGAT ATGCGGCGCA
251 TTATGCCCGA TTTGGGTTT GAGGCGAAAG GCTATGCCCT GTCTTTCGAA
301 CAGCTCGCGC AGTTGAAAAT CCCCCTCATC GTGTATCTGA AATACCGCAA
351 AGACGACCAT TTTCGGTAT TCGCGGAGT GGATGGCAAT ACGGTTTIGC
401 TTGCCGACCC GTCGCCGGT CATGTTTCGA TGAGCAGGGC GCASTTTTTC
451 GAGGCTTGCC AAACCGTGA GGGAAATTG GCAGGCAAAA TTTTGGCGST
501 CGTGCCGAAA AAAGCGGAGG CGATTTCAAA TAAATTGTTT TTCACACATC
551 ATCCCAAGCG GCAGACGGAG TTTCAGTCG GACAGGTAAA ATGGTGGCGT

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601 GCTTATTGA

This corresponds to the amino acid sequence <SEQ ID 2910; ORF 952.ng>:

g952.pep (partial)
 1 ..LSYRLNAAPM FNDNPVVYGR IKLQSWKARR DFNIVKQDLD FSCGAASVAT
 51 LLNNFYGQKL TEEEVLEKLG KEQMRASFED MRRIMPDLGF EAKGYALSFE
 101 QLAQLKIPVI VYLKVRKDDH FSVLRGVDGN TVLLADPSPG HVSMSRAQFL
 151 EAWQTREGNL AGKILAVVPR KAEAISNKL FTHHPKRQTE FAVGQVKWWR
 201 AY*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2911>:

m952.seq
 1 ATGATGAAGT TCAAATATGT TTTTCTGTTG GCGTGTGTTG TCGTTTCTTT
 51 ATCTTATCGT TTGAATGCTG CACCGATGTT TAACGATAAT CCTGTTGTTT
 101 ACGGAAAAAT CAAAGTGCAG AGTTGGAAG CGCGGCGGGA TTTCAATATT
 151 GTAAAGCAGG ATTTGGATT TTTCTGTGGG GCGGCTTCGG TGCGCAGCT
 201 TTGAACAAT TTTTACGGGC AAACGCTGAC GGAAGAAGAA GTGTTGAAAA
 251 AGCTGGATAA GGAGCAGATG CGCGCTCGT TTGAGGATAT GCGGCGCAT
 301 ATGCTGATT TGGGTTTGA GCGGAAGGCG TATGCCCTGT CTTTCGAGCA
 351 GCTCGCGCAG TTGAAAATCC CCGTCATCGT GTATCTGAAA TACCGCAAAG
 401 ACGACCATTT TTCGGTATTG CGCGGTATAG ACGGCAATAC GGTTTTCGCT
 451 GCCGACCCGT CGCTGGGGCA TGTTTCAATG AGCAGGGCGC AGTTTTTGA
 501 TGCTTGGCAA ACCCGTGAGG GAAATTTGGC AGGTAAGATT TTGGCTGTCA
 551 TACCGAAAAA AGCCGAGACA ATTTCAAATA AATTGTTTTT CACACAACAC
 601 CCAAAACGCG AGACGGAGTT TACAGTCGGA CAAATCAGGC AAGCACGTGC
 651 AGAGTAA

This corresponds to the amino acid sequence <SEQ ID 2912; ORF 952>:

m952.pep
 1 MMKFYVFL ACVVVLSYR LNAAPMFNDN PVVYGKIKVQ SWKARRDFNI
 51 VKQDLDFSCG AASVATLLNN FYGQTLTEE VLKLDKEQM RASFEDMRR
 101 MPDLGFEAKG YALSFEQLAQ LKIPVIVYLK YRKDDHFSVL RGIDGNTVLL
 151 ADPSLGHVSM SRAQFLDAWQ TREGNLAGKI LAVIPKKAET ISNKLFFTQH
 201 PKRQTEFTVG QIRQARAE*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 952 shows 92.5% identity over a 201 aa overlap with a predicted ORF (ORF 952) from *N. gonorrhoeae*

g952/m952; 92.5% identity in 201 aa overlap

		10	20	30	40
g952.pep		LSYRLNAAPMFNDNPVVYGR IKLQSWKARRDFNIVKQDLD FSCG			
m952	MMKFYVFLACVVVLSYRLNAAPMFNDNPVVYGR IKVQSWKARRDFNIVKQDLD FSCG				
	10 20 30 40 50 60				
	50 60 70 80 90 100				
g952.pep	AASVATLLNNFYGQKL TEEEVLEKLG KEQMRASFEDMRRIMPDLGF EAKGYALSFEQLAQ				
m952	AASVATLLNNFYGQTL TEEEVLEKLD KEQMRASFEDMRRIMPDLGF EAKGYALSFEQLAQ				
	70 80 90 100 110 120				
	110 120 130 140 150 160				
g952.pep	LKIPVIVYLKVRKDDHFSVLRGVDGNTVLLADPSPGHVSMSRAQFL EAWQTREGNLAGKI				
m952	LKIPVIVYLKVRKDDHFSVLRGIDGNTVLLADPSLGHVSMSRAQFLDAWOTREGNLAGKI				
	130 140 150 160 170 180				
	170 180 190 200				
g952.pep	LAVVPKKA E AISNKLFFTHHPKRQTEFAVGQVKWWRAYX				
m952	LAVIPKKAETISNKLFFTHHPKRQTEFTVGQIRQARAE				
	190 200 210				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2913>:

a952.seq
 1 ATGATGAAGT TCAAATATGT TTTTCTGTTG GCGTGTGTTG TCGTTTCTTT

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```

51 ATCTTATCGT TTGAATGCTG CACCGATGTT TAACGATAAT CCTGTTGTTT
101 ACGGAAAAAT CAAAGTGCAG AGTTGGAAG AAAGGCGGGA TTTCATATT
151 GTAAAGCAGG ATTTGGATT TTCCTGCGG GCGGCTTCGG TGGCGACGCT
201 TTTGAACAAT TTTTACGGG AAACGCTGAC GGAAGAAGAA GTGTTGAAA
251 AGCTGGATAA GGAGCAGATG CGCGCTCGT TTGAGGATAT GCGGCGCATT
301 ATGCCAGATT TGGGTTTGA AGCGAAAGG CATGCCCTGT CTTTCGAGCA
351 GCTCGCACAG TTGAAAATCC CCGTCATCGT GTATCTGAAA TACCGCAAGG
401 ATGATCATTT CTCGGTATTG CGCGGGATAG ACGGCAATAC GGTTTTGCTT
451 GCCGACCCGT CGCTGGGTCA TGTTTCAATG AGCAGGGCGC AGTTTNGGA
501 TGCTTGGCAA ACCCGTGAGG GAAATTTGGC AGGTAAGATT TTGGCGGTCG
551 TGCCGAAAAA AGCCGAGACA ATTTCAAATA AATTGTTTTT CACACATCAT
601 CCCPAGCGGC AGACGGAGTT TGCAGTCGGA CAAATCAGGC AAGCACGTGC
651 AGAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2914; ORF 952.a>:

```

a952.pep
1  MMKFKYVLL ACVVVLSYR LNAAPMFNDN PVVYGKIKVQ SWKERRDFNI
51 VKQDLDFSCG AASVATLLNN FYGQTLTEEE VLKKLDKEQM RASFEDMRRI
101 MPDLGFEEKG YALSFEQLAQ LKIPVIVYLK YRKDDHFSVL RGIDGNTVLL
151 ADPSLGHVSM SRAQFXDAWQ TREGNLAGKI LAVVPKKAET ISNKLFFTHH
201 PKRQTEFAVG QIRQARAE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 952 shows 97.7% identity over a 218 aa overlap with a predicted ORF (ORF 952) from *N. meningitidis*

```

a952/m952 97.7% identity in 218 aa overlap

a952.pep      10      20      30      40      50      60
MMKFKYVLLACVVVLSYRLNAAPMFNDNPNVVYGKIKVQSWKERRDFNIVKQDLDFSCG
|||||
m952          10      20      30      40      50      60
MMKFKYVLLACVVVLSYRLNAAPMFNDNPNVVYGKIKVQSWKARRDFNIVKQDLDFSCG
|||||

a952.pep      70      80      90      100     110     120
AASVATLLNNFYGQTLTEEEVLKKLDKEQMRASFEDMRRI MPDLGFEEKGYALSFEQLAQ
|||||
m952          70      80      90      100     110     120
AASVATLLNNFYGQTLTEEEVLKKLDKEQMRASFEDMRRI MPDLGFEEKGYALSFEQLAQ
|||||

a952.pep      130     140     150     160     170     180
LKIPVIVYLK YRKDDHFSVL RGIDGNTVLLADPSLGHVSM SRAQFXDAWQ TREGNLAGKI
|||||
m952          130     140     150     160     170     180
LKIPVIVYLK YRKDDHFSVL RGIDGNTVLLADPSLGHVSM SRAQFLDAWQ TREGNLAGKI
|||||

a952.pep      190     200     210     219
LAVVPKKAETISNKLFFTHHPKRQTEFAVGQIRQARAE
|||:|||||
m952          190     200     210
LAVIPKKAETISNKLFFTHHPKRQTEFTVQIRQARAE
|||||

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2915>:

```

g953.seq
1  ATGAAAAAAA TCATCTTCGC CGCGCTCGCA GCGGCAGCCG TCGGCACTGC
51 CTCCGCCACC TACAAAGTGG ACGAATATCA CGCCAACGTC CGTTTCGCCA
101 TCGACCACTT CAACACCAGC ACCAACGTCG GCGGTTTTTA CGGTCTGACC
151 GGTTCGGTCG AGTTCGATCA AGCAAAACGC GACGGCAAAA TCGACATCAC
201 CATTCCCGTC GCCAACCTGC AAAGCGGTTC GCAACCTTC ACCGGCCACC
251 TGAAATCCGC CGACATCTTC GATGCCGCTC AATATCCGGA CATCCGCTTC
301 GTTTCACCA AATTCAACTT CAACGGCAAA AAACCTGTTT CCGTTGACGG
351 CAACCTGACC ATGCGCGGCA AAACCGCCCC CGTCAAATC AAAGCCGAAA
401 AATTCAACTG CTACCAAGC CCGATGGCGG AAACCGAAGT TTGCGGCGGC
451 GACTTCAGCA CCACCATCGA CCGCACCAAA TGGGGCGTGG ACTACCTCGT
501 TAACGCCGGT ATGACCAAAA ACGTCCGCAT CGACATCCAA ATCGAAGCTG
551 CAAAACAATA A

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2917>:

This corresponds to the amino acid sequence <SEQ ID 2918; ORF 953>:

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 953 shows 93.0% identity over a 187 aa overlap with a predicted ORF (ORF 953) from *N. gonorrhoeae*

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 2919>:

a953.seq					
1	ATGAAAAAAA	TCATCATCGC	CGCGCTCGCA	GCAGCGCGCA	TCGGCACTGC
51	TCTCGCGCGC	ACCTACAAAG	TGGACGAATA	TCACGCCAAC	GCCCGTTTCT
101	CTATCGACCA	TTTCAACAC	AGCACAACG	TCGGCGGTTT	TTACGGTCTG
151	ACCGGTTCCG	TTGAGTTCGA	CCAAGCAAAA	CGCGACGGTA	AAATCGACAT
201	CACCATCCCC	GTTCGCAACC	TGCMAAGCGG	TTCGCAACAT	TTTACCGACC
251	ACCTGAATAT	AGCCGACATC	TTTCGATGCG	CCCAATATCC	GGACATCTCG
301	TTTGGTTTCCA	CCAAATTTCAA	CCTCAGACGG	AXAAAACTGG	TTTCCGTGGA

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351 CGGCAACCTG ACCATGCACG GCAAAACCGC CCCCCTCAAA CTCAAAGCCG
401 AAAAATTCAA CTGCTACCAA AGCCCCGATG TGAACACCGA AGTTTGCGGC
451 GCGGACTTCA GCACCACCAT CGACCGCACC AAATGGGCA TGGACTACCT
501 CGTTAACGTT GGTATGACCA AAAGCGTCCG CATCGACATC CAAATCGAGC
551 CAGCCAAACA ATAA

```

This corresponds to the amino acid sequence <SEQ ID 2920; ORF 953.a>:

```

a953.pep
  1 MKKIIIAALA AAAIGTASAA TYKVDEYHAN ARFSIDHENT STNVGGFYGL
  51 TGSVEFDQAK RDGKIDITIP VANLQSGSQH FTDHLKSADI FDAAQYPDIR
 101 FVSTKFNFG KKLVSVDGNL TMHGKTAPVK LKAEFNCYQ SPMLKTEVCG
 151 GDFSTTIDRT KWGMDYLVNV GMTKSVRIDT QIEAAKQ*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 953 shows 97.3% identity over a 187 aa overlap with a predicted ORF (ORF 953) from *N. meningitidis*

```

a953/m953    97.3% identity in 187 aa overlap

      10      20      30      40      50      60
a953.pep  MKKIIIAALAAAAIGTASAATYKVDEYHANARFSIDHENTSTNVGGFYGLTGSVEFDQAK
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m953      MKKIIIFAALAAAAISTASAATYKVDEYHANARFAIDHENTSTNVGGFYGLTGSVEFDQAK
          10      20      30      40      50      60

      70      80      90      100     110     120
a953.pep  RDGKIDITIPVANLQSGSQHFTDHLKSADIFDAAQYPDIRFVSTKFNFGKKLVSDGNL
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m953      RDGKIDITIPANLQSGSQHFTDHLKSADIFDAAQYPDIRFVSTKFNFGKKLVSDGNL
          70      80      90      100     110     120

      130     140     150     160     170     180
a953.pep  TMHGKTAPVKLKAEFNCYQSPMLKTEVCGGDFSTTIDRTKWGMDYLVNVGMTKSVRIDT
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m953      TMHGKTAPVKLKAEFNCYQSPMEKTEVCGGDFSTTIDRTKWGMDYLVNVGMTKSVRIDT
          130     140     150     160     170     180

a953.pep  QIEAAKQX
          |||||
m953      QIEAAKQX

```

g954.seq not found yet

g954.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2921>:

```

m954.seq
  1 ATGAAAAAGT TTTATTTTGT GCTGCTGCGG TTGGGTTTGG CAGCGTGTGG
  51 GCAAGAACAA TCGCAGAAAG CTGATGCGGA GCAGTATTTT TTGCCAATA
 101 AATATCAATT TGCAGATGAG AAACAGCCTT TTTATTTTGA ACGCGCCGCC
 151 CGTTTCCGTG TATTGCAACA AGGCCTTGGC GGGGATTTTG AGAGGTTTTT
 201 AAAAGGAGAA ATACCTAATC AAGAAAATCT TSCAAAGTAT CGTGAAAATA
 251 TTAICTAAGC AGTCGCTTAT TATGCGGACA CSAATGGAGA TGATGACCCA
 301 TACCGCGTCT GCAAACAGGC TGCACAAGAT GCAGAAATCC TGATGAAGAG
 351 TATGGTAACA AGCGGTGGAG GCGGTACAAC TGATTTAGAT AAGGAAAGTT
 401 ATCAAAATTA CCGAAAATCA ATGCAAGAAT GCGTAAAC AATAACGGAA
 451 GCTGAAGCCA ATTTGCCGAA AAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2922; ORF 954>:

```

m954.pep
  1 MKKFFVLLA LGLAACGQEQ SQKADAEQYF FANKYQFADE KQAFYFERAA
  51 RFRVLQQLG GDFERFLKE IPNQENLAKY RENITQAVAY YADTNGDDDP
 101 YRVCKQAAQD AEILMKSMVT SGGGGTTDLD KESYQNYRKS MQECRKTITE
 151 AEANLPKK*

```

a954.seq not found yet

a954.pep not found yet

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2923>:

```

g957.seq (partial)
1  ATGTTTAAAA AATTCAAACC GGTACTGTTG TCATTTTGTG CACTTGTATT
51  TGCCTTTTGG CTGGGAACAG GTATTGCCTA TGAGATTAAT CCGCGTTGGT
101 TTTTGAGCGA TACGGCAACT GAAGTACCTG AAAATCCGAA TGCTTTTGTG
151 GCGAAACTTG CCCGCCTGTT CCGAAATGCC GACAGGGCGG TTGTCATCGT
201 GAAGGAATCG ATGAGGACGG AGGAAAGCCT TGCCGGAGCT GTGGATGACG
251 GTCCGTTGCA GTCGGAGAAG GATTATCTCG CGCTCGCTAT CCGGCTCAGT
301 CGTTTGAAAG AAAAGGCGAA ATGGTTTCAC GTAACGGAGC AGGAACATGG
351 GGAAGAGGTT TGGCTGGATT ACTATATCGG CGAGGGCGGT TTGGTTGCGG
401 TTTCGCTTTC GCAACGCTCG CCGGAAGCGT TTGTTAATGC CGAATATCTG
451 TATCGGAACG ATCGTCCGTT TTCTGTAAT GTGTACGGCG GAACGGCTCA
501 CCGGGAAAAAT TATGAAACGA CAGGAGAATA TCGGGTTGTT TGGCAACCGG
551 ACGGTTCCGT ATTTGATGCG GCGGGGCGCG GGAATAATCG GGAAGATGTT
601 TATGAGCATT GCCTCGGGTG TTATCAGATG GCCCAGGTAT ATTTGGCGAA
651 ATACCGGGAT GTCGCGAATG ACGAGCAGAA GGTTTGGGAC TTCCGCGAAG
701 AGAGCAACCG GATTGCATCG GACTCGCGCG ATTATGTGTT TTATCAGAAT
751 ATGCGGGAAT TGATGCCCCG GGGGatgaaG gcgaacagtc ttgtggtcgg
801 ctatgatgcg gacggtCtgc CgcaAAAagt ctattggagt gtcgacaatg
851 gaaaaaaacc ccaaagtgtc gaattattt tgaaaaacgg aaatcttttt
901 attgccaat cttcgacggt aaccttgaaa acggatggcg taacggcgga
951 tatgcaaac tatcatgctc aacaaacgtt ctatttggat ggg...

```

This corresponds to the amino acid sequence <SEQ ID 2924; ORF 957.ng>:

```

g957.pep (partial)
1  MFKKFKPVLL SFFALVFAFW LGTGIAYEIN PRWFLSDTAT EVPENPNAFV
51  AKLARLFRNA DRAVVIVKES MRTEESLAGA VDDGPLOSEK DYLAALAIRLS
101 RLKEKAKWFH VTEQENGEEV WLDYYIGEGG LVAVSLSQRS PEAFFVNAEYL
151 YRNDRPFVSU VYGGTAHGEN YETTGEYRVV WQPDGVSFDA AGRGKIGEDV
201 YEHCLGCVQM AQVYLAKYRD VANDEQKVDW FREESNRIAS DSRDYVFYQN
251 MRELMPRGNK ANSLVVGYYDA DGLPKQVYWS VDNKKPKQSV EYYLKNGNLF
301 IAQSSTVTLK TDGVTADMOT YHAQOTLYLD G...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2925>:

```

m957.seq
1  ATGTTTAAAA AATTCAAACC GGTACTGTTG TCATTTTGTG CACTTGTATT
51  TGCCTTTTGG CTGGGAACGG GTATTGCCTA TGAGATTAAT CCGCGTTGGT
101 TTTTGAGCGA TACGGCAACT GAAGTACCTA AAAATCCGAA TGCTTTTGTG
151 GCGAAACTTG CCCGCCTGTT CCGAAATGCC GACAGGGCGG TTGTCATCGT
201 GAAGGAATCG ATAGGACGGG AGGAAAATCT TGCCGGAACG GTGGATGACG
251 GTCCSTTGCA GTCGGAGAAG GATTATCTCG CGCTCGCTAT CCGGCTCAGT
301 CGTTTGAAAG AAAAGGCGAA ATGGTTTCAC GTAACGGAGC AGGAACATGG
351 GAAAGAGGTT TGGCTGGATT ACCATATCGG CGAGGGCGGT TTGGTTGCGG
401 TTTCGCTTTC GCAACGCTCG CCGGAAGCAT TTGTTAATGC CGAATATCTG
451 TATCGGAACG ATCGTCCGTT TTCTGTAAT GTGTACGGCG GAACGGTCA
501 CCGGSAATAAT TATGAAACGA CAGGAGAATA TCGGGTTGTT TGGCAACCGG
551 ACGGTTCCGT ATTTGATGCG GCGGGGCGCG GGAATAATCG GGAAGATGTT
601 TATGAGCATT GCCTCGGGTG TTATCAGATG GCCCAGGTAT ATTTGGCGAA
651 ATACCGGGAT GTCGCGAATG ACGAGCAGAA GGTTTGGGAC TTCCGCAAAAG
701 AGAGCAACCG AATTGCGTCT GACTCGCGCA ATTCTGTGTT TTATCAGAAT
751 ATGCGGGAAT TGATGCCCCG AGGGATCAAG GCGAACAGTC TTGTGGTCCG
801 CTATGATGCG GACGGTCTCG CGCAAAAAGT CTATTGGAGT TTCGACAATG
851 GAAAAAAGCG CCAGAGTTTC GAATATTATT TSAAAAACCG AAATCTTTTT
901 ATTGCACAAAT CTTGACGGGT AGCATTGAAA GCGGATGGCG TAACGGCGGA
951 TATGCAGACC TATCATGCGC AACAGACGTG GTATTGGAT GCGGGCGGA
1001 TTGTCCCGGA AGAGAAACAG GGAGACAGAC TSCCTGATT TCCTTTGAAC
1051 TTGGAATAAT TGGAAAAGA GGTGCGCGGT TATGCAGAGG CTGCGGCGAG
1101 ACGTTCGGGC GGCAGGCGCG ACCTTTCTCA CTGA

```

This corresponds to the amino acid sequence <SEQ ID 2926; ORF 957>:

```

m957.pep
1  MFKKFKPVLL SFFALVFAFW LGTGIAYEIN PRWFLSDTAT EVPKNPNAFV
51  AKLARLFRNA DRAVVIVKES IRTEENLAGT VDDGPLQSEK DYLAALAIRLS
101 RLKEKAKWFH VTEQENGKEV WLDYHIGEGG LVAVSLSQRS PEAFFVNAEYL
151 YRNDRPFVSU VYGGTVHGEN YETTGEYRVV WQPDGVSFDA AGRGKIGEDV
201 YEHCLGCVQM AQVYLAKYRD VANDEQKVDW FRKESNRIAS DSRNSVFYQN

```


1368

251 MRELMPRGNK ANSLVVG YDA DGLPQKVYWS FDNGKKRQSF EYYLKNGNLF
 301 IAQSSSTVALK ADGVTADMOT YHAQQTWYLD GGRIVREEKQ GDRLPDFPLN
 351 LENLEKEVRR YAEAAARRSG GRDLSSH*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 957 shows 95.2% identity over a 331 aa overlap with a predicted ORF (ORF 957) from *N. gonorrhoeae*

g957/m957 95.2% identity in 331 aa overlap

g957.pep	10	20	30	40	50	60
	MFKKFKPVLLSFFALVF	AWLGTG	IAYEIN	PRWFLSD	TATEVP	ENPNFAVAKLARLFRNA
m957	MFKKFKPVLLSFFALVF	AWLGTG	IAYEIN	PRWFLSD	TATEVP	KNPNFAVAKLARLFRNA
g957.pep	70	80	90	100	110	120
	DRAVVIVKESMRTEES	LAGAVDDG	PLQSEKDY	LALAIRL	SRLKEKAK	WFWHVTQE
m957	DRAVVIVKESIRTEEN	LAGAVDDG	PLQSEKDY	LALAIRL	SRLKEKAK	WFWHVTQE
g957.pep	130	140	150	160	170	180
	WLDYYIGEGGLVAVSL	SQRSPEAF	VNAEYLYR	NDPFSVNV	YGGTAHGE	NYETTGEYRVV
m957	WLDYHIGEGGLVAVSL	SQRSPEAF	VNAEYLYR	NDPFSVNV	YGGTVHGE	NYETTGEYRVV
g957.pep	190	200	210	220	230	240
	WQPDGVSF	DAAGRGKIG	DVYEHCLG	CYQMAQVY	LAKYRDVAN	DEQKVWDF
m957	WQPDGVSF	DAAGRGKIG	DVYEHCLG	CYQMAQVY	LAKYRDVAN	DEQKVWDF
g957.pep	250	260	270	280	290	300
	CSR	DYVFYQNM	RELM	PRGMKAN	SLVVG	YDADGLPQKVYWS
m957	DSR	NSVFYQNM	RELM	PRGMKAN	SLVVG	YDADGLPQKVYWS
g957.pep	310	320	330			
	IAQSSSTV	LKT	DGVTADM	QTYHAQQ	TWYLDG	
m957	IAQSSSTV	LKT	DGVTADM	QTYHAQQ	TWYLDG	
m957	YAEAAARRSG	GRDLSSH				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2927>:

a957.seq

1	ATGTTTAAAA	AATCAAACC	GGTACTGTTG	TCATTTTGTG	CACCTGTATT
51	TGCCTTTTGG	CTGGGAACGG	GTATTGCCTA	TGAGATTAA	CCGCGTTGGT
101	TTTTGAGCGA	TACGGCAACT	GAAAATCCGA	ATGCTTTTGT	GGCGAAACTT
151	GCCCGCCTGT	TCCGAAATGC	CGACAGGGCG	GTGTGCATCG	TGAAGGAATC
201	GATGAGGACG	GAGGAAAGTC	TTGCCGGAGC	IGTGGATGAC	GGTCCGTTGC
251	AGTCGGAGAA	GGATTATCTT	GCACTCGCTG	ICCGGCTCAG	TCGTTTGAAA
301	GAAAAGGCGA	AATGGTTTCA	CGTAACGGAG	CAGGAACATG	GGGAAGAGGT
351	TTGGCTGGAT	TACTATATCG	GCGAGGGCGG	TTTGGTTGCG	GTTTCGCTTT
401	CGCAACGCTC	GCCGGAAGCG	TTTGTAAATG	CCGAATATCT	GTATCGGAAC
451	GATCGTCCGT	TTTCTGTAAA	TGTGTACGGC	GGAACGGTTC	ACGGGGAAAA
501	TTGATGAAAC	ACAGGAGAAT	ATCGGGTTGT	TTGGCAACCG	GACGGTTCGG
551	TATTTGATGC	GTCGGGGCGC	GGGAAAATCG	GGGAAGATGT	TTATGAGCAT
601	TGCCICGGGT	GTTATCAGAT	GGCCAGGTA	TATTGGCGA	AAATCGGGGA
651	TGTCGCGAAT	GATGAGCAGA	AGGTTTGGGA	CTTCCGCGAA	GAGAGTAACC
701	GGATTGCGTC	GGACTCGCGC	GATTCTGTGT	TTTATCAGAA	TATGCGGGAA
751	TTGATGCCCC	GAGGGATGAA	GGCAAAACGT	CTTGTGGTCG	GCTATGATGC
801	GGACGGTCTG	CCGCAGAAAG	TCTATTGGAG	TTTCGACAAT	GGGAAAAAAC
851	GCCAGAGTTT	CGAATATTAT	TGAAAAACG	GAAATCTTTT	TATTGCACAA
901	TCTTCGACGG	TAGCATTGAA	AGCGGATGGC	GTAACGGCGG	ATATGCAGAC

1369

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951 CTATCATGCG CAACAGACGT GGTATTAGA TGGCGGCGG ATTGTCCGG
1001 AAGAGAAACA GGGGACAGA CTGCTGATT TTCCTTGAA CTGGGAAGAT
1051 TTGGAAAAAG AGGTGAGCCG TTATGCAGAG GCTCGGCGA GACGTCGGG
1101 CGGCAGCGCG GACCTTCTC ACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2928; ORF 957.a>:

```

a957.pep
1  MFKKFKPVLL SFFALVFVFW LGTGIAYEIN PRWFLSDTAT ENPNAFVAKL
51  ARLFRNADRA VVIVKESMRT EESLAGAVDD GPLQSEKDYI ALAVRLSRLK
101 EKAKWFHVTE QEHGEEVWLD YYIGEGGLVA VLSQRSPEA FVNAEYLYRN
151 DRPFSVNVYG GTVHGENYET TGEYRVVWQP DGSVFDASGR GKIGEDVYEH
201 CLGICYMAQV YLAKYRDVAN DEQKVWDFRE ESNRIASDSR DSVFYQNMRE
251 LMPRGMKANS LVVGYDADGL POKVYWSFDN GKQRQSFEYY LKNGNLFIAQ
301 SSTVALKADG VTADMQTYHA QOTWYLDGGR IVREEKQGRD LPDFPLNLED
351 LEKEVSRVAE AAARRSGGRR DLSH*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 957 shows 96.3% identity over a 377 aa overlap with a predicted ORF (ORF 957) from *N. meningitidis*

```

a957/m957 96.3% identity in 377 aa overlap

      10      20      30      40      50
a957.pep MFKKFKPVLLSFFALVFVFWLGTGIAYEINPRWFLSDTATE---NPNAFVAKLARLFRNA
      |||
m957      MFKKFKPVLLSFFALVFVFWLGTGIAYEINPRWFLSDTATEVPKNPNAFVAKLARLFRNA
      |||
      10      20      30      40      50      60
a957.pep DRVVIVKESMRTEESLAGAVDDGPLQSEKDYIALAVRLSRLKEKAKWFHVTEQEHGEEV
      |||
m957      DRVVIVKESIRTEENLAGTVDDGPLQSEKDYIALAIRLSRLKEKAKWFHVTEQEHGKEV
      |||
      60      70      80      90      100     110
a957.pep WLDYYIGEGGLVAVSLSQRSPEAFVNAEYLYRNDRPFSVNVYGGTVHGENYETTGEYRVV
      |||
m957      WLDYHIGEGGLVAVSLSQRSPEAFVNAEYLYRNDRPFSVNVYGGTVHGENYETTGEYRVV
      |||
      120     130     140     150     160     170
a957.pep WQPDGVSVDASGRGKIGEDVYEHCLGICYMAQVYLAKYRDVANDEQKVWDFREESNRIAS
      |||
m957      WQPDGVSVDAAAGRGKIGEDVYEHCLGICYMAQVYLAKYRDVANDEQKVWDFRKEENRIAS
      |||
      180     190     200     210     220     230
a957.pep DSRDVSFYQNMRELMPRGMKANSLVVGYDADGLPOKVYWSFDNGKKRQSFEYYLKNGNLF
      |||
m957      DSRNSVIFYQNMRELMPRGMKANSLVVGYDADGLPOKVYWSFDNGKKRQSFEYYLKNGNLF
      |||
      240     250     260     270     280     290
a957.pep IAQSSTVALKADGVTADMQTYHAQOTWYLDGGRIVREEKQGRDLPDFPLNLEDLEKEVSR
      |||
m957      IAQSSTVALKADGVTADMQTYHAQOTWYLDGGRIVREEKQGRDLPDFPLNLENLEKEVRR
      |||
      300     310     320     330     340     350
a957.pep YAEAAAARRSGGRRDLSHX
      |||
m957      YAEAAAARRSGGRRDLSHX
      |||
      360     370
a957.pep
m957

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2929>:

```

g958.seq
1  TTGGCTCGTT TATTTTCACT CAAACCACTG GTGCTGGCAT TGGGCTTCTG
51  TTTCGGCAGC CATTGCGCCG CCGATACCGT TCGCGCGGAA GAGCGGACG

```

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101 GCGGTGTCGC AGAAGGCGGT GCGCAGGGCG CGTCCGAATC CGCACAAGCT
151 TCCGATTGTA CCTTCGGTTC GACCTGCCTG TTTTGCAGTA ACAGAAAGCGG
201 CAGCCCCGAG AGAACCGAAG CCGCCGTCGA AGGCAGCGGC GAAGCATCCG
251 TCCCCGAAGA CTATACGCGC ATTGTTGCCG ACAGGATGGA AGGACAGTCG
301 AAGGTTAAGG TCGCGCGCGA AGGAAGCGTT ATCATCGAAC GGGACGGCGC
351 AGTCCTCAAT ACCGATTGGG CGGATTACGA CCAGTCGGGC GACACCGTTA
401 CCGTAGGCGA CCGGTTTCGCC CTCCAACAGG ACGGTACGCT GATTTCGGGGC
451 GAAACCTGTA CCTACAATCT CGATCAGCAG ACCGGCGAAG CGCACAACGT
501 CCGTATGGAA ACCGAACAAG GCGGACGGCG GCTGCAAGC GTCAGCCGCA
551 CCGCCGAAAT GTTGGGCGAA GGGCGTTACA AACTGACGGA AACCCAAATC
601 AACACCTGTT CCGCCGGAGA TGCCGGCTGG TATGTCAAAG CCGCCTCTGT
651 CGAAGCCGAT CCGGGAAAAG GCATAGGCGT TGCCAAACAC GCCGCCCTTCG
701 TGTTCCGCGG CGTTCCCTTT TTTCTATACG CTTGGGCGGA CTTCCCGCTT
751 GACGSCAACC GCAAAAGCGG ACTGCTCGTC CCGTCCGTAT CTGCCGGTTC
801 GGACGCGGTT TCCCTTTCCG TCCCTTATTA TTTCAACCTT GCCCCCAACT
851 TCGATGCCAC TTTCGCCCCC GGCATTATCG GCGAACGCGG CGCGACGTTT
901 GACGSAACAA TCCGTTACCT GCGTCCCGAT TACAGCGGAC AGACCGACCT
951 GACCTGGTTG CCGCACGATA AGAAAAGCGG CAGGAACAAC CGCTATCAGG
1001 CAAAATGGCA GCACCGGCAC GACATTTCCG ACACGCTTCA GCGGGGTGTC
1051 GATTTCGAAC AAGTCTCCGA CAGCGGCTAC TACCGCGACT TTTACGGCGG
1101 CGAAGAAATC GCCGCAACG TCAACCTCAA CCGCCGCGTA TGCTGGATT
1151 ATGGCGGCAG GCGGCGGGA GGCAGCCTGA ATGCCGGCCT TTCGGTTCAG
1201 AAATACCAGA CGCTGGCAA CCAAAGCGGC TACAAAGACG AACCTTACGC
1251 CATCATGCCC CGCCTTTCTG CCGATTGGCA TAAAAACGCA GGCAGGGCGC
1301 AAATCGGCGT GTCCGCACAA TTTACCCGCT TCAGCCACGA CGGCCGCCAA
1351 GACGSCAGCC GACTGGTCTG GTATCCCGGT ATCAAAATGG ATTTCAGCAA
1401 CAGCTGGGGC TACGTCCGCC CCAAACCTCG GCTGCAGGCC ACTTATTACA
1451 GCCTCGACAG TTTCCGGCGG AAGCATCCC GCAGCGTCGG CCGCGTTTGT
1501 CCCGTTGTCA ATATCGACGG CCGCACAAAC TTCGAACGCA ATACGCGCCT
1551 GTTCGGCGGC GGAGTCGTGC AAACCATCGA GCCGCGCCTG TTCTACAAC
1601 ATATTCTDGC CAAATCTCAA AACGACCTGC CCAATTTCGA TTCGTCGGAA
1651 AGCAGCTTCG GCTACGGGCA GCTTTCCGCG GAAAACCTCT ATTACGGCAA
1701 CGACCGCATC AACGCCGCCA ACAGCCTTTC CACCGCGCTG CAGAGCCGTA
1751 TTTTGGACGG CGCGACGGGG GAGGAGCGTT TCCGCGCCGG TATCGGTCAG
1801 AAATTCTATT TCAAGGATGA TCGGCTGATG CTTGACGGCA GCGTCGGCAA
1851 AAATCCGCGC AGCGTTCGCG ACTGGGTGGC ATTGCGCTCC GCGGCGATAG
1901 ETLTYNLDQQ TGEAHNVME TEQGGRRLOS VSRTAEMLGE GRYKLTETQF
1951 CCGCGCGAAC ATTACGCGCT CCGCGCAGGC TACCGCCCGC CCCCCGAAA
2001 AGTGTGAAC GCCCGCTACA AATACGGCGC CACGAAAAAA ATCTACCTGC
2051 AGCGCGACGG TTCCTATTTT TACGACAAAC TCAGCCAGCT CGACCTGTCC
2101 GCACAATGGC CGCTGACGCG CAACCTGTCT GCGTCTGTCC GCTACAAC
2151 CGGTTTTGAA GCCAAAAAAC CGATAGAAAT GTTGCCTGGT GCAGAATACA
2201 AAAGCAGTTG CGGCTGCTGG GCGCGGGGCG TGTACGCCCA ACGCTACGTT
2251 ACCGGCGAAA ACACCTACAA AAACGCGGTC TTTTTCAC TTCAAGTTGAA
2301 AGACCTCAGC AGCGTCGGCA CAAACCCCGC AGCAGGATG GATGTCGCCG
2351 TTCCCGGCTA CATCCCCGCC CACTCTCTTT CCGCCGGACG CAACAAACGG
2401 CCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2930; ORF 958.ng>:

```

g958.pep
1  LARLFLSKPL VLALGFCEGT HCAADTVAAE EADGRVAEGG AQGASESAQA
51  SDLTGLSTCL FCSNESGSPE RTEAAVCGSG EASVPEDYTR IVADRMEGQS
101 KVKVRAEGSV IIERDGAVLN TDWADYDQSG DTVTVGDRFA LQQDGTLLRG
151 ETLTYNLDQQ TGEAHNVME TEQGGRRLOS VSRTAEMLGE GRYKLTETQF
201 NTCAGDAGW YVKAASVEAD RKGIGVAKH AAFVFGGVPL FYTPWADFPL
251 DGNRKSGLLV PSVSAGSDGV SLSVPYFNL APNFDATFAP GIIGERGATF
301 DGQIRYLRPD YSGQDILTWL PHDKKSGRNN RYQAKWQHRH DISDTLQAGV
351 DFNQVSDSGY YRDFYGGEEI AGNVNLNRRV WLDYGGRAAG GSNAGLSVQ
401 KYQTLANQSG YKDEPYAIMP RLSADWHKNA GRAQIGVSAQ FTRFSDHGRQ
451 DGSRLVVYPG IKWDFNSWG YVRPKLGLHA TYSLDSFGG KASRSVGRVL
501 PVVNIDGTTT FERNTLFGG GVVQTIETPL FYNYPKASQ NDLPNFDSSSE
551 SSFGYGQLFE ENLYYNDRI NAANSLSTAV QSRILDGATG EERFRAGIGQ
601 KFYFKDDAVM LDGSVGKNPR SRSDWVAFAS GGIGGRFTLD SSIHYNQNDK
651 RAEHYAVGAG YRPAPGKVLN ARYKYGRNEK IYLDAGDSYF YDKLSQLDLS
701 AQWPLTRNLS AVVRYNYGFE AKKPIEMLAG AEYKSSCGCW GAGVYAQRVY
751 TGENYKNAV FFSLLQLDLS SVGRNPAGRM DVAVPGYIPA HSLSAGRNRK
801 P*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2931>:

```

n958.seq
1  TTGGCTCGTT TATTTTCACT CAAACCACTG GTGCTGGCAT TGGGCTCTTG
51  CTTCCGCGAC CATTGCGCCG CCGCCGATGC CGTTGCGGCG GAGGAAACGG
101 ACAATCCGAC CGCCGGAGAA AGCGTTCGGA GCGTGTCCGA ACCCATACAG

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1371

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151 CCTACCAGCC TGAGCCTCGG TTCGACCTGC CTGTTTTCGA GTAACGAAAG
201 CGGCAGCCCC GAGAGAACCG AAGCCGCCGT CCAAGGCAGC GGCGAAGCAT
251 CCATCCCCGA AGACTATACG CGCATGTGTG CCGACAGGAT GGAAGGACAG
301 TCGCAGGTGC AGGTGCGTGC CGAAGGCAAC GTCGTCGTGC AACGCAACCG
351 GACGACCCCTC AATACCGATT GGGCGGATTA CGACCAAGTC GGCACACCCG
401 TTACCGCAGG CGACCGGTTT GCCCTCCAAC AGGACGGTAC GCTGATTTCG
451 GGCAGAAACC TGACCTACAA TCTCGAGCAG CAGACCGGGG AAGCGCACAA
501 CGTCCGCATG GAAATCGAAC AAGCGGACG GCGGCTGCAA AGCGTCAGCC
551 GCACCGCCGA AATGTTGGGC GAAGGGCATT ACAAACTGAC GGAACCCCAA
601 TTCAACACCT GTTCCGCCG CGATGCCGGC TGGTATGTCA AGCGACCCTC
651 TGTCAAGGCC GATCGGGAAG AAGGCATAGG CGTTGCCAAA CACGCCGCCT
701 TCGTGTTCGG CGCGGTTCCC ATTTTCTACA CCCCTTGGGC GGACTTCCCG
751 CTCGATTTCA ACCGCAAAAG CGGCCTGCTT GTTCCCTCAC TGTCCGCCGG
801 TTCGACGGCG GTTCCCTTTT CCGTTCCCTA TTATTTC AACCTTGCCTCC
851 ATCTCGATGC CACGTTTCGG CCCAGCGTGA TCGGCGAAGC CGGCGCGGTC
901 TTTGACGGCG AGGTACGCTA CCTGCGGGCG GATTATGCCG GCCAGTCCGA
951 CCTGACCTGG CTGCCGCACG ACAAGAAAAG CGGCAGGAAT AACCGCTATC
1001 AGGCGAAATG GCAGCATCGG CACGACATT CCGACACGCT TCAGGCGGGT
1051 GTCGATTTCA ACCAAGTCTC CGACAGCGCG TACTACCGCG ACTTTTACGG
1101 CAACAAAGAA ATCGCCGGCA ACGTCAACCT CAACCGCGCT GTATGGCTGG
1151 ATTTATGGCG CAGGGCGGCG GCGCGCAGCC TGAATGCCGG CCTTTCGGTT
1201 CTGAATAACC AGACGCTGGC AAACCAAGG GGTACAAAG ACAAAACGTA
1251 TGCCCTCATG CCGCGCCTTT CGGTGAGTGC GCGTAAAAAC ACCGGCAGGG
1301 CGCAATTCGG CGTGTCCGCA CAATTTACCC GATTTCAGCA CGACAGCCGC
1351 CAAGACGGCA GCGCGCTGGT CGTCTATCCC GACATCAAT GGGATTTCAG
1401 CAACAGCTGG GGCTATGTCC GTCCCAAAC CGGACTGCAC GCCACCTATT
1451 ACAGCCTCAA CCGCTTCGGC AGCCAAGAG CCCGACGCGT CAGCGCACT
1501 CTGCCCATTC TCAACATCGA CAGCGCGCA ACTTTTGAGC GGAATACGCG
1551 GATGTTCCGG GGAGAAGTCC TGCAAAACCT CGAGCCGCGC CTGTTCTACA
1601 ACTATATTCG TGCCAAATCC CAARACGACC TGCCCAATT CGATTGCTCG
1651 GAAAGCAGCT TCGGCTACGG GCAGCTCTTT CGCGAAAACC TCTATTACGG
1701 CAACGACAGG ATTAACACCG CAACAGCCTT TCCGCCGCC GTGCAAGGCC
1751 GTATTTTGA CGGCGCGACG GGGGAAGAGC GTTCCGCGC CGGCATCGGT
1801 CAGAAATCTT ATTTCAAGGA TGATGCGGTG ATGCTTGACG GCAGCGTCGG
1851 CAAAAAACCG CGCAACCGTT CCGACTGGGT GGCATTTGCC TCCGGCAGCA
1901 TCGGCAGCCG CTTCATCCTC GACAGCAGCA TCCACTACAA CCAAAACGAC
1951 AAACCGCCCG AGAATACGC CSTCGGTGCA AGCTACCGTC CCGCACAGGG
2001 CAAAGTGTCT AACGCCCGCT ACAATAACGG GCGCAACGAA AAAATCTACC
2051 TGAAGTCCGA CGGTTCCCTT TTTTACGACA AACTCAGCCA GCTCGACCTG
2101 TCCGCACAAAT GGCCGCTGAC GCGCAACCTG TCGGCCGTCG TCCGTTACAA
2151 CTACGCTTTT GAAGCCAAAA AACCGATAGA GGTGCTGGCG GGTGCGGAAT
2201 ACAAAGCAG TTGCGGCTGC TGGGCGCGG CGGTGTACGC CCAACGCTAC
2251 GTTACCGGCG AAAACACCTA CAAAACGCT GTCTTTTCT CACTTCAGTT
2301 GAAAGACCTC AGCAGTGTG GCAGAAACCC CGCAGACAGG ATGGATGTG
2351 CCGTTCCCGG CTATATCACC GCCACCTCTC TTTCCGCCGG ACGCAACAAA
2401 CGACCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2932; ORF 958>:

```

m958.pep
1 LARLFSLKPL VLALGLCFGT HCAAADAVAA EETDNPTAGE SVRSVSEPIQ
51 PTSLSLGSTC LFCSNESGSP ERTEAAVQGS GEASIPEDYT RIVADRMEOG
101 SQVQVRAEGN VVVERNRTTL NTDWADYDQS GDTVTAGDRF ALQQDGTLLR
151 GETLTYNLEQ QTGEAHNVRM EIEQGGRRLO SVSRTAEMLG EGHYKLTETO
201 FNTCSAGDAG WYVKAASVEA DREKGIGVAK HAAFFVGGVP IFYTPWADFP
251 LDGNRKSGLL VPSLSAGSDG VSLSVPPYYFN LAPNLDATFA PSVIGERGAV
301 FDGQVRYLRP DYAGQSDLTW LPHDKKSGRN NRYQAKWQHR HDISDTLQAG
351 VDFNQVSDG YYRDFYGNKE IAGNVNLNRR VWLDYGGRAA GGSINAGLSV
401 LKYQTLANQS GYKDKPYALM PRLSVEWRN TGRAQIGVSA QTRFSDSR
451 QDGSRLVVYP DIKWDFSNSW GYVRPKLGLH ATYYSLNRFQ SQAARRVSRT
501 LPIVNI DSGA TFERNTRMFG GEVLQTLFPR LFYNYIPAKS QNDLPNFDSS
551 ESSFGYGQLF RENLYYGNDR INTANSLSAA VQSRILDGAT GEERFRAGIG
601 QKFYFKDDAV MLDGSGVKKP RNRSDWVAF SSGISGRFIL DSSIHYNQND
651 KRAENYAVGA SYRPAQKVL NARYKYGRNE KIYKSDGSY FYDKLSQLDL
701 SAQWPLTRNL SAVVRYNYGF EAKKPIEVL GAELYKSSCGG WAGVYAORY
751 VTGENTYKNA VFFSLQLKDL SSVGRNPADR MDVAVPGYIT AHSLSAGRNK
801 RP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 958 shows 89.3% identity over a 802 aa overlap with a predicted ORF (ORF 958) from *N. gonorrhoeae*

1372

m958/g958 89.3% identity in 802 aa overlap

m958.pep	10	20	30	40	50	60
	LARLFSLKPLVLALGLCFGTHCAAADAVAAEETDNPTAGESVRSVSEPIOPTSLSLGSTC					
g958	LARLFSLKPLVLALGLCFGTHCAA-DTVAEEADGRVAEGGAQGAESAQASDLTLGSTC					
	10	20	30	40	50	
m958.pep	70	80	90	100	110	120
	LFCSNESGSPERTEAAVQGSGEASIPEDYTRIVADRMEGSQVQVRAEGNVVVVERNRTTL					
g958	LFCSNESGSPERTEAAVQGSGEASVPEDYTRIVADRMEGSQVQVRAEGSVIIERDGAVL					
	60	70	80	90	100	110
m958.pep	130	140	150	160	170	180
	NTDWADYDQSGDVTAGDRFALQQDGLIRGETLTYNLEOOTGEAHNVREIEQGGRRLO					
g958	NTDWADYDQSGDVTVGDRFALQQDGLIRGETLTYNLDQQTGEAHNVRETEQGGRRLO					
	120	130	140	150	160	170
m958.pep	190	200	210	220	230	240
	SVSRTAEMLGEGHYKLTETCFNTCSAGDAGWYVKAASVEADREKIGVAKHAAVFVGGVP					
g958	SVSRTAEMLGEGRYKLTETCFNTCSAGDAGWYVKAASVEADRGKIGVAKHAAVFVGGVP					
	180	190	200	210	220	230
m958.pep	250	260	270	280	290	300
	IFYTPWADFPDGNRKSGLLVPSLSAGSDGVSLSVPYYFNLPNLDATFAPSVIGERGAV					
g958	IFYTPWADFPDGNRKSGLLVPSVSAGSDGVSLSVPYYFNLPNFDATFAPGIIGERGAT					
	240	250	260	270	280	290
m958.pep	310	320	330	340	350	360
	FDGQVRYLRPDYAGQSDLTWLPKDKKSGRNNRYQAKWQHRHDSITLQAGVDFNQVSDSG					
g958	FDGQIRYLRPDYSGQDLTWLPKDKKSGRNNRYQAKWQHRHDSITLQAGVDFNQVSDSG					
	300	310	320	330	340	350
m958.pep	370	380	390	400	410	420
	YYRDFYGNKEIAGNVNLRVWLDYGGRAAGGSLNAGLSVLKYQTLANQSGYKDKPYALM					
g958	YYRDFYGGEEIAGNVNLRVWLDYGGRAAGGSLNAGLSVQKYQTLANQSGYKDEPYAIM					
	360	370	380	390	400	410
m958.pep	430	440	450	460	470	480
	PRLSVEWRNTGRAQIGVSAQFTRFSHDSRQDGSRLVVPDIKWDFSNSWGYVRPKLGLH					
g958	PRLSADWHKAGRAQIGVSAQFTRFSHDSRQDGSRLVVPDIKWDFSNSWGYVRPKLGLH					
	420	430	440	450	460	470
m958.pep	490	500	510	520	530	540
	ATYYSLNREFGSQEARRVSRTLPIVNI DSGATFERNTRMFGGEVLQTLERLFYNYIPAKS					
g958	ATYYSLDSFGGKASRSVGRVLPVVNI DGGTTFERNTRLFGGGVVQTIEPRLFYNYIPAKS					
	480	490	500	510	520	530
m958.pep	550	560	570	580	590	600
	QNDLPNFDSESSFGYGQLFRENLYYGNDRINTANSLAAVQSRILDGATGEERFRAGIG					
g958	QNDLPNFDSESSFGYGQLFRENLYYGNDRINAANSLTAVQSRILDGATGEERFRAGIG					
	540	550	560	570	580	590
m958.pep	610	620	630	640	650	660
	QKFYFKDDAVMLDGSVGKKPRNRSDWVAFASGSIGSRFILDSSIHYNQNDKRAENYAVGA					
g958	QKFYFKDDAVMLDGSVGKNPRSRSDWVAFASGGIGGRFTLDSSIHYNQNDKRAEHYAVGA					
	600	610	620	630	640	650
m958.pep	670	680	690	700	710	720
	SYRPAQGVKVLNARYKYGRNEKIYKSDGSYFYDKLSQDLDSAQWPLTRNL SAVVRNYGF					
g958	GYRPAQGVKVLNARYKYGRNEKIYKQADGSYFYDKLSQDLDSAQWPLTRNL SAVVRNYGF					
	660	670	680	690	700	710

730 740 750 760 770 780
m958.pep EAKKPIEVLGAGYEYKSSCGCWAGVYAQRYYVTGENTYKNVFFSLQLKDLSVGRNPADR
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g958 EAKKPIEMLAGAEYKSSCGCWAGVYAQRYYVTGENTYKNVFFSLQLKDLSVGVGNPAGR
 720 730 740 750 760 770

790 800
m958.pep NDVAVPGYITAHSLSAGRNRKP
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g958 NDVAVPGYIPAHSLSAGRNRKPX
 780 790 800

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2933>:

```

a958.seq
1      TTGGCTCGTT TATTTTCACT CAAACCACTG GTGCTGGCAT TGGGCTTCTG
51     TTTCCGCACG CATTCGCCTG CGCCCGATGC CGTTCGGCGG GAGGAAACCG
101    ACAATCCGAG CCGCGGAGGA AGCGTTCCGA CGGTGTCCGA ACCCATACAG
151    CCTACCAGCC TGAGCCTCGG TTCGACCTGC CTGTTTTCGA GTAACGAAAG
201    CGGCAGCCCC GAGAGAACC GAAAGCCCGT CCAAGGCAGC GGCAGGACAT
251    CCATCCCCGA GAGCTATACG CGCATTTTGT CCAGACAGAT GGAAGGACAG
301    TCGCAGGTGC AGGTGCGTGC CGAAGGCAAC GTCGTCTGTG AACGCAATCG
351    GACGACCCCT AATGCGGATT GGGCGGATTA CGACCAAGTC GGCACACCCG
401    TTACCGCAGG CGACCGGTTT GCCTCTCAAT AGGACGCTAC GTTGATTTCG
451    GGGCAAAACC TGACCTACAA TCTCGAGCAG CAGACCGGGG AAGCGCACAA
501    CGTCCGATTA GAAACCGAAG CAGGGCGSAG CGGGCTGCAA AGCGTCACCC
551    GCACCGCTAG AATGTTGGGC GAAGGCGCATT ACAACCTGAC GGAACACGCA
601    TTCAACACCT GTTCGCGCGG CGATGCGCGC TGTATGTGTA AGGCCGCTTC
651    CGTCGAAGCC CATCGGGAAA AAGGCATATG CGTTGCCAAA CACGCCGCTC
701    TCGTGTTCGG CGCGCTTCCC ATTTTCTAGA CCGCTTGGCG GGACTTCCCG
751    CTTGACGGCA ACCGCAAAAG CGGCTTGCTC GTTCCCTCAC TGTCCGCGCG
801    TTCGAGCGGC GTTTCCTTTT CCGTTCCTTA TTATTTCAAC CTGCGCCCTC
851    ATCICGATGC CACGTTCTGC CGCGCGGTGA TCGGCGAAGC CGCGCGCGTC
901    TTTGACGGGC AGGTACGCTA CCTGCGGCGG GATTATGCCG GCCAGTCCCA
951    CCTGACCTGG CTGCGCGACG ACAGAAAGAG CGGCAGGAAT AACCGCTATC
1001   AGGCGAAATG CGAGCACCGG CAGCAGATTT CCGACAGCCT TCAGCGGGET
1051   GTCGATTTCA ACCAAGTCTC CGACAGCGGC TACTACCGCG ACTTTTACGG
1101   CAACAAAGAA ATPCGCGGCA ACCTCAACCT CAACCCGCGT GTATGCTGTG
1151   ATTAATGGCG CAGGGCGGCG GCGCGCAGCC TGAATCCGGG CTATTCGGTT
1201   CTGAAATACC AGACGCTGGC AAACCAAAGC GGTACAAAGG ACAAACCGTA
1251   TGCCCTGATG CCGCGCCTTT CGCGCGATTG CGCCAAAAC ACCGGCAGGG
1301   CGCAATTCGG GCGTCTCGCC CATTATACCC GTTTCAGCCA CGACAGCCGC
1351   CAAGACGGCA CGCGCTCTGT CGTCTATCCC GACATCAAAAT GGGATTTCAG
1401   CAACAGCTGG GGTACGTCC GTCCCAAATC CGGACTGCAC GCCACCTATT
1451   ACAGCGCTCA CCGCTTCGGC AGCCAAGAAG CCCGACCGCT CACCCGCATC
1501   CTGCCCATCG TCAACATCGA CAGCGCGATG ACCTTCGAAC GCAATACCGG
1551   GATGTTTCGG GCGCGAGTCC TGCAAAACCT CGAGCCGCGC CTGTTCTACA
1601   ACTATATTTC TGCCAAATCC CAAAACGACC TGCCCAATTT CTGATTCTGC
1651   GAAAGCAGCT TCGGCTACGG CGAGCTTTTT CGTGAAAACC TGTATTACGG
1701   CAACGACAGG ATTAACACCG CAACAGCCTT TTCGCGCGCC GTGCAAGCC
1751   GTATTTTTGA CGCGCGGACG GGGGAAGAGC GTTTCGCGCG CGGCATCTGG
1801   CAGAAATCTT ACTTCAAAAA CGACGCGATC ATGCTGTAGC GCGATGTCTG
1851   CAAAAAACCG CGCAGCGGTT CGGACTGGGT GGCATTCCGC TCCAGCGGCA
1901   TCGCGCAGCG CTTTATCTCT CAGACGACGA TCCACTACAA CCAAAACGAC
1951   AAACGCGCGC AGAATACGCG CCGTGGTGCA AGCTACCGTC CGGCACAGGG
2001   CAAAGTGCTG AACGCCGCT CAAAAATACG CGGCAACGAA AAAATCTACC
2051   TGAAGTCCGA CGGTTCTCTT TTTTACGACA AACTCAGCCA TCTGCACTGT
2101   TCCGCACAAT GCGCGCTGAC GCGCAACCTG TCGGCCGCTG GCGCTTACAA
2151   CTACGGTTTT GAAGCCAAAA AACCGATAGA GGTGCTGGCG GGTGCGGAAT
2201   ACAAAAGCAG TPGCGGCTGC TSGGGCGCGG CGTGTATACG CCAACCGTAC
2251   GTTACCGCGG AAAACACCTA CAAAACGCTG GCTTTTTTCT CACTTCACTT
2301   GAAAGACCTC AGCAGTGTCT GCAGAAACCC CGCAGACAGG ATGATTGTCT
2351   CCGTGTCCCG CTATATCCCC GCCCACTCTC TTTCCGCGCG ACBCAACAAA
2401   CGGCGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2934; ORF 958.a>:

a958.pep

1	LARFLSLKPL	VLALGFCFCGT	HCAAADAVAA	EETDNPAGG	SVRSVSEPIQ
51	PTSLSLGSTC	LFCNSNCGSP	ERTEAAVQGS	GEASIPEDYT	RIVADRMEGQ
101	SQVQRAEGH	VVVERNRTTL	NADWADYDOS	EDTVTAGDRF	ALQQDGTLLR
151	GETLLYNLEQ	QTGEAHHNVR	ETDEHGGRRLQ	SVSRTEAEMLG	EGHYKLLTETQ
201	FNTCSAGDAG	WYKVAASVEA	DREKGIGVAK	HAAFVFCGGP	IIFYTPWADFQ

1374

```

251 LDGNRKSGLL VPSLSAGSDG VSLSVPYFFN LAPNLDATFA PGVIGERGAV
301 FDGQVRYLRP DYAGQSDLTW LPHDKKSGRN NRYQAKWQHR HDISDTLQAG
351 VDFNQVSDSG YYRDFYGNKE IAGNVNLRNR VWLDYGGRAA GGS LNAGLSV
401 LKYQTLANQS GYKDKPYALM PRLSADWRKN TGRAQIGVSA QFTRFSDSR
451 QDGERLVVYP DIKWDFSNSW GYVRPKLGLH ATYYSLNRFQ SQAARRVSRT
501 LPIVNIDSGM TFERNTRMFG GGVLTLEPR LFYNYIPAKS QNDLPNFDSS
551 ESSFGYGOLF RENLYYGNDR INTANSLSAA VQSRILDGAT GEERFRAGIG
601 QKFYFKNDV MLDGSVGKKP RSRSDWVAF SSGIGSRFIL DSSIHYNQND
651 KRAENYAVGA SYRPAQGVK NARYKYGRNE KIYKSDGSY FYDKLSQLDL
701 SAQWPLTRNL SAVVRYNYGF FAKKPTFVLA GA EYKSSCGC WGAGVYAQRY
751 VTGENTYKNA VFFSLQLKDL SSVGRNPADR MDVAVPGYIP AHSLSAGRKN
801 RP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 957 shows 96.3% identity over a 377 aa overlap with a predicted ORF (ORF 957) from *N. meningitidis*

a958/m958 98.1% identity in 802 aa overlap

	10	20	30	40	50	60
a958.pep	LARLFS	LKPLVL	LALGFC	FGTHCA	ADAVAA	EETDNPT
m958	LARLFS	LKPLVL	LALGFC	FGTHCA	ADAVAA	EETDNPT
	10	20	30	40	50	60
	70	80	90	100	110	120
a958.pep	LFCSNE	SGSPER	TEAAVQ	GSSEAS	IPEDYTR	IVADRM
m958	LFCSNE	SGSPER	TEAAVQ	GSSEAS	IPEDYTR	IVADRM
	70	80	90	100	110	120
	130	140	150	160	170	180
a958.pep	NADWAD	YDQSGD	TVTAGD	RFALQQ	DGTLIR	GETLT
m958	NADWAD	YDQSGD	TVTAGD	RFALQQ	DGTLIR	GETLT
	130	140	150	160	170	180
	190	200	210	220	230	240
a958.pep	SVSRTE	AMLGEG	HYKLT	TETQFN	TCSAGD	AGWYKA
m958	SVSRTE	AMLGEG	HYKLT	TETQFN	TCSAGD	AGWYKA
	190	200	210	220	230	240
	250	260	270	280	290	300
a958.pep	IFYTPW	ADFP	LDGNRK	SGLLV	VPSLSA	GS
m958	IFYTPW	ADFP	LDGNRK	SGLLV	VPSLSA	GS
	250	260	270	280	290	300
	310	320	330	340	350	360
a958.pep	FDGQVR	YLRPD	YAGQSD	LTWLP	HDKKSG	RNNRYQ
m958	FDGQVR	YLRPD	YAGQSD	LTWLP	HDKKSG	RNNRYQ
	310	320	330	340	350	360
	370	380	390	400	410	420
a958.pep	YYRDFY	GNKEI	IAGNVN	LRNVW	LDYGG	RAAGGS
m958	YYRDFY	GNKEI	IAGNVN	LRNVW	LDYGG	RAAGGS
	370	380	390	400	410	420
	430	440	450	460	470	480
a958.pep	PRLSAD	WRKNT	TGRAQI	GVSAQ	FTRFSD	SRQDGS
m958	PRLSAD	WRKNT	TGRAQI	GVSAQ	FTRFSD	SRQDGS
	430	440	450	460	470	480
	490	500	510	520	530	540
a958.pep	ATYYSL	NRFSG	QEAARR	VSRTLP	IVNIDSG	M
m958	ATYYSL	NRFSG	QEAARR	VSRTLP	IVNIDSG	M

1375

	490	500	510	520	530	540
a958.pep	550	560	570	580	590	600
	QNDLPNFDSESSFGYGQLFRENLYYGNDRIANTANSLSAAVQSRILDGATGEERFRAGIG					
m958	QNDLPNFDSESSFGYGQLFRENLYYGNDRIANTANSLSAAVQSRILDGATGEERFRAGIG					
	550	560	570	580	590	600
a958.pep	610	620	630	640	650	660
	QKFYFKNDVAVMLDGSVGKKPRSRSDWVAFASGIGSRFILDSSIHYNQHKRAENYAVGA					
m958	QKFYFKNDVAVMLDGSVGKKPRSRSDWVAFASGIGSRFILDSSIHYNQHKRAENYAVGA					
	610	620	630	640	650	660
a958.pep	670	680	690	700	710	720
	SYRPAQGVNLNARYKYGRNEKIYKSDGSGYFYDKLSQDLDSAQWPLTRNLSAVVRNYGF					
m958	SYRPAQGVNLNARYKYGRNEKIYKSDGSGYFYDKLSQDLDSAQWPLTRNLSAVVRNYGF					
	670	680	690	700	710	720
a958.pep	730	740	750	760	770	780
	EAKKPIEVLAGAEYKSSCGCWGAGVYAQRVVTGENTYKNAVFESLQKDLSSVGRNPADR					
m958	EAKKPIEVLAGAEYKSSCGCWGAGVYAQRVVTGENTYKNAVFESLQKDLSSVGRNPADR					
	730	740	750	760	770	780
a958.pep	790	800				
	MDVAVPGYIPAHSLSAGRNRKPX					
m958	MDVAVPGYIPAHSLSAGRNRKP					
	790	800				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2935>:

```
g959.seq
1  ATGAACATCA AACACCTTCT CTTGACCGCC GCCGCAACCG CACTGTTGGG
51  CATTTCGGCC CCCGCGCTCG CCCACCACGA CGGACACGGC GATGACGACC
101 ACGGACACGC CGCACACCAA CACGGCAAAC AAGACAAAAT CATCAGCCGC
151 GCGCAAGCCG AAAAAGCGGC TTGGCGCGT GTCGGCGGCA AAATCACCAG
201 CATCGATCTC GAACACGACG ACGGCCGTCC GCACTATGAT GTCGAAATCG
251 TCAAAAACGG ACAGGAATAC AAAGTCGTTG TCGATGCCCG TACCGGCCGC
301 GTGATTTCCT CCCGCCGCGA CGACTGA
```

This corresponds to the amino acid sequence <SEQ ID 2936; ORF 959.ng>:

```
g959.pep
1  MNIKHLLLTA AATALLGISA PALAHHDGHG DDDHGHAHQ HGKQDKIISR
51  AQAEKAARAR VGGKITDIDL EHDDGRPHYD VEIVKNGQEQ KVVVDARTGR
101 VISSRRDD*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2937>:

```
m959.seq
1  ATGAACATCA AACACCTTCT CTTGACCTCC GCCGCAACCG CACTGCTGAG
51  CATTTCGGCC CCCGCGCTCG CCCACCACGA CGGACACGGC GATGACGACC
101 ACGGACACGC CGCACACCAA CACAACAAAC AAGACAAAAT CATCAGCCGC
151 GCGCAAGCCG AAAAAGCAGC GTTGGCGCGT GTCGGCGGCA AAATCACCAG
201 CATCGATCTC GAACACGACA ACGGCCGTCC GCACTATGAT GTCGAAATCG
251 TCAAAAACGG ACAGGAATAC AAAGTCGTTG TCGATGCCCG TACCGGCCGC
301 GTGATTTCCT CCCGCCGCGA CGACTGA
```

This corresponds to the amino acid sequence <SEQ ID 2938; ORF 959>:

```
m959.pep
1  MNIKHLLLTS AATALLSISA PALAHHDGHG DDDHGHAHQ HNKQDKIISR
51  AQAEKAALAR VGGKITDIDL EHDNGRPHYD VEIVKNGQEQ KVVVDARTGR
101 VISSRRDD*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 959 shows 95.4% identity over a 108 aa overlap with a predicted ORF (ORF 959) from *N. gonorrhoeae*

1376

m959/g959 95.4% identity in 108 aa overlap

```

      10      20      30      40      50      60
m959.pep  MNIKHLLLTSAATAIISISAPALAHHDGHGDDDHGHAHQHNKQDKIISRAQAEKAALAR
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g959      MNIKHLLLTAAATALLGISAPALAHHDGHGDDDHGHAHQHNKQDKIISRAQAEKAALAR
          10      20      30      40      50      60

      70      80      90     100     109
m959.pep  VGGKITDIDLEHDNGRPHYDVEIVKNGQEYKVVVDARTGRVISSRRDDX
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g959      VGGKITDIDLEHDDGRPHYDVEIVKNGQEYKVVVDARTGRVISSRRDDX
          70      80      90     100

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2939>:

```

a959.seq
1  ATGAACTTCA AACGCCTTCT CTTGACCGCC GCCGCAACCG CACTGATGGG
51 CATTTCGCC CCCGCACTCG CCCACCACGA CGGACACGGC GATGACGACC
101 ACGGACACGC CGCACACCAA CACAGCAAAC AAGACAAAAT CATCAGCCGC
151 GCCCAAGCCS AAAAAGCAGC GTTGGCGCGT GTCGGCGGCA AAATCACCAG
201 CATCGATCTC GAACACGACA ACGGCCGTCC GCACTATGAT GTCGAAATCG
251 TCAAAAACGG ACAGGAATAC AAAGTCGTTG TCGATGCCCG TACCGGCCGC
301 GTGATTTCTC CCCGCCGCGA CGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2940; ORF 959.a>:

```

a959.pep
1  MNFKRLLLLTA AATALMGISA PALAHHDGHG DDDHGHAHQ HSKQDKIISR
51  AQAEKAALAR VGGKITDIDL EHDNGRPHYD VEIVKNGQEY KVVVDARTGR
101 VISSRRDD*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*ORF 959 shows 94.4% identity over a 108 aa overlap with a predicted ORF (ORF 959) from *N. meningitidis*

a959/m959 94.4% identity in 108 aa overlap

```

      10      20      30      40      50      60
a959.pep  MNFKRLLLLTAATALMGISAPALAHHDGHGDDDHGHAHQHSKQDKIISRAQAEKAALAR
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m959      MNIKHLLLTSAATALLSISAPALAHHDGHGDDDHGHAHQHNKQDKIISRAQAEKAALAR
          10      20      30      40      50      60

      70      80      90     100     109
a959.pep  VGGKITDIDLEHDNGRPHYDVEIVKNGQEYKVVVLEARTGRVISSRRDDX
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m959      VGGKITDIDLEHDNGRPHYDVEIVKNGQEYKVVVDARTGRVISSRRDDX
          70      80      90     100

```

g960.seq not found yet

g960.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2941>:

```

m960.seq
1  ATGCAAGTAA ATATTCAGAT TCCCTGTATG CTGTACAGAC GCGGGAGTGT
51 TAAGCCCCCT TTGTTTGAAG CTCGCGCGCT CTTGCCGAGC TTCACCGACC
101 CCGTTGTGCC CAAGCTCTCT GCTCCCGCGC GCTACATTGT CGACATCCCC
151 AAAGGCAATC TGAAAACCGA AATCGAAAAG CTGCCCAAAC AGCCCCAGTA
201 TGCTATCTCG AACAGCTCC AAGTAGCGAA AACGCTAAC TGGAAACCAG
251 TGCAACTGGC TTACGATAAA TGGGACTATA AGCAGGAAGG CTTAACCAGA
301 GCCGGTGCAG CGATTATCGC GCTGGCTGTT ACCGTGGTTA CTGCGGCGCG
351 GGGACTCGGA GCCGCACTAG GCTTAAACGG CGCAGCGGCA GCAGCGGCCG
401 ATGCCGCCTT TGCCTCACTC GCTTCTCAGG CTTCCGTATC GCTCATCAAC
451 AATAAAGGCG ATGTCGGCAA AACCTCAAG GAACTGGGCA GAAGCCGCAC
501 GGTAAAAAAT CTGGTTGTAG CGCGGCAAC GGCAGGCGTA TCCAACAAAC

```

```

551 TCGGTGCCCTC TTCCCTTGCC ACTTGGAGCG AAACCCCTTG GGTAACAAC
601 CTCACGTTA ACCTGGCCAA TGGGGCAGT GCCCGCTGA TCAACACCCG
651 TGTTAACGGC GGCAGCCTGA AAGACAATCT GGAGGCAAT ATCCTGGCGG
701 CATTGGTGAA TACCGCGCAT GGGGAGGCGG CGAGTAAGAT CAAAGGACTG
751 GATCAGCACT ATGTGCGCCA CAAAATCGCT CATGCCGTAG CGGGCTGTGC
801 GGCTGCAGCG CGGAATAAGG CCAATGTCA GGACGGCGCG ATCGGTGCGG
851 CTGTGGGTGA GATTGTGCGG GAGGCTTTGG TAAAAATAC CGATTTTAGC
901 GATATGACCC CGGAACAATT AGATCTGGAA GTTAAGAAA TTACCGCCTA
951 TGCCAACTT GCGGCAGGTA CAGTTGCAGG CGTAACGGGA GGAGATGTCA
1001 ATACTGCTTC ACAACCCGCA CAAAACGCGG TAGAAAAATA TGCGGTTAAA
1051 GCTGTGTGTA CTGCTGCAAA AGTGGTTTAT AAGGTAGCCA GAAAAGGATT
1101 AAAAAACGGG AAAATCAACG TTAGAGATT AAAACAGACG TTGAAAGACG
1151 AAGGTTATAA TTTAGCCGAC AACCTGACCA CCTTATTGGA CGAAACATTG
1201 GATTGGAACG ATGCCAAAGC CGTTATTGAT ATTGTCGTCG GAACAGAGCT
1251 GAAATCGCGCT AATAAAGGGG AAGCGGCACA AAAGGTCAAG GAAGTTTATG
1301 AAAAAAATCG TCCTTATATC CCTAATAAAG GTGCTGTACC GAATATGAGT
1351 ACATACATGA AAAATAATCC TTTTGAAAAA CAGCTGGCTC AAATTCAGA
1401 AAAGACAACG CTTCCGACGC AGCAAGGGCA GTCTGTCTTC TTGGTAAAAA
1451 GAAACCAAGG GTTATTAAAA ACCGGTGATA GGTTTATTT AGATGGCCAA
1501 CATAAAATC ATTTAGAGGT TTTTGATAAA AATGGAACT TTAAGTTTGT
1551 TCTAAATATG GATGGTTCGC TTAACCAAT GAAAACTGGG GCAGCAAAA
1601 GTCGTAAATT AAACCTAAAA TAG

```

This corresponds to the amino acid sequence <SEQ ID 2942; ORF 960>:

```

m960.pep
1  MQVNIQIPCM LYRRGSVKPF LFEAPRLLPs FTDPVVPKLS APGGYIVDIP
51  KGNLKEIEK LAKQPEYAYL KQLOVAKNVN WNQVQLAYDK WDKQEGLTR
101 AGAAIALAV TVVTAGAGVG AALGLNGAAA AAADAASFASL ASQASVSLIN
151 NKGDVGGKPLK ELGRSRTVKN LVVAAATAGV SNKLGAASSL TWSETPWVNN
201 LNVNLANAGS AALINTAVNG GSLKDNLEAN ILAALVNTHA GEAAASKIKGL
251 DQHYVAHKIA HAVAGCAAAA ANKGKCDJGA IGAARVEIVG EALVKNTDFS
301 DMTPEQLDLE VKKITAYARK AAGTVASVTG GDVNTAAQTA QNAVENNAVK
351 AVVTAAKVYV KVARGLKNG KINVRDLKQT LKDEGYNLAD NLTLFDETL
401 DWNDKAVID IVVGTELNRA NKGEEAQKVK EVLEKNRPYI PNKGAVPNMS
451 TYMKNNPFCK QLAQISEKTT LPTQQGQSVF LVKRNQGLLK TGDRFYLDGQ
501 HKNHLEVFCK NGNFKFVLMN DGSLNQMKTG AAKGRKLNK *

```

a960.seq not found yet

a960.pep not found yet

g961.seq not found yet

g961.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2943>:

```

m961.seq
1  ATGAGCATGA AACACTTTCC AGCCAAAGTA CTGACCACAG CCATCCTTGC
51  CACTTTCTGT AGCGGCGCAC TGGCAGCCAC AAGCGACGAC GATGTTAAAA
101 AAGCTGCCAC TGTGGCCATT GTTGCTGCCT ACAACAATGG CCAAGAAATC
151 AACGGTTTCA AAGCTGGAGA GACCATCTAC GACATTGGTG AAGACGGCAC
201 AATTACCCAA AAAGACGCAA CTGCAGCCGA TGTGAAGCC GACGACTTIA
251 AAGGTCTGGG TCTGAAAAAA GTCGTGAATA ACCTGACCAA AACCGTCAAT
301 GAAPACAAAC AAAACGTCGA TGCCAAAGTA AAAGCTGCAG AATCTGAAAT
351 AGAPAAAGTTA ACAACCAAGT TAGCAGACAC TGATGCCGCT TTAGCAGATA
401 CTGATGCCGC TCTGGATGAA ACCACCAACG CCTTGAATAA ATTGGGAGAA
451 AATATAACGA CATTTGCTGA AGAGACTAAG ACAAAATATCG TAAAAATTGA
501 TGAPAAATTA GAAGCCGTGG CTGATACCGT CGACAAGCAT GCCGAAGCAT
551 TCAACGATAT CGCCGATTCA TTGGATGAAA CCAACACTAA GGCAGACGAA
601 GCCGTCAAAA CCGCCAATGA AGCCAAACAG ACGGCCGAAG AAACCAACAA
651 AAACGTCGAT GCCAAAGTAA AAGCTGCAGA AACTGCAGCA GGCAAGCCG
701 AAGCTGCCGC TGGCACAGCT AATACTGCAG CCGACAAGGC CGAAGCTGTC
751 GCTCAAAAAG TTACCGACAT CAAAGCTGAT ATCGCTACGA ACAAAGCTGA
801 TATIGCTAAA AACTCAGCAC GCATCGACAG CTTGGACAAA AACGTAGCTA
851 ATCTGCGCAA AGAAACCCGC CAAGGCCTTG CAGAACAAGC CGCGCTCTCC
901 GGCCTGTTCC AACCTTACAA CGTGGGTCGG TTCAATGTAA CGGCTGCACT
951 CGGCGGCTAC AAATCCGAAT CGGCAGTCGC CATCGGTACC GGCTTCCGCT
1001 TTACCGAAAA CTTTCCCGCC AAAGCAGGCG TGGCAGTCGG CACTTCGTCC
1051 GGTCTCTCCG CAGCCTACCA TGTCGGCGTC AATTACGAGT GGTAA

```

This corresponds to the amino acid sequence <SEQ ID 940; ORF 2944>:

```

m961.pep
1  MSMKHFEPAKV LTTAILATFC SGALAAATSDD DVKKAATVAI VAAVNNQGEI

```

```

51  NGFKAGETIY DIGEDGTITQ KDATAADVEA DDFKGLGLKK VVTNLTKTVN
101 ENKQNVDAKV KAAESEIEKL TTKLADTDAA LADTDAALDE TTNALNKLGE
151 NITTFAEETK TNIVKIDEKL EAVADTVDKH AEA FNDIADS LDETNTKADE
201 AVKTANEAKQ TAEETKQNV D AKV KAAETAA GKAEAAA GTA NTAADKAEAV
251 AAKVTDIKAD IATNKADIAK NSARIDSLDK NVANLRKETR OGLAEQAAALS
301 GLFQPINVGR FNVTAAVGGY KSESAVAIGT GFRFTENFAA KAGVAVGTSS
351 GSSAAYHVG V NYEW*

```

a961.seq not found yet

a961.pep not found yet

g972.seq not found yet

g972.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2945>:

```

m972.seq
1  TTGACTAACA GGGGGGGAGC GAAATTAAAA ACCAATTCCA AGAGTAGTGA
51  ACGAATGAGT GAAGTTGAAT ATTTCTCACA CTTTATATCG GACGGAAAAG
101 GGAAGCTTTT AGAAATTCCG CAGCGAAGAG GTAAGCAAGA CggGGTTTTT
151 GTTGATTGGA TTTCATTCAC ATTCCATGAA GATACTTTAC TGAAAGTTTC
201 CGGTTGCCCT TTATTTCTG ATGCTGAATA CATGTATGTA TTAAGCAGAA
251 AGCTGGAAGA AATTCTAGGT TTTGGCATAA CGCGCAAATG CAAATCAAGG
301 GGCAACAAAT TCTATGAATC CATGTATAGG TTAGGTTCCG ATGATGTTGA
351 TTATGGAGAG GTGCATTTCTG GArGTCAGCG CAATACTGTT TTAGTTGAGT
401 TGAAAGGTAC TGGTTGCAGC GTTGCAAGTC CGGGTTGGGA GTTGAGGCTA
451 AAGCAGTTTC TCGATGATT C GATAAGGACA AGAATAACGC GAATTGACCT
501 AGCACTTGAT TTTTTTGATG GAGAGTACAC GCCGGATCAG GCGTTGTTAG
551 ATCAGCATAA TGGTTTTTTT GATAACAGCA ATCAAAGGCC GAAATCTGAA
601 ACGATCGGTA CGGCTTGGCG GAATGAGGAC GGGAGCGGCA AGACATTTTA
651 TGTAGGTCGC AAGAAAAATT CTCGTTTGT TCGTGTATTAT GAGAAAGGCA
701 GGCAGCTTGG AGATAAAGAA AGCAAATGGG TAAGGTTCTGA GATCCAGTTT
751 AATTATGGAG ATATAGAAAT ACCCTTGGAT ATTTTAATAA ATCAGGTTTC
801 GTATTTCTGT GGAGCTTTTC CAATTGTAG AAAATTTAAA AATATGCCGG
851 TTCCCGAAAG GTTTGATCAG AGAAAGAAAA AGCTTAATTT AACTTTTCGAG
901 CATAAATTGC ATTACGCGAA AAACGCGGTT GGAAAACTGG TCAATTTTCAT
951 GATTGAAATG GGTTTTGATA ATAGCGAAAT TGTGGAATCT TTAAGGCGAG
1001 ATTCGGGATT TCCCAAAGGA TTAGAACCTG AAAAATATGC TCTGGAAATG
1051 TTAAGGGACG GTTTGAAACA CGGTTTATT CATGAACAGC CGGATATTGA
1101 TTTGAAATT GAACCTGATG AATTGGGGGT TATTGCTTTT AAAAATTCTG
1151 ACAAATTCGA TAGGGAAAAA AGGCTTTTTA GTCCTGATTA TGATGTCGAG
1201 AAAGAAAGGA AATATCAGGA ATATTTAAGT AAAGTTTATC ATCAAATGT
1251 AGATTATGAT TATTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2946; ORF 972>:

```

m972.pep
1  LTNRGGAKLK TXSKSSERMS EVEYFSHFIS DGKGKLEIP QRRGKQDGVF
51  VDWISFTFHE DTLLKVSGCP LFSDAEYMYV LSRKLEEILG FGITRKCKSR
101 GNKFYESMYR LGSDDVDYGE VHFGXQRNTV LVELKGTGCS VASPGWELRL
151 KQFLDDSI RTITRIDLALD FFDGEYTPDQ ALLDHDNGFF DNSNORPKSE
201 TIGTAWRNE DSGKTFYVGR KKNSRFVRVY EKGRQLGDKE SKNVRFEIQF
251 NYGDIPIPLD ILINQGSYFC GAFFICRKFK NMPVPERFDQ RKXKLNLTFE
301 HKLHYAKNAV GKLNVNFIEM GFDNSEIVES LKADSGFPKG LEPEKYALEM
351 LRDGLKHGFI HEQPDIDLEI ELDELGVIAF KNSDKFDREK RLSPDYDVE
401 KERKQYEYLS KVIYHONVDYD YF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2947>:

```

a972.seq
1  TTGACTAACA GGGGGGGAGC GAAATTAAAA ACCAATTCCA AGAGTAGTGA
51  ACGAATGAGT GAAGTTGAAT ATTTCTCACA CTTTATATCG GACGGAAAAG
101 GGAAGCTTTT AGAAATTCCG CAGCGAAGAG GTAAGCAAGA CGGGGTTTTT
151 GTTGATTGGA TTTCATTCAC ATTCCATGAA GATACTTTAC TGAAAGTTTC
201 CGGTTGCCCT TTATTTCTG ATGCTGAATA CATGTATGTA TTAAGCAGAA

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```

251 AGCTGGAAGA AATTCTAGGT TTTGGCATAA CGCGCAAATG CAAATCAAGG
301 GGCAACAAAT TCTATGAATC CATGTATAGG TTAGGTTTCG ATGATCTTGA
351 TTATGGAGAG GTGCATTTTC GAGGTCAGCG CAATACTGTT TTAGTTGAGT
401 TGAAAGGTAC TGGTTGCAGC GTTGCAAGTC CGGGTTGGGA GTTGAGGCTA
451 AAGCAGTTTC TCGATGATTC GATAAGGACA AGAATAACGC GAATTGACCT
501 AGCACTTGAT TTTTTTGATG GAGAGTACAC GCCGGATCAG GCGTTGTTAG
551 ATCACGATAA TGGTTTTTTT GATAACAGCA ATCAAAGGCC GAAATCTGAA
601 ACGATCGGTA CGGCTTGGCG GAATGAGGAC GGGAGCGGCA AGACATTTTA
651 TGTAGGTCGC AAGAAAAATT CTCGTTTGT TCGTGTTTAT GAGAAAGGCA
701 GGCAGCTTGG AGATAAGAA AGCAAATGGG TAAGGTTTCGA GATCCAGTTT
751 AATTATGGAG ATATAGAAAT ACCCTTGGAT ATTTTAATAA ATCAGGGTTC
801 GTATTTCTGT GGAGCTTTTC CAATTGTAG AAAATTTAAA AATATGCCGG
851 TTCCCGAAAG GTTTGATCAG AGAAAGAAAA CGCTTAATTT AACTTTCGAG
901 CATAAATTGC ATTACGCGAA AAACGCGGTT GGAAAACCTGG TCAATTTTCA
951 GATTGAAATG GGTTTTGATA ATAGCGAAAT TGTGGAATCT TTAAAGGCAG
1001 ATTCGGGATT TCCCAAAGGA TTAGAACCTG AAAAATATGC TCTGGAATG
1051 TTAAGGGACG GTTTGAAACA CGGTTTTATT CATGAACAGC CGGATATTGA
1101 TTTGGAATTT GAACCTTGATG AATTGGGGGT TATTGCTTTT AAAAAATCTG
1151 ACAAATTCGA TAGGGAAAAA AGGCTTTTTA GTCCTGATTA TGATGTCGAG
1201 AAAGAAAGGA AATATCAGGA ATATTAAAGT AAAGTTTATC ATCAAATGT
1251 AGATTATGAT TATTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2948; ORF 972.a>:

```

a972.pep
1  LTNRGGAKLK TNSKSSERMS EVEYFSHFIS DGKKGKLEIP QRRGKQDGVF
51  VDWSIFTFHE DTLKVS GCP LFSDAEYMYV LSRKLEEILG FGITRKCKSR
101 GNKFYESMYR LGSDDVDYGE VFHGGQRNTV LVELKGTGCS VASPGWELRL
151 KQFLDDSI RTITRIDLALD FFDGEYTPDQ ALLDHDNGFF DNSNQRPKSE
201 TTGTAWRNED GSGKTFYVGR KKNRSFVRVY EKGRQLGDKE SKWVRFEIQF
251 NYGDIEIPLD ILINQGSYFC GAFFICKRKF NMPVPERFDQ RKKTNLNLTFE
301 HKLHYAKNAV GKLVNFMIE M GFDNSEIVES LKADSGFPG LEPEKYALEM
351 LRDGLKHGFI HEQPDIDLEI ELDELGVIAF KNSDKFDREK RLFSPDYDVE
401 KERKYQEYLS KVIHQNVVDYD YF*

```

m972/a972 99.3% identity in 422 aa overlap

	10	20	30	40	50	60
m972.pep	LTNRGGAKLKTXSKSSERMSEVEYFSHFISDGKKGKLEIPQRRGKQDGVFVDWSIFTFHE					
a972	LTNRGGAKLKTNKSSERMSEVEYFSHFISDGKKGKLEIPQRRGKQDGVFVDWSIFTFHE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m972.pep	DTLLKVS GCP LFSDAEYMYVLSRKLEEILGFGITRKCKSRGNKFYESMYRLGSDDVDYGE					
a972	DTLLKVS GCP LFSDAEYMYVLSRKLEEILGFGITRKCKSRGNKFYESMYRLGSDDVDYGE					
	70	80	90	100	110	120
	130	140	150	160	170	180
m972.pep	VFHGXQRNTVLVELKGTGCSVASPGWELRLKQFLDDSI RTITRIDLALD FFDGEYTPDQ					
a972	VFHGGQRNTVLVELKGTGCSVASPGWELRLKQFLDDSI RTITRIDLALD FFDGEYTPDQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
m972.pep	ALLDHDNGFFDNSNQRPKSETIGTAWRNEDGSGKTFYVGRKKNSRFVRVYEKGRQLGDKE					
a972	ALLDHDNGFFDNSNQRPKSETIGTAWRNEDGSGKTFYVGRKKNSRFVRVYEKGRQLGDKE					
	190	200	210	220	230	240
	250	260	270	280	290	300
m972.pep	SKWVRFEIQFNYGDIEIPLDILINQGSYFCGAFFICKRKFKNMPVPERFDQKKKLNLTFE					
a972	SKWVRFEIQFNYGDIEIPLDILINQGSYFCGAFFICKRKFKNMPVPERFDQKKKLNLTFE					
	250	260	270	280	290	300

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	310	320	330	340	350	360
m972.pep	HKLHYAKNAVGKLVNEMIEMGFDNSEIVESLKADSGFPKGLEPEKYALEMLRDGLKHGFI					
a972	HKLHYAKNAVGKLVNEMIEMGFDNSEIVESLKADSGFPKGLEPEKYALEMLRDGLKHGFI					
	310	320	330	340	350	360
	370	380	390	400	410	420
m972.pep	HEQPDIDLEIELDELGVIAFKNSDKFDREKRLFSPDYDVEKERKYQEYLSKVYHQNVVDYD					
a972	HEQPDIDLEIELDELGVIAFKNSDKFDREKRLFSPDYDVEKERKYQEYLSKVYHQNVVDYD					
	370	380	390	400	410	420
m972.pep	YFX					
a972	YFX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2949>:

g973.seq

```

1  ATGGACGGCG CACAACCGAA AACAAATTTT TTTGAACGCC TGATTGCCCG
51  actCGCCCGC GAACCCGATT CCGCCGAAGA CGTATTAAAC CTGCTTCGGC
101 AGGCGCACGA ACAGGAAGTT TTTGATGCCG ACACACTGAC CCGCTGGAA
151 AAAGTATTGG ACTTTGCCGA GCTGGAAGTG CGCGATGCGA TGATTACGCG
201 CAGCCGCATG AACGTATTGA AAGAAAACGA CAGCATCGAA CGCATACCG
251 CCTACGTCAT CGATACCGCC CATTCGCGCT TCCCGTCAT CGCGGAAGAC
301 AAAGACGAAG TTTTGGGCAT TTTGCACGCC AAAGACCTGC TCAAATATAT
351 GTTCAACCCC GAGCAGTTCC ACCTGAAATC CGTCTTGCGC CCTGCCGTTT
401 TCGTGCCCGA AGGCAAATCT TTGACCGCCC TTTTAAAAGA GTTCCGCGAA
451 CAGCGCAACC ATATGGCAAT CGTCATCGAC GAATACGGCG GCACGTCGGG
501 TTTGGTCACC TTTGAAGACA TCATCGAGCA aatcgtcggt gacaTCGAAG
551 ACGAGTTTGA CGAAGACGAA AGCGccgacg acatCCACTC cgTTTccgCC
601 GAACGCTGGC GCATCCacgc ggctaCCGAA ATCGAAGaca TCAACGCCTT
651 TTTCCGTACG GAatacggca gcgaaagaagc cgacaccatc ggcggtTGG
701 TCATTCAGGA ATTGGGACAC CTGCCCGTGC GCGGCGAAAA AGTCCTTatc
751 .ggcgGTTTGC agttcaccgt CGCCCGCGCC GACAACCGCC GCCTGCACAC
801 GCTGATGGCG ACCCGCGTGA AGTAAGCAGA GCCTGCCcgc accgcggttT
851 CTGCacAGTT TAG

```

This corresponds to the amino acid sequence <SEQ ID 2950; ORF 973.ng>:

g973.pep

```

1  MDGAQPKTNF FERLIARLAR EPDSAEDVLN LLRQAHEQEV FDADTLTRLE
51  KVLDFAELEV RDAITRSM NVLKENDSIE RITAYVIDTA HSRFPVIGED
101 KDEVLGILHA KDLLKYMFPN EQPHLKSCLR PAVFVPEGKS LTALLKEFRE
151 QRNHMAIVID EYGGTSGLVF FEDIIEQIVG DIEDEFDEDE SADDIHSVSA
201 ERWRIHAATE IEDINAFPGT EYGSEEDTI GGLVIQELGH LPVRGEKVL
251 GGLQFTVARA DNRRHLTLMA TRVK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2951>:

m973.seq

```

1  ATGGACGGCG CACAACCGAA AACGAATTTT TTTGAACGCC TGATTGCCCG
51  ACTCGCCCGC GAACCCGATT CCGCCGAAGA CGTATTAAAC CTGCTTCGGC
101 AGGCGCACGA GCAGGAAGTT TTTGATGCCG ATACGCTTTT AAGATTGGAA
151 AAAGTCTCTG ATTTTCCGA TTTGGAAGTG CGCGACGCGA TGATTACGCG
201 CAGCCGTATG AACGTTTTAA AAGAAAACGA CAGCATCGAG CGCATACCG
251 CCTACGTTAT CGATACCGCC CATTCGCGCT TCCCGTCAT CGCGGAAGAC
301 AAAGACGAAG TTTTGGGCAT TTTGCACGCC AAAGACCTGC TCAAATATAT
351 GTTTAACCCC GAGCAGTTCC ACCTCAAATC CATTCTCCGC CCCGCCGTCT
401 TCGTCCCCGA AGGCAAATCG CTGACCGCCC TTTTAAAAGA GTTCCGCGAA
451 CAGCGCAACC ATATGGCGAT TGTATCGAC GAATACGGCG GCACATCCGG
501 CTTGGTCACC TTTGAAGACA TCATCGAGCA AATCGTCGGC GAAATCGAAG
551 ACGAGTTTGA CGAAGACGAT AGCGCCGACA ATATCCATGC CGTTTCTTCm
601 GaACGcTGCG GCATCCATGC AGTACCAGAA ATCGAAGACA TCAACACCTT

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651 CTTCCGCACG GAATACAGCA kCGAAGAAGC CGACACCATT GCGGGCCTGG
701 TCATTCAAGA GTTGGGACAT CTGCCCCGTGC GCGGCGAAAA AGTCCTTATC
751 GCGCGTTTGC AGTTCACCGT CGCACGCGCC GACAACCGCC GCCTGCATAC
801 GCTGATGGCG ACCCGCGTGA AGTAA

m973.ppt

1	MDGAQPKTN	FERLIARLAR	EPDSAEDVLN	LLRQAHEQEV	FADTLLRLR
51	KVLEDFSDLE	RDAMITRSRM	NVLKENDSIE	RITAYVIDTA	HSRFVPIGED
101	KDEVLGILHA	KDLKXYMFNP	EQFHLKSILR	PAVFVPEKGS	LTALLKEVER
151	QRNHMAIVID	EYGGTSGLVT	FEDIIEQIVG	EIEDEFDEDD	SADNIHAVSS
201	ERWRTHAATE	IEDINTFFGT	EYSXEEADTI	GGLVIQBLGH	LPVRGEKVL
251	GGLOFTVARA	DNRRLHLMTA	TRVK*		

Homology with a predicted ORF from *N. gonorrhoeae*

from *N. gonorrhoeae*:

m973/q973

	10	20	30	40	50	60
m973 . pep	MDGAQPKTNFFERLIARLAREPDSAEDVLNLLRQAHEQEVFDADTLRLREKVLDFSDLEV					
g973	MDGAQPKTNFFERLIARLAREPDSAEDVLNLLRQAHEQEVFDADTLRLREKVLDFAELEV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m973 . pep	RDAMITRSRMNVLKENDSIERITAYVIDTAHSRFPVIGEDKDEVLGILHAKDLLKYMFPN					
g973	RDAMITRSRMNVLKENDSIERITAYVIDTAHSRFPVIGEDKDEVLGILHAKDLLKYMFPN					
	70	80	90	100	110	120
	130	140	150	160	170	180
m973 . pep	EQFHLKSIILRPVFPVEGKSLTALLKEFREQRNHMAIVIDEYGGTSGLVTFEDIIEQIVG					
g973	EQFHLKSVLRPAVFPVEGKSLTALLKEFREQRNHMAIVIDEYGGTSGLVTFEDIIEQIVG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m973 . pep	EIEDEFDEDDSDADNIHAVSSERWRIHAATEIEDINTFFGTEYSXEADTIGGLVIQELGH					
g973	DIEDEFDEDESADDIHSVAERWRIHAATEIEDINAFFGTEYGSBADTIGGLVIQELGH					
	190	200	210	220	230	240
	250	260	270			
m973 . pep	LPVRGEKVLIGGLQFTVARADNRRLHTLMATRVKX					
g973	LPVRGEKVLIGGLQFTVARADNRRLHTLMATRVKX					
	250	260	270			

a973.seq

1	ATGGACGGCG	CACAACCGAA	AACAAATTTT	TTTGAACGCC	TGATTGCCCG
51	ACTCGCCCGC	GAACCCGATT	CCGCGGAGA	CGTATTGACC	CTGTTGCCCG
101	AAGCGCAGCA	ACAGGAAGTA	TTTGATCGGT	ATACGCTTTT	AGAATTGGAA
151	AAAGTCTCTG	ATTTTCTGA	TTTGAAGTG	CGCGACGGCA	TGATTACCGC
201	CAGCCGTATG	AACGTTTTAA	AAGAAAACGA	CAGCATCGAA	CGCATCACCG
251	CCTACGTTAT	CGATACCCGC	CATTCTCGCT	TCCCGCATAT	CGGTGAAGAC
301	AAAGACGAAG	TTTTGGGTAT	TTTGCACGCC	AAAGACCTGC	TCAAATATAT
351	GTTCAACCCC	GAGCAGTTC	ACCTCAAATC	GATATTGGCG	CTCGCGCTCT
401	TCGTCCCCGA	AGGCAAATCG	CTGACCGCCC	TTTTAAAAGA	GTTCGCGGAA
451	CAGCGCAACT	ATATGGCAAT	CGTATCGCAC	GAATACGGCG	GCACCTCGGG
501	TTTGGTAACC	TTTGAAGACA	TCATCGAGCA	AATCGTCGGC	GACATCGAAG
551	ATGAGTTTGA	CGAAGACGAA	AGCGCGGACA	ACATCCACGC	CGTTTCCGGC

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601 GAACGCTGGC GCATCCACGC GGCTACCGAA ATCGAAGACA TCAACGCCTT
651 TTTCGGCACG GAATACAGCA GCGAAGAAGC CGACACCATC GGCGGCCTGG
701 TCATTCAGGA ATTGGGACAC CTGCCCCTGC GCGGGCAAAA AGTCCTTATC
751 GGCGGTTTGC AGTTCACCGT CGCCCGCGCC GACAACCGCC GCCTGCATAC
801 GCTGATGGCG ACCCGCGTGA AGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2954; ORF 973.a>:

```

a973.pep
  1 MDGAQPKTNF FERLIARLAR EPDSAEDVLT LLRQAHEQEV FDADTLRLLE
 51 KVLDFSDLEV RDAMITRSRM NVLKENDSIE RITAYVIDTA HSRFPVIGED
101 KDEVLGILHA KDLLKYMFP EQFHLKSILR PAVFVPEGKS LTALLKEFRE
151 QRNHMAIVID EYGGTSGLVF FEDIIEQIVG DIEDEFDEDE SADNIHAVSA
201 ERWRIHAATE IEDINAFFGT EYSSEEADTI GGLVIQELGH LPVRGEKVL I
251 GGLQFTVARA DNRRLHTLMA TRVK*

```

m973/a973 97.8% identity in 274 aa overlap

	10	20	30	40	50	60
m973.pep	MDGAQPKTNFFERLIARLAREPDSAEDVLTLLRQAHEQEVFDADTLRLLEKVLDFSDLEV					
a973	MDGAQPKTNFFERLIARLAREPDSAEDVLTLLRQAHEQEVFDADTLRLLEKVLDFSDLEV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m973.pep	RDAMITRSRMNVLKENDSIERITAYVIDTAHSRFPVIGEDKDEVILGHAKDLLKYMFP					
a973	RDAMITRSRMNVLKENDSIERITAYVIDTAHSRFPVIGEDKDEVILGHAKDLLKYMFP					
	70	80	90	100	110	120
	130	140	150	160	170	180
m973.pep	EQFHLKSILRPAVFVPEGKSLTALLKEFREQRNHMAIVIDEYGGTSGLVTFEDIIEQIVG					
a973	EQFHLKSILRPAVFVPEGKSLTALLKEFREQRNHMAIVIDEYGGTSGLVTFEDIIEQIVG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m973.pep	EIEDEFDEDDSDADNIHAVSSERWRIHAATEIEDINTFFGTEYSXEEADTIGGLVIQELGH					
	:					
a973	DIEDEFDEDESADNIHAVSAERWRIHAATEIEDINAFFGTEYSSEEADTIGGLVIQELGH					
	190	200	210	220	230	240
	250	260	270			
m973.pep	LPVRGEKVLIGGLQFTVARADNRRLHTLMATRVKX					
a973	LPVRGEKVLIGGLQFTVARADNRRLHTLMATRVKX					
	250	260	270			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2955>:

```

g981.seq
  1 ATGAAAAAAT GGATTGCCGC CGCCCTTGCC TGTTCGCAC TCGCGCTGTC
 51 TGCCCTGCGC GGTCAAGGCA AAGATGCCGC CGCGCCTGCC GCCAACCCCG
101 GCAAAGTGTA CCGCGTGGCT TCCAACGCCG AGTTTGCCCC CTTTGAATCT
151 TTAGACTCGA AAGGCAATGT CGAAGGTTTC GACGTGGATT TGATGAACGC
201 GATGGCGAAG GCGGGCAATT TAAAAATCGA ATTCAAACAC CAGCCGTGGG
251 ACAGCCTTTT CCCCGCCTTG AACAAACGGC ATGCGGACGT TGTGATGTCG
301 GCGTAACCA TTACCGACGA CCGCAAACAG TCTATGGATT TCAGCGACCC
351 GTATTTTGAA ATCACCCAAG TCGTCCTCGT TCCGAAAGGC AAAAAAGTAT
401 CTCTCTCCGA AGATTGAAA AAGATGAACA AAGTCGGCGT GGTACCGGC
451 CACACGGGCG ATTTCTCGT TTCCAAACTC TTGGGCAACG ACAATCCGAA
501 AATCGCGCGC TTCGAAAACG TCCCCCTGAT TATCAAAGAA CTGGAACACG
551 GCGGCTTGGA TTCCGTGGTC AGCGACAGCG CGGTACATCG CAATTATGTG
601 AAAACAACCC CGGCCAAAGG AATGGACTTC GTTACCCTGC CCGACTTCAC
651 CACCGAACAC TACGGCATCG CGGTACGCAA AGGCGACGAA GCAACCGTCA
701 AAATGCTGAA CGATGCGTTG GAAAAAGTAC GCGAAAGCGG CGAATACGAC
751 AAGATCTACG CCAATATTTT TGCCAAAGAG GCGGACAGG CTGCGAAATA
801 A

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1383

This corresponds to the amino acid sequence <SEQ ID 2956; ORF 981.ng>:

g981.pep
 1 MKKWIAAALA CSALALSACG GQKDAAPA ANPGKVYRVA SNAEFAPFES
 51 LDSKGNVEGF DVDLMNAMAK AGNFKIEFKH QPWSLFPAL NNGDADVMS
 101 GVTITDDRKO SMDFPSDPYFE ITQVVLVPGK KKVSSSEDLK KMNKVGVTG
 151 HTGDFSVSKL LGNDNPKIAR FENVPLIIKE LENGGLDSVV SDSAVIANV
 201 KNNPAKGMDF VTLPDFTTEH YGIAVRKGDE ATVKMLNDAL EKVRESGEYD
 251 KIYAKYFAKE GGQAAK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2957>:

m981.seq
 1 ATGAAAAAAT GGATTGCCGC CGCCCTTGCC TGTTCGCGC TCGCGCTGTC
 51 TGCCTGCGGC GGTCAGGGCA AAGA7ACCGC CGCGCTGCCC GCCAACCCCG
 101 ACAAAAGTGA CCGCGTGGCT TCCAACGCCG AGTTTGCCCC CTTTGAATCT
 151 TTAGACTCGA AAGGCAATGT CGAAGGTTTC GATGTGGATT TGATGAACGC
 201 GATGGCGAAG GCGGGCAATT TTAATAATCGA ATTCAAACAC CAGCCGTGGG
 251 ACAGCCTTTT CCCCGCCTTA AACACGGCG ATGCGGACGT TGTGATGTCG
 301 GCGGTAACCA TTACCGACGA CCGCAAACAG TCTATGGACT TCAGCGACCC
 351 GTATTTTGAA ATCACCAGG TCGTCTCTGT TCCGAAAGGC AAAAAAGTAT
 401 CTCTCTCCGA AGATTTGAAA AACATGAACA AAGTCGGCGT GGTACCCGGC
 451 TACACGGGCG ATTTCTCCGT ATCCAACTC TTGGGCAACG ACAATCCGAA
 501 AATCGCGCGC TTGAAAACG TTCCCTGAT TATCAAAGAA CTGGAACG
 551 GCGGCTTGA TTCCGTGGTC AGCGACAGCG CGGTATCGC CAATTATGTG
 601 AAAACAATC CGGCCAAGG GATGGACTTC GTTACCCTGC CCGACTTCAC
 651 CACCGAACAC TACGGCATCG CGGTACGCAA AGGCGACGAA GCAACCGTCA
 701 AAATGCTGAA CGATGCGTTG GAAAAGTAC GCGAAAGCGG CGAATACGAC
 751 AAGATTACG CCAATATTT TGCAAAAGAA GACGGACAGG CCGCAAAATA
 801 A

This corresponds to the amino acid sequence <SEQ ID 2958; ORF 981>:

m981.pep
 1 MKKWIAAALA CSALALSACG GQKDTAAPA ANPDKVYRVA SNAEFAPFES
 51 LDSKGNVEGF DVDLMNAMAK AGNFKIEFKH QPWSLFPAL NNGDADVMS
 101 GVTITDDRKO SMDFPSDPYFE ITQVVLVPGK KKVSSSEDLK KMNKVGVTG
 151 YTGDFSVSKL LGNDNPKIAR FENVPLIIKE LENGGLDSVV SDSAVIANV
 201 KNNPAKGMDF VTLPDFTTEH YGIAVRKGDE ATVKMLNDAL EKVRESGEYD
 251 KIYAKYFAKE DGQAAK*

m981/g981 98.1% identity in 266 aa overlap

	10	20	30	40	50	60
981.pep	MKKWIAAALACSALALSACGGQKDTAAPAANPDKVYRVASNAEFAPFESLDSKGNVEGF					
g981	MKKWIAAALACSALALSACGGQKDAAPAAANPGKVYRVASNAEFAPFESLDSKGNVEGF					
	10	20	30	40	50	60
981.pep	DVDLMNAMAKAGNFKIEFKHQPWDSLFPALNNGDADVMSGVTITDDRKSMDFPSDPYFE					
g981	DVDLMNAMAKAGNFKIEFKHQPWDSLFPALNNGDADVMSGVTITDDRKSMDFPSDPYFE					
	70	80	90	100	110	120
981.pep	ITQVVLVPGKKVSSSEDLKMNKVGVTGTYTGDVSVSKLLGNDNPKIARFENVPLIIKE					
g981	ITQVVLVPGKKVSSSEDLKMNKVGVTGHTGDVSVSKLLGNDNPKIARFENVPLIIKE					
	130	140	150	160	170	180
981.pep	LENGGLDSVVSDSAVIANVYKNNPAKGMDFVTLPDFTTEHYGIAVRKGDEATVKMLNDAL					
g981	LENGGLDSVVSDSAVIANVYKNNPAKGMDFVTLPDFTTEHYGIAVRKGDEATVKMLNDAL					
	190	200	210	220	230	240
981.pep	EKVRESGEYDKIYAKYFAKEDGQAAKX					
g981	EKVRESGEYDKIYAKYFAKEGGQAAKX					
	250	260				
981.pep	EKVRESGEYDKIYAKYFAKEDGQAAKX					
g981	EKVRESGEYDKIYAKYFAKEGGQAAKX					
	250	260				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2959>:

```
a981.seq
1  ATGAAAAAAT GGATTGCCGC CGCCCTTGCC TGTTCCGCGC TCGCGCTGTC
51  TGCCTGCGGC GGTGAGGGTA AAGATGCCGC CGCGCCCGCC GCAAAATCCCG
101 ACAAAGTGTA CCGCGTGGCT TCCAACGCCG AGTTTCCCCC CTTTGAATCT
151 TTAGACTCGA AAGGCAATGT CGAAGGTTTC GATGTGGATT TGATGAACGC
201 GATGGCGAAG GCGGGCAATT TTAAATCGA ATTCAAACAC CAGCCGTGGG
251 ACAGCCTTTT CCCCGCCTTG AACACGGCG ATGCGGACGT TGTGATGTCG
301 GGCGTAACCA TTACCGACGA CCGCAAACAG TCTATGGACT TCAGCGACCC
351 GTATTTTGAA ATCACCACAG TCGTCTCGT TCCGAAAGGC AAAAAAATAT
401 CTTCTTCCGA AGATTGAAA AACATGAACA AAGTCGGCGT GGTAAACGGC
451 TACACGGGCG ATTTCTCCGT ATCCAAACTC TTGGGCAACG ACAACCCGAA
501 AATCGCGCGC TTTGAAAACG TTCCCTGAT TATCAAAGAA CTGGAAAACG
551 GCGGCTTGA TCCGTGGTC AGCGACAGCG CAGTCATCGC CAATTATGTG
601 AAAACAATC CGACCAAAGG GATGGACTTC GTTACCCTGC CCGACTTCAC
651 ACCGGAACAC TACGGCATCG CGGTACGCAA AGGCGACGAA GCAACCGTCA
701 AAATGCTGAA CGATGCGTTG AAAAAAGTAC GCGAAAGCGG CGAATACGAC
751 AAAATCTACG CCAATATTT TGCAAAAGAA GACGGACAGG CCGCAAAATA
801 A
```

This corresponds to the amino acid sequence <SEQ ID 2960; ORF 981.a>:

```
a981.pep
1  MKKWIAAALA CSALALSACG GQGKDAAAPA ANPDKVYRVA SNAEFAPFES
51  LDSKGNVEGF DVDLMNAMAK AGNFKIEFKH QPWSLFPAL NNGDADVMS
101 GVTITDDRKO SMDFSDPYFE ITQVVLVPKG KKISSSEDLK NMNKGVVGTG
151 YTGDFSVS KL LGNDNPKIAR FENVPLIIKE LENGGLDSV SV SDSAVIAN YV
201 KNNPTKGMDF VTLPDFTTEH YGIAVRKGDE ATVKMLNDAL KKVRESGEYD
251 KIIYAKYFAKE DGQAAK*
```

m981/a981 98.5% identity in 266 aa overlap

	10	20	30	40	50	60
m981.pep	MKKWIAAALACSALALSACGGQGKDAAAPAANPDKVYRVASNAEFAPFESLDSKGNVEGF					
a981	MKKWIAAALACSALALSACGGQGKDAAAPAANPDKVYRVASNAEFAPFESLDSKGNVEGF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m981.pep	DVDLMNAMAKAGNFKIEFKHQPWDSLFPALNNGDADVVMSSGVTITDDRKQSMDFSDPYFE					
a981	DVDLMNAMAKAGNFKIEFKHQPWDSLFPALNNGDADVVMSSGVTITDDRKQSMDFSDPYFE					
	70	80	90	100	110	120
	130	140	150	160	170	180
m981.pep	ITQVVLVPKGKVVSSSEDLKNMNKVGVTGYTGDFSVS KLLGNDNPKIARFENVPLIIKE					
a981	ITQVVLVPKGKVISSSEDLKNMNKVGVTGYTGDFSVS KLLGNDNPKIARFENVPLIIKE					
	130	140	150	160	170	180
	190	200	210	220	230	240
m981.pep	LENGGLDSVSDSAVIAN YVKNPNPAKGMDFVTLPDFTTEHYGIAVRKGDEATVKMLNDAL					
a981	LENGGLDSVSDSAVIAN YVKNPNPAKGMDFVTLPDFTTEHYGIAVRKGDEATVKMLNDAL					
	190	200	210	220	230	240
	250	260				
m981.pep	EKVRESGEYDKIIYAKYFAKEDGQAAKX					
a981	KKVRESGEYDKIIYAKYFAKEDGQAAKX					
	250	260				

1385

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2961>:

```

g982.seq
1   atcgcatcgc aaaaccttcg attcgacaat cgattcctcc aaaaaatggt
51  caacggcgTg aatattttgc cggccgcCga ttgggtagcC ttgGGcgCgCA
101 AAGGCCGCAA CGTGGTGGT GACCGCGCTT TCGGCGGCC GCACATCACC
151 AAAGACGGCG TAACCGTCGC CAAAGAAATC GAACTGAAAG ACAAGTTTGA
201 AAATATGGGC GCGCAAATGG TAAAAGAAGT CGCGTCCAAA ACCAaCgaCg
251 tagCCGgcga cggtagcact accgCCACCG TATTGGCACA ATCCATCGTT
301 GCCGAaggcA TGAAATACGT TACCGCCGGC ATGAACCCGA CCGATCTGAA
351 ACGCGGCATC GACAAAGccg ttgCCGCTtt ggttgAAGAg cTGAAAAACA
401 TCGCCAAACC TTGCGATACT TCCAAAGAAA TCGCCCAAGT CGGCTCGATT
451 TCCGCCAACT CCGACGAACA AGtcgGCCGg ATTATCGCCG AAGCGATGGA
501 AAAAGTCGGC AAAGAAGgcg tgattacCGT TGAAGACGGC AAATCTTTGG
551 AAAACGAGCT GGACGTGGTT GAAGGTATGC AGTTCGACCG CGGCTACCTG
601 TCCCTTACT TTATCAACGA CGCGAAAAA CAAATCGCCG GTCTGGACAA
651 TCCGTTTGTG TTGCTGTTTCG ACAAAAAAAT CAGCAACATC CGCGACCTG
701 TGCCCGTGTG GGAACAAGTG GCGAAAGCCA GCCGCCGCT GTTGATTATC
751 GCTGAAGACG TAGAAGGCGA AGCCTTGGCG ACTTTGGTCG TGAACAACAT
801 CCGCGGCATC CTGAAAACCG TTGCCGTCAA AGCccccggc tTCGGcGACC
851 GCCGCAAAAGC GATgctgcaa gaCATCGCCA TCCTGACcgg cggcgTagtG
901 ATTtccGAAG Aagtccggcct GTCTTTGGAA AAAgcgactT TGgacgaCTT
951 Gggtcaaacc aaACGcatCG AAATCGGtga agaaaacact ACCGTcATcg
1001 acgGCTTCGG CGACGcagcC CAAAtcgaag cgCGTGTTCG CGAAATCCGC
1051 CAACAAATCG AAACCGCGAC CAGCGATTAC GACAAAGAAA AACTGCAAGA
1101 GCGCGTTGCC AAATGGCAG GAGGCGTGGC AGTGATCAA STCGGCGCGG
1151 CGACCGAAGT CGAAATGAAA GAGAAAAAAG ACCGCGTGA AGACGCGCTG
1201 CACGCTACCC GCGCAGCCGT TGAAGAAGGC GTGGTTGCAG SCGGCGGCGT
1251 AGCCCTGTTG CGCGCCCGTG CCGCTTTGGA AAACCTGCAC ACCGGCAATG
1301 CCGACCAAGA CGCAGGCGTA CAAATCGTAT TCGCGCGCGT TGAGTCTCCG
1351 CTGCGCCAAA TCGTTGCCAA CGCAGGCGGA GAACCCAGCG TGGTGGTGAA
1401 CAAAGTGTTC GAAGGCAAAG GCAactacgG TTACAACGCa ggctcCGGCG
1451 AATACGgcga CATGATCGGA ATGGGCGTAC TCGACCTGCG CAAAGTAACC
1501 CGTTCCGCGC TGCAACACGC CGGCTCTatC GCCGGTCTGA TGCTeACGAC
1551 CGACTGCATG ATTGCCGAAA TCCCTGAAGA AAAACCGGCT GTGCCCGATA
1601 TGGGGGGAAT GGGCGGTATG GCGGCATGA TGTA

```

This corresponds to the amino acid sequence <SEQ ID 2962; ORF 982.ng>:

```

g982.pep
1   IASQNLRFDN RFLQKMVNGV NILPAADWVA LGAKGRNVVV DRAFGGPHIT
51  KDGVTVAKEI ELKDKFENMG AQMVKEVASK TNOVAGDGTT TATVLAQSIV
101 AEGMKYVTAG MNPTDLKRGI DKAVAALVEE LKNIAPCDT SKEIAQVGS
151 SANGDEQVGA IIAEAMEKVG KEGVITVEDG KSELELDVV EGMQFDRGYL
201 SPYFINDAEK QIAGLDNPFV LFLDKKISNI RDLLPVLEQV AKASRPLLI
251 AEDVEGEALA TLVVNNIRGI LKTVAVKAPG FGDRRKAMLQ DIAILTGGVV
301 ISEEVGLSLE KATLDDLQGT KRIEIGEENT TVIDGFGDAA QIEARVAEIR
351 QQIETATSDY DKEKLQERVA KLAGGVAVIK VGAATEVEMK EKKDRVEDAL
401 HATRAAVEEG VVAGGGVALL RARAALNLH TGNADQDAGV QIVLRAVES
451 LRQIVANAGG EPSVVVNKVL EGKNGYGYNA GSGEYDMIG MGVLDPAKVT
501 RSALQHAASI AGLMLTTDCM IAEIPEEKPA VPDMGGMGM GMM*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2963>:

```

m982.seq
1   ATGGCAGCAA AAGACGTACA GTTCGGCAAT GAAGTCCGTC AAAAAATGGT
51  AAACGGCGTG AACATTCTGG CAAACGCCGT CCGCGTAACC TTGGGCCCCA
101 AAGGTCGCAA CETAAGTCGT GACCGCGCAT TCGGCGGCC GCACATCACC
151 AAAGACGGCG TAACCGTCGC CAAAGAAATC GAACTGAAAG ACAAGTTTGA
201 AAATATGGGC GCGCAAATGG TAAAAGAAGT TGCGTCCAAA ACCAACGACG
251 TGGCAGGCGA CGGTACGACT ACCGCCACCG TACTGGCGCA ATCCATCGTT
301 GCCGAAGGTA TGAAATATGT TACCGCAGGT ATGAATCCGA CCGACCTGAA
351 ACGGGGTATC GATAAAGCCG TCGCCGCTTT GGTGACGAA CTGAAAAACA
401 TCGCCAAACC TTGCGACACT TCTAAAGAAA TCGCCCAAGT CGGCTCTATT
451 TCCGCCAACT CCGACGAACA AGTCGGCGCG ATTATCGCCG AAGCGATGGA
501 AAAAGTCGGC AAAGAAGGCG TGATTACCGT TGAAGACGGC AAGTCTTTGG
551 AAAACGAGCT GGACGTAGTT GAAGGTATGC AGTTCGACCG CGGCTACCTG
601 TCTCCTTACT TCATCAACGA TGCGGAAAAA CAAATCGCTG CTTTGGACAA

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651	TCCGTTTGTA	TTGTTGTTGC	ACAAAAAAT	CAGCAACATC	CGCGACCTGC
701	TGCCTGTTT	GGAAACAAGTG	GCAAAAGCCA	GCCGTCCGCT	GTGTGATTATC
751	CGTAGAAGC	TAGAAGGCCA	AGCCTTTGGC	ACTTTGGTCG	TGAAACAACAT
801	CCGAGGCAT	CTGAAAAACCG	TTCGGCTCAA	AGCCCTTGGC	TTCCGGACAC
851	GCCGCAAAGC	GATGTTGCAA	GACATCGCCA	TCCTGACCGG	CGGCGTGGTG
901	ATTTCCGAAG	AACTCGGTCT	GTCTTTGGAA	AAAGCGACTT	TGGACGACTT
951	GGTCAAGCC	AAACGCATCG	AAATCGGTAA	AGAAAAACCC	ACCATCATCG
1001	ACGGCTTTGG	CGACGCAGCC	CAAAATCGAG	CGCGTGTTCG	CGAAATCCGC
1051	CAACAAATCG	AAACCGCAAC	CAGCGATTAC	GACAAAGAAA	AATGCAAGA
1101	GCGCTGGCT	AAATTGGCAG	GCGGCTGGC	AGCTCATCAA	GTCCGTGCCG
1151	CGACCGAAGT	CGAAATGAAA	GAGAAAAAAG	ACGCCGTGGA	AGACCGCTGC
1201	CACGCTACCC	CGCGAGCCGT	TGAAGAAGCG	GTGTTGCAAG	CGGGCGCGGT
1251	AGCCCTGTTG	CGTGCCCGTG	CTGCTTTGGA	AAACCTGCAC	ACCGGCAATG
1301	CCGACCAAGA	CGCAGGCGTA	CAAAATCGTCT	TGACCGCCGT	TGAGTCTCCG
1351	CTGCGCCAAA	TCGTTGCCAA	CGCAGGCGGC	GACACCGCG	TGGTGTGAAA
1401	CAAGTATTG	GAAAGCAAAG	SCAATCATCG	TTACAACGCT	GGCAGCGCGC
1451	AATACGGCGA	TATGATCGAA	ATGGGCGTAC	TCGACCCCGC	CAAAGTAACC
1501	CGTTCTGCGC	TGCAACACGC	CGCATCTATC	GCCGGCTTGA	TGCTGACCAC
1551	TGATTGCGAT	ATCGCTGAAA	TCCCTCGAAG	CAAAACGGCT	GTGCGCTGATA
1601	TGGCGGCCAT	GGGTGGTATG	GCCGCGCATGA	TGTA	

m982.seq

1	ATGGCAGCAA	AAGACGTACA	GTTCCGCAAT	GAAGTCCGTC	AAAAAATGGT
51	AAACGGCGTG	AACATCTCTGG	CAAACGCCGT	CCGGTAACC	TTGGGCCCA
101	AAGGTCTCGAA	CGTAGTCGTT	GACCGCGCAT	TCGGCGGCC	GCACATCCC
151	AAAGACGGCG	TAACTGTCGC	CAAGAAGAA	GAATCGAAG	ACAAGTTTAC
201	AAATATGGGC	CGCCAAATGG	TGAAAGAAGT	TGCGTCCAAA	ACCAACGACG
251	TGGCAGGCGA	CGGTACGACT	ACCGCCACCG	TACTGGCGCA	ATCCATCGT
301	GCCGAAGGTA	TGAAATATGT	TACCGCAGGT	ATGAATCCGA	CCGACCTGAA
351	ACGCGGTATC	GATAAGCCG	TCGCGCTTT	GGTTGACGAA	CTGAAAAACA
401	TCGCCAAACC	TTGCGACACT	TCATAAGAAA	TCGCCCAAGT	CCGCTCTATT
451	TCGCCCAACT	CCGACGAACA	AGTCGGCGCG	ATTATCGCCG	AAGCGATGGA
501	AAAAGTCGCG	AAAGAAGCG	TGATTACCGT	TGAAGACGCG	AAGTCTTTGG
551	AAACGAGCT	GGACGTAGT	GAGGTATGC	AGTTCGACCG	CGCTACCTG
601	TCCTCTTACT	TCATCAACGA	TGCGGAAAA	CAAAATCGTG	CTTTGGACAA
651	TCCGTTTGTA	TTGTTGTTTC	ACAAAAAAT	CAGCAACATC	CGCGACCTGC
701	TGCTGTGTTT	GGAAACATGT	GCAAAAGCCA	GCGCTCCGCT	GTGTGATTATC
751	CGTGAAGACG	TAGAAGCGCA	AGCCTTGGCG	ACTTTGGTCG	TGAACAACAT
801	GCGAGGCATC	CTGAAACCG	TTCGCGTCAA	AGCCCTTGGC	TTCCGCGACC
851	GCCGCAAAGC	GATGTTGCAA	GACATCGCCA	TCTTGACCGG	CGGCGTGGTG
901	ATTTCCGAAG	AAGTCGGTCT	GTCTTTGGAA	AAAGCGCACT	TGGACGACTT
951	GGGTCAAGCC	AAACGCATCT	AAATCGGTAA	AGAAAACACC	ACCATCATCT
1001	ACGGCTTTGG	CAGCGCAGCC	CAAAATCGAG	CGCGTGTTCG	CGAAATCCGC
1051	CAACAAATCG	AAACCGCAAC	CAGCGATTAC	GACAAAGAAA	AACTGCAAGA
1101	GCGCGTGGCT	AAATTGGCAG	GCGCGCTGGC	AGCTCATCAA	GTCCGTTCCG
1151	CGACCGAAGT	CGAAATGAA	GAGAAAAAG	ACCGCGTGA	AGACGCGCTG
1201	CACGCTACCC	CGCAGCCGT	TGAAGAAAGC	GTGCTTGACG	CGGCGCGCGT
1251	AGCCCTGTTG	CGTGCCCGTG	CTGCTTTGGA	AAACCTGCAC	ACCGGCAATG
1301	CCGACCAAGA	CGCAGGCGTA	CAAATCGTCT	TGCGCGCGCT	TGAGTCTCCG
1351	CTGCGCCAAA	TCGTTGCCAA	CGCAGCGCGC	GACCCGACG	TGGTTGTGAA
1401	CAAAGTATTG	GAAAGCAAAG	GCAACTACGG	TTACAACGCT	GCGACGCGCG
1451	AATACGGCGA	TATGATCGAA	ATGGGCGTAC	TCGACCCCGC	CAAAGTAACC
1501	CGTTCTGCGC	TGCAACACGC	CGCATCTAGA	GCCGGCTTGA	TGCTGACCAC
1551	TGATTGCGAT	ATCGTGTAAA	TCCCCTGAAT	CAAAACCGCT	GTGCCTGATA
1601	TGGTCGGCAT	GGGTGGTATG	CGCGGCGATGA	TGTA	

Homology with a predicted ORF from *N. gonorrhoeae*

m982/g982 95.8% identity in 544 aa overlap

m982.pep MAAKDVFQGNEVRQKMNVGNI LANAVRVT LGPKGRNVVDRAFGGP HITKDGVTVAKEI
::: :: | : ||||| | : || |||||

1387

g982	IASQNLRFDNRFLQKMVNGVNILPAADWVALGAKGRNVVVDRAFGGPHITKDGVTVAKEI
	10 20 30 40 50 60
m982.pep	ELKDKFENMGAQMVKEVASKTNDVAGDGTATVLAQSIVAEGMKYVTAGMNPDLKRG
	70 80 90 100 110 120
g982	ELKDKFENMGAQMVKEVASKTNDVAGDGTATVLAQSIVAEGMKYVTAGMNPDLKRG
	70 80 90 100 110 120
m982.pep	DKAVAALVDELKNIAPCDTSKEIAQVGSISANSDEQVGAIIEAMEKVGKEGVITVEDG
	130 140 150 160 170 180
g982	DKAVAALVDELKNIAPCDTSKEIAQVGSISANSDEQVGAIIEAMEKVGKEGVITVEDG
	130 140 150 160 170 180
m982.pep	KSLENELDVVEGMQFDRGYLSPYFINDAEKQIAALDNPFVLLFDKKISNIRDLLPVLEQV
	190 200 210 220 230 240
g982	KSLENELDVVEGMQFDRGYLSPYFINDAEKQIAGLDNPFVLLFDKKISNIRDLLPVLEQV
	190 200 210 220 230 240
m982.pep	AKASRPLIIAEDVEGEALATLVVNNIRGILKTVAVKAPGFGDRRKAMLQDIAILTG
	250 260 270 280 290 300
g982	AKASRPLIIAEDVEGEALATLVVNNIRGILKTVAVKAPGFGDRRKAMLQDIAILTG
	250 260 270 280 290 300
m982.pep	ISEEVGLSLEKATLDDLQAKRIEIGKENTTIIDGFGDAAQIEARVAEIRQIETATSDY
	310 320 330 340 350 360
g982	ISEEVGLSLEKATLDDLQAKRIEIGKENTTIIDGFGDAAQIEARVAEIRQIETATSDY
	310 320 330 340 350 360
m982.pep	DKEKLQERVAKLAGGVAVIKVGAATEVENKEKKDRVEDALHATRAAVEEGVVAGGGVALL
	370 380 390 400 410 420
g982	DKEKLQERVAKLAGGVAVIKVGAATEVENKEKKDRVEDALHATRAAVEEGVVAGGGVALL
	370 380 390 400 410 420
m982.pep	RARAALENLHTGNADQDAGVQIVLRAVESPLRQIVANAGGEPSSVVNVKVLGKNGYGYNA
	430 440 450 460 470 480
g982	RARAALENLHTGNADQDAGVQIVLRAVESPLRQIVANAGGEPSSVVNVKVLGKNGYGYNA
	430 440 450 460 470 480
m982.pep	GSGEYGDMIEMGVLDPAKVTRSAHQHAASIAGLMLTTDCMIAEIPEDKPAVPDMGGMGM
	490 500 510 520 530 540
g982	GSGEYGDMIEMGVLDPAKVTRSAHQHAASIAGLMLTTDCMIAEIPEDKPAVPDMGGMGM
	490 500 510 520 530 540
m982.pep	GGMMX
g982	GGMMX

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2965>:

```

a982.seq
1  ATGGCAGCAA AAGACGTACA ATTCGGCAAT GAAGTCCGCC AAAAAATGGT
51  AAACGGCGTG AACATTTTGG CAAACGCCGT GCGCGTAACC TTGGGTCCCA
101 AAGGCCGCAA CGTGGTGTT GACCGCGCTT TCGGCGGCC GCACATCACC
151 AAAGACGGCG TAACCGTCGC CAAAGAAATC GAACTGAAAG ACAAGTTTGA
201 AAATATGGGC GCGCAAATGG TGAAAGAAGT CGCGTCCAAA ACCAACGACG
251 TGGCGGGCGA CGGTACGACT ACCGCCACCG TATTGGCGCA ATCCATCGTT
301 GCCGAAGGTA TGAAATACGT TACCGCCGT ATGAACCGA CCGACCTGAA
351 ACGCGGTATC GACAAAGCCG TCGCGCTTT GGTGAAGAG CTGAAAAACA

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1388

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401 TCGCCAAACC TTGCGACACT TCTAAAGAAA TCGCCCAAGT CGGCTCTATT
451 TCCGCCAACT CTGACGAACA AGTCGGCGCG ATTATTGCCG AAGCGATGGA
501 AAAAGTCGGC AAAGAAGGCG TGATTACCGT TGAAGACGGC AAATCTTTGG
551 AAAACGAGCT GGACGTGGTT GAAGGTATGC AATTCCACCG CGGCTACCTG
601 TCTCCTTACT TCATCAACGA TCGGGAAGAA CAAATCGCCG GCTTGGACAA
551 TCCGTTTGTA TTGCTGTTG ACAAATAAT CAGCAATATC CGCGACCTGC
701 TGCCTGTTTT GGAACAAGTG GCCAAAGCCA GCCGTCCGCT GTTGATTATC
751 GCTGAAGACG TAGAAGGCGA AGCCTTGGCG ACTTTGGTCG TGAACAACAT
801 CCGCGGCATT CTGAAAACCG TTGCCGTTAA AGCTCCGGGC TTCGGCGACC
851 GCCGCAAAGC GATGCTGCAA GACATCGCTA TCCTGACCGG CGGCACAGTG
901 ATTTCCGAAG AAGTCGGCCT GTCTTTGGAA AAAGCGACTT TGGACGACTT
951 GGGTCAGGCC AAACGCATCG AAATCGGTAA AGAAAACACC ACCATCATCG
1001 ACGGCTTCGG CGACGCAGCC CAAATCGAAG CGCGTGTTCG CGAAATCCGC
1051 CAACAAATCG AAACGCAAC CAGCGATTAC GACAAAGAAA AACTGCAAGA
1101 GCGCGTTGCC AAATGGCAG GCGGCGTGGC AGTAATCAAA GTCGGTGGCG
1151 CGACCGAAGT GGAAATGAAA GAGAAAAAAG ACCGCGTGGA AGACGCGCTG
1201 CACGCTACCC GCGCAGCCGT TGAAGAAGGC GTGGTTGCAG GCGGCGGCGT
1251 AGCCCTGTTG CGCGCCCGTG CCGCTCTGGA AAACCTGCAC ACCGGCAATG
1301 CAGACCAAGA CGCAGGCGTA CAAATCGTCT TCGCGCGCGT TGAGTCTCCG
1351 CTGCGCCAAA TCGTTGCCAA CGCAGGCGGC GAACCCAGCG TGGTTGTGAA
1401 CAAAGTGTTG GAAGGCARAG GCAACTATGG TTACAACGCT GGCAGCGGCG
1451 AATACGGCGA CATGATCGAA ATGGGCGTAC TCGACCCCGC CAAAGTAACC
1501 CGTTCCGCGC TGCAACACGC CGCGTCTATC GCCGGCCTGA TGCTGACCAC
1551 AGACTGCATG ATTGCTGAAA TCCCTGAAGA CAAACCGGCT ATGCCTGATA
1601 TGGGCGGCAT GGGTGTATG GCGGCATGA TGTA

```

This corresponds to the amino acid sequence <SEQ ID 2966; ORF 982.a>:

a982.pep

```

1  MAAKDVFQGN EVRQKMNNGV NILANAVRVT LGPKGRNVVV DRAFGGPHIT
51  KDGVTVAKEI ELKDKFENMG AQMVKEVASK TNDVAGDGT TATVLAQSIV
101 AEGMKYVTAG MNPTDLKRG I DKAVALVEE LKNIAPCDT SKEIAQVGS I
151 SANSDEQVGA IIAEAMEKVG KEGVITVEDG KLENELDVV EGMQFDRGYL
201 SPYFINDAEK QIAGLDNPFV LFDKKISNI RDLLPVLEQV AKASRPLLI I
251 AEDVEGEALA TLVNNIRGI LKTVAVKAPG FGDRRKAMLQ DIAILTGGTV
301 ISEEVGLSLE KATLDDLQQA KRIEIGKENT TIIDGFGDAA QIEARVAEIR
351 QQIETATSDY DKEKLQERVA KLAGGVAVIK VGAATEVEMK EKKDRVEDAL
401 HATRAAVEEG VVAGGGVALL RARAALNLH TGNADQDAGV QIVLRAVESP
451 LRQIVANAGG EPSVVVNKVL EGKNGYGYNA GSGEYGDME MGVLDPKAVT
501 RSALQHAASI AGLMLTTDCM IAEIPEKPA MPDMGGMGM GMM*

```

m982/a982 99.3% identity in 544 aa overlap

	10	20	30	40	50	60
m982.pep	MAAKDVQFGNEVRQKMNNGV NILANAVRVT LGPKGRNVVV DRAFGGPHIT KDGVTVAKEI					
a982	MAAKDVQFGNEVRQKMNNGV NILANAVRVT LGPKGRNVVV DRAFGGPHIT KDGVTVAKEI					
	10	20	30	40	50	60
m982.pep	ELKDKFENMG AQMVKEVASK TNDVAGDGT TATVLAQSIV AEGMKYVTAG MNPTDLKRG I					
a982	ELKDKFENMG AQMVKEVASK TNDVAGDGT TATVLAQSIV AEGMKYVTAG MNPTDLKRG I					
	70	80	90	100	110	120
m982.pep	ELKDKFENMG AQMVKEVASK TNDVAGDGT TATVLAQSIV AEGMKYVTAG MNPTDLKRG I					
a982	ELKDKFENMG AQMVKEVASK TNDVAGDGT TATVLAQSIV AEGMKYVTAG MNPTDLKRG I					
	130	140	150	160	170	180
m982.pep	DKAVALVDEL KNIAPCDT SKEIAQVGS ISANSDEQV GAI IAEAMEKVG KEGVITVEDG					
a982	DKAVALVEEL KNIAPCDT SKEIAQVGS ISANSDEQV GAI IAEAMEKVG KEGVITVEDG					
	130	140	150	160	170	180
m982.pep	KLENELDVVEGMQFDRGYL SPYFINDAEK QIAGLDNPFV LFDKKISNI RDLLPVLEQV					
a982	KLENELDVVEGMQFDRGYL SPYFINDAEK QIAGLDNPFV LFDKKISNI RDLLPVLEQV					
	190	200	210	220	230	240

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	250	260	270	280	290	300
m982.pep	AKASRPLLIIAEDVEGEALATLVVNNIRGILKTVAVKAPGFGDRRKAMLQDIAILTTGGVV					
a982	AKASRPLLIIAEDVEGEALATLVVNNIRGILKTVAVKAPGFGDRRKAMLQDIAILTTGGTV					
	250	260	270	280	290	300
	310	320	330	340	350	360
m982.pep	ISEEVGLSLEKATLDDLGOAKRIEIGKENTTIIDGFGDAAQIEARVAEIRQQIETATSDY					
a982	ISEEVGLSLEKATLDDLGOAKRIEIGKENTTIIDGFGDAAQIEARVAEIRQQIETATSDY					
	310	320	330	340	350	360
	370	380	390	400	410	420
m982.pep	DKEKLQERVAKLAGGVAVIKVGAATEVEMKEKKDRVEDALHATRAAVEEGVVAGGGVALL					
a982	DKEKLQERVAKLAGGVAVIKVGAATEVEMKEKKDRVEDALHATRAAVEEGVVAGGGVALL					
	370	380	390	400	410	420
	430	440	450	460	470	480
m982.pep	RARAALENLHTGNADQDAGVQIVLRAVESPLRQIVANAGGEPSSVVVNKVLEGKNGYGYNA					
a982	RARAALENLHTGNADQDAGVQIVLRAVESPLRQIVANAGGEPSSVVVNKVLEGKNGYGYNA					
	430	440	450	460	470	480
	490	500	510	520	530	540
m982.pep	GSGEYGDMIEMGVLDPAKVTRSALQHAASIAGLMLTTDCMIAEIPEDKPAVPMGGMGGM					
a982	GSGEYGDMIEMGVLDPAKVTRSALQHAASIAGLMLTTDCMIAEIPEDKPAMPDMGGMGGM					
	490	500	510	520	530	540
m982.pep	GGMMX					
a982	GGMMX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2967>:

g986.seq

1	GTGTTCAAAA	AATACCAATA	CTTCGCTTTG	GCGGCACTGT	GTGCCGCTTT
51	GCTGGCAGGC	TGCGAARAGG	CAGGCAGCTT	TTTCGGTGCG	GACAAAAAAG
101	AAGCATCCTT	CGTAGAACGC	ATCGAACACA	CCAAAGACGA	CGGCASTGTC
151	AGTATGCTGC	TGCCCCGACTT	TGCCCAACTG	GTTCAAAGCG	AAGGCCCGGC
201	AGTCGTCAAT	ATTCAGGCAG	CCCCCGCCCC	GCGCACCCAA	AACGGCAGCG
251	GCAATGCCGA	AACCGATTCC	GACCCGCTTG	CCGACAGCGA	CCCGTTCTAC
301	GAATTTTCA	AACGCCTCGT	CCCGAACATG	CCCGAAATCC	CCCAAGAAGA
351	AGCAGATGAC	GGCGGATTGA	ACTTCGGTTC	GGGCTTCATC	ATCAGCAAAA
401	ACGGCTACAT	CCTGACCAAT	ACCCACGTCG	TTGCCGGTAT	GGGCAGTATC
451	AAAGTCCTGC	TCAACGACAA	GCGCGAATAT	ACCGCCAAAC	TCATCGGTTC
501	GGATGTCCAA	TCCGATGTCG	CCCTTCTGAA	AATCGACGCA	ACGGAAGAGC
551	TACCCGTCGT	CAAAATCGGC	AATCCCAAAA	ATTTGAAACC	GGGCGAATGG
601	GTCGCTGCCA	TCGGCGCGCC	CTTCGGCTTT	GACAAACAGC	TGACCGCCGG
651	CATCGTGTCC	GCCAAAGGCA	GAAGCCTGCC	CAACGAAAgc	tACACACCCT
701	TCATCCAAAC	CGACGTTGCC	ATCAATCCGG	GCAATTCCGG	CGGCCCGCTG
751	TTCAACTTAA	AAGGACAGGt	cgTCGGCATC	AATTCGCAAA	TATACAGCCG
801	CAGCGgcgga	ttCATGGGCA	TCTCCTTTGC	CATCCCGATT	GACGTTGCCA
851	TGAATGTCGC	CGAACAGCTG	AAAAACACCG	GCAAAGTCCA	ACGCGGACAA
901	CTGGGCGTGA	TTATTTCAGGA	AGTATCCTAC	GGTTTGGCAC	AGTCGTTCCG
951	TCTGGATAAA	GCCAGCGGCG	CATTGATTGC	CAAAATCCTT	CCCGGCAGCC
1001	CCGCAGAACG	TGCCGGCCTG	CAGGCGGGCG	ACATCGTCCT	CAGCCTCGAC
1051	GGCGGAGAAA	TACGTTCTTC	CGGCGACCTT	CCCGTCATGG	TCGGCGCCAT
1101	TACGCCGGGA	AAAGAAGTCA	GCCTCGGCGT	ATGGCGCAAA	GGCGAAGAAA
1151	TCACAATCAA	AGCCAAGCTG	GGCAACGCCg	cggagcATAC	CGGCgcatCA
1201	TCCAAAACAG	ATGAAGcccc	ctacaccgAA	CAGCAATCCG	GTACGTTCTC
1251	GGTCGAATCC	GCAGGCATTA	CCCTTCAGAC	ACATACCGAC	AGCAGCGGca
1301	aacacctcgt	cgtcgtacgg	gtttccgacg	cggcagaacg	cGCAGGCTTA

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1351 AGgcgcggcg acgaaatcct cgcggtcggg caagtccccg tcaatgacga
1401 agccgGTTTC cgcaaaGCTA TGGACAAGGC AGGCAAAAAC GTCCCCCTGC
1451 TGGTCatgcg ccgTGGCAAC ACGCTGTTCA TCGCATTAAA CCTGCAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2968; ORF 986.ng>:

```

g986.pep
  1 VFKKYQYFAL AALCAALLAG CEKAGSFFGA DKKEASFVER IEHTKDDGSV
 51 SMLLPDFAQL VQSEGPAVVN IQAAPAPRTQ NGSGNAETDS DPLADSDPFY
101 EFFKRLVPMN PEIQEEADD GGLNFGSGFI ISKNGYILT NTHVVGAMGSI
151 KVLNDKREY TAKLIGSDVQ SDVALLKIDA TEELPVVKIG NPKNLKPGEW
201 VAAIGAPFGF DNSVTAGIVS AKGRSLPNES YTPFIQTDVA INPGNSGGPL
251 FNLKGQVVGI NSQIYSRSGG FMGISFAIPI DVAMNVAEQL KNTGKVQRGQ
301 LGVLIQEVSY GLAQSFGLDK ASGALIAKIL PGSPAERAGL QAGDIVLSLD
351 GGEIRSSGDL PVMVGAITPG KEVSLGVWRK GEEITIKAKL GNAAEHTGAS
401 SKTDEAPYTE QSGTFSVES AGITLQTHTD SSGKHLVVVR VSDAAERAGL
451 RRGDEILAVG QVPVNDEAGF RKAMDKAGKN VPLLVMRRGN TLFIALNLQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2969>:

```

m986.seq
  1 GTGTTCAAAA AATACCAATA CCTCGCTTTG GCAGCACTGT GTGCAGCCTC
 51 GCTGGCAGGC TGGCACAAGG CAGGCAGCTT CTTCGTGGCG GACAAAAAAG
101 AAGCATCCTT CGTAGAACGC ATCGAACACA CCAAAGACGA CGGCAGCGTC
151 AGTATGCTGC TGCCCGACTT TGCCCAACTG GTTCAAAGTG AAGGTCCGGC
201 AGTCGTCAAT ATTCAAGGCAG CCCC GCCGCC CCGCACCCAA AACGGCAGCG
251 GCAATGCCGA AAACGATTCC GACCCGATTG CCGACAACGA CCGTTCTAC
301 GAATTTTTCA AACGCCTCGT CCCGAATATG CCCGAATCC CCCAAGAAGA
351 AGCAGATGAC GGCAGATTGA ACTTCGGTTC GGGCTTCATC ATCAGCAAAG
401 ACGGCTACAT CTTGACCAAT ACCCACGTCG TTACCGGCAT GGGCAGTATC
451 AAAGTCTGCG TCAACGACAA GCGGAATAT ACCGCCAAAC TCATCGGTTT
501 GGATGTCCAA TCCGATGTCG CCCTTCTGAA AATCGACGCA ACGGAAGAGC
551 TGCCCGTCGT CAAATCGGC AATCCCAAAG ATTTGAAACC GGGCGAATGG
601 GTCGCGGCCA TCGGCGCGCC CTTCGGCTTC GACAACAGCG TGACCGCCGG
651 CATCGTGTCC GCCAAAGGCA GAAGCCTGCC CAACGAAAGC TACACACCCT
701 TCATCCAAAC CGACGTTGCC ATCAATCCGG GCAACTCCGG CGGCCCGCTG
751 TTCAACTTAA AAGGACAGGT CGTCGGCATC AACTCGCAA TATACAGCCG
801 CAGCGGCGGA TTCATGGGCA TTCTCTTCGC CATCCCGATT GACGTTGCCA
851 TGAATGTCGC CGAACAGCTG AAAACACCG GCAAAGTCCA ACGCGGACAA
901 CTGGGCGTGA TTATTCAAGA AGTATCCTAC GGTTCGACAC AATCGTTCGG
951 TTTGGACAAA GCCGGCGGCG CACTGATTGC CAAAATCCTG CCCGGCAGCC
1001 CCGCAGAACG TCGCGGCTG CAGGCGGGCG ACATCGTCTT CAGCCTCGAC
1051 GGGCGAGAAA TACGTTCTTC CGGCGACCTT CCCGTATATG TCGGCGCCAT
1101 TACGCGGGGA AAAGAAGTCA GCCTCGGCGT ATGGCGCAAA GCGGAAGAAA
1151 TCACAATCAA AGTCAAGCTG GGCAACGCCG CCGAGCATAT CGGCGCATCA
1201 TCCAAAACAG ATGAAGCCCC CTACACCGAA CAGCAATCCG GTACGTCTC
1251 GGTGCAATCC GCAGGCATTA CCCTTCAGAC ACATACCGAC AGCAGCGGCG
1301 GACACCTCGT CGTCGTACGG GTTCCGACG CGGCAGAACG CGCAGGCTTG
1351 AGGCGCGGCG ACGAAATTCT TGCCGTCGGG CAAGTCCCCG TCAATGACGA
1401 AGCCGTTTTC CGCAAAGCTA TGGACAAGGC AGGCAAAAAC GTCCCCCTGC
1451 TGATCATGCG CCGTGGCAAC ACGCTGTTTA TCGCATTAAA CCTGCAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2970; ORF 986>:

```

m986.pep.
  1 VFKKYQYLAL AALCAASLAG CDKAGSFFVA DKKEASFVER IEHTKDDGSV
 51 SMLLPDFAQL VQSEGPAVVN IQAAPAPRTQ NGSGNAENDS DFIADNDPFY
101 EFFKRLVPMN PEIQEEADD GGLNFGSGFI ISKNGYILT NTHVVTGMGSI
151 KVLNDKREY TAKLIGSDVQ SDVALLKIDA TEELPVVKIG NPKDLKPGEW
201 VAAIGAPFGF DNSVTAGIVS AKGRSLPNES YTPFIQTDVA INPGNSGGPL
251 FNLKGQVVGI NSQIYSRSGG FMGISFAIPI DVAMNVAEQL KNTGKVQRGQ
301 LGVLIQEVSY GLAQSFGLDK AGGALIAKIL PGSPAERAGL QAGDIVLSLD
351 GGEIRSSGDL PVMVGAITPG KEVSLGVWRK GEEITIKVKL GNAAEHIGAS
401 SKTDEAPYTE QSGTFSVES AGITLQTHTD SSGHLVVVR VSDAAERAGL
451 RRGDEILAVG QVPVNDEAGF RKAMDKAGKN VPLLIMRRGN TLFIALNLQ*

```

Computer analysis of this amino acid sequence gave the following results:

	10	20	30	40	50	60
m986.pep	VFKKYQYLALCAASLAGCDKAGSFFVADKKEASFVERIEHTKDDGSGVSM LLPDFAQL					
g986	VFKKYQYFALCAALLAGCEKAGSFFGADKKEASFVERIEHTKDDGSGVSM LLPDFAQL					
	10	20	30	40	50	60
m986.pep	70	80	90	100	110	120
	VQSEGPAVVNIQAAPAPRTQNGSGNAENDSDPIADNDPFYEFFKRLVPMPEIPQEEADD					
g986	VQSEGPAVVNIQAAPAPRTQNGSGNAETDSDPLADSDPFYEFFKRLVPMPEIPQEEADD					
	70	80	90	100	110	120
m986.pep	130	140	150	160	170	180
	GGLNFGSGFIISKDGYILTNTHVVTGMGSIKVLNDKREYTAKLIGSDVQSDVALLKIDA					
g986	GGLNFGSGFIISKNGYILTNTHVVAGMGSIKVLLNDKREYTAKLIGSDVQSDVALLKIDA					
	130	140	150	160	170	180
m986.pep	190	200	210	220	230	240
	TEELPVVKIGNPKDLKPGEWVAAIGAPFGFDNSVTAGIVSAKGRSLPNESYTPFIQT DVA					
g986	TEELPVVKIGNPKNLKPGEWVAAIGAPFGFDNSVTAGIVSAKGRSLPNESYTPFIQT DVA					
	190	200	210	220	230	240
m986.pep	250	260	270	280	290	300
	INPGNSGGPLENLKGQVVGINSQIYSRSGGFMGISFAIPIDVAMNVAEQLKNTGKVQRGQ					
g986	INPGNSGGPLENLKGQVVGINSQIYSRSGGFMGISFAIPIDVAMNVAEQLKNTGKVQRGQ					
	250	260	270	280	290	300

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	310	320	330	340	350	360
m986.pep	LGVIIQEVSYGLAQSFGLDKAGGALIAKILPGSPAERAGLCAGDIVLSLDGGEIRSSGDL					
g986	LGVIIQEVSYGLAQSFGLDKAGGALIAKILPGSPAERAGLCAGDIVLSLDGGEIRSSGDL					
	310	320	330	340	350	360
	370	380	390	400	410	420
m986.pep	PVMVGAITPGKEVSLGVWRKGEEITIKVKLGNAAEHIGASSKTDEAPYTEQQSGTFSVES					
g986	PVMVGAITPGKEVSLGVWRKGEEITIKVKLGNAAEHTGASSKTDEAPYTEQQSGTFSVES					
	370	380	390	400	410	420
	430	440	450	460	470	480
m986.pep	AGITLQTHTDSSGGHLVVVRVSDAAERAGLRRGDEILAVGQVPVNDGFRKAMDKAGKN					
g986	AGITLQTHTDSSGGHLVVVRVSDAAERAGLRRGDEILAVGQVPVNDGFRKAMDKAGKN					
	430	440	450	460	470	480
	490	500				
m986.pep	VPLLIMRRGNTLFIALNLQX					
g986	VPLLVMRRGNTLFIALNLQX					
	490	500				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2971>:

```

a986.seq
1  GTGTTCAAAA AATACCAATA CCTCGCTTGT GCAGCACTGT STGCCGCCTC
51  GCTGGCAGGC TGCACAAAG CCGGCAGCTT TTTCGGTGCG GACAAAAAAG
101 AAGCATCCTT TGTAGAACGC ATCAAACACA CCAAAGACGA CGGCAGCGTC
151 AGTATGCTGC TGCCCGACTT TGTCCAACGT GTTCAAAGCG AAGGCCCGGC
201 AGTCGTCAAT ATTACGGCAG CCCC GCCGCC CCGCACCCAA AACGGCAGCA
251 GCAATGCCGA AACCGATTCC GACCGCTTG CCGACAGCGA CCCGTTCTAC
301 GAATTTTTC AACGCCTCGT CCGGAACATG CCGGAAATCC CCAAGAAGA
351 AGCAGATGAC GNGGATTGA ACTTCGGTTC GGGCTTCATC ATCAGCAAAG
401 ACGGCTATAT TCTGACCAAT ACGCACGTCG TTACCGGCAT GGGCAGTATC
451 AAAGTCTGTC TCAACGACAA GCGCGAATAT ACCGCCAAAC TCATCGGTTT
501 GGATGTCCTA TCCGATGTCG CCCTTCTGAA AATCGACGCA ACGGAAGAGC
551 TGCCCGTCGT CAAAATCGGC AATCCCAAAG ATTTGAAACC GGGCGAATGG
601 GTCGCGGCCA TCGGCGCGCC CTTCGGCTTC GACAACAGCG TGACCGCCGG
651 CNTCGTGTCC GCCAAAGGCA GAAGCCTGCC CAACGAAAGC TACACACCCT
701 TCATCCAAAC CGACGTTGCC ATCAATCCGG GCAACTCCGG CGGCCCGCTG
751 TTCAACTTAA AAGGACAGGT CGTCGGCATC AACTCGCAA TATACAGCCG
801 CAGCGGGCGA TTTCATGGCA TTTCCTTCGC CATCCCATT GACGTTGCCA
851 TGAATGTCGC CGAACAGCTG AAAAACACCG GCAAAGTCCA ACGCGGACAA
901 CTGGGCGTGA TTATTCAAGA AGTATCCTAC GGTTCGGCAC AATCGTTCGG
951 TTTGGACAAA GCCGGCGGCG CACTGATTGC CAAAATCCTG CCCGGCAGCC
1001 CCGCAGAACG TGCCGGCCTG CGGGCGGGCG ACATCGTCCT CAGCCTCGAC
1051 GGCGGAGAAA TACGTTCTTC CGGCGACCTT CCCGTTATGG TCGGCGCCAT
1101 TACGCGGGGA AAAGAAGTCA GCCTCGGCGT ATGGCGCAAA GGCGAAGAAA
1151 TCACAATCAA AGTCAAGCTG GGCAACGCCG CCGAGCATAT CGGCGCATCA
1201 TCCAAAACAG ATGAAGCCCC CTACACCGAA CAGCAATCCG GTACGTTCTC
1251 GGTCGAATCC GCAGGCATTA CCCTTCAGAC ACATACCGAC AGCAGCGGCG
1301 GACACCTCGT CGTCGTACGG GTTTCGACG CGGCAGAACG CGCAGGCTTG
1351 AGGCGCGGCG ACGAAATCTT TGCCGTCGGG CAAGTCCCCG TCAATGACGA
1401 AGCCGGTTTC CGCAAAGCTA TGGACAAGGC AGGCAAAAC GTCCCCCTGC
1451 TGATCATGCG CCGTGGCAAC ACGCTGTTTA TCGCATTAAA CCTGCAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2972; ORF 986.a>:

```

a986.pep
1  VFKKYQYLAL AALCAASLAG CDKAGSFFGA DKKEASFVER IKHTKDDGSV
51  SMLLPDFVQL VQSEGPAVVN IQAAPAPRTQ NGSSNAETDS DPLADSDPFY
101 EFFKRLVPNM PEIPQEEADD GGLNFGSGFI ISKDGYILT NTHVVTGMGSI
151 KVLNDKREY TAKLIGSDVQ SDVALLKIDA TEELPVVKIG NPKDLKPGEW
201 VAAIGAPFGF DNSVTAGXVS AKGRSLPNES YTPFIQTQDVA INPGNSGGPL
251 FNLKGQVVGI NSQIYSRSGG FMGISFAIPI DVAMNVAEQL KNTGKVQRGQ

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301 LGVIIQEVSY GLAQSFGLDK AGGALIAKIL PGSPAERAGL RAGDIVLSLD
 351 GGEIRSSGDL PVMVGAITPG KEVSLGVWRK GEEITIKVKL GNAAEHIGAS
 401 SKTDEAPYTE QQSGTFSVES AGITLQTHTD SSGHLVVVR VSDAERAGL
 451 RRGDEILAVG QVPVND EAGF RKAMD KAGN VPLLIMRRGN TLFIALNLQ*

m986/a986 98.2% identity in 499 aa overlap

	10	20	30	40	50	60
m986.pep	VFKKYQYLALALCAASLAGCDKAGSFFVADKKEASFVERIEHTKDDGSVSMLLPDFAQL					
a986	VFKKYQYLALALCAASLAGCDKAGSFFGADKKEASFVERIKHTKDDGSVSMLLPDFVQL					
	10	20	30	40	50	60
m986.pep	70	80	90	100	110	120
	VQSEGPVVNIQAAPAPRTQNGSGNAENDSDPIADNDPFYEFFKRLVPMPEIPQEEADD					
a986	VQSEGPVVNIQAAPAPRTQNGSSNAETSDPLADSDPFYEFFKRLVPMPEIPQEEADD					
	70	80	90	100	110	120
m986.pep	130	140	150	160	170	180
	GGLNFGSGFIISKDGYILTNTHVVTGMSIKVLLNDKREYTAKLIGSDVQSDVALLKIDA					
a986	GGLNFGSGFIISKDGYILTNTHVVTGMSIKVLLNDKREYTAKLIGSDVQSDVALLKIDA					
	130	140	150	160	170	180
m986.pep	190	200	210	220	230	240
	TEELPVVKIGNPKDLKPGEWVAAIGAPFGFNSVTAGIVSAKGRSLPNESYTPFIQTQVA					
a986	TEELPVVKIGNPKDLKPGEWVAAIGAPFGFNSVTAGXVSAKGRSLPNESYTPFIQTQVA					
	190	200	210	220	230	240
m986.pep	250	260	270	280	290	300
	INPGNSGGPLENLKGQVVGINSQIYSRSGGFMGISFAIPIDVAMNVAEQLKNTGKVQRGQ					
a986	INPGNSGGPLENLKGQVVGINSQIYSRSGGFMGISFAIPIDVAMNVAEQLKNTGKVQRGQ					
	250	260	270	280	290	300
m986.pep	310	320	330	340	350	360
	LGVIIQEVSYGLAQSFGLDKAGGALIAKILPGSPAERAGLQAGDIVLSLDGGEIRSSGDL					
a986	LGVIIQEVSYGLAQSFGLDKAGGALIAKILPGSPAERAGLRAGDIVLSLDGGEIRSSGDL					
	310	320	330	340	350	360
m986.pep	370	380	390	400	410	420
	PVMVGAITPGKEVSLGVWRKGEETIKVKLGNAAEHIGASSKTDEAPYTEQQSGTFSVES					
a986	PVMVGAITPGKEVSLGVWRKGEETIKVKLGNAAEHIGASSKTDEAPYTEQQSGTFSVES					
	370	380	390	400	410	420
m986.pep	430	440	450	460	470	480
	AGITLQTHTDSSGGHLVVVRVSDAERAGLRRGDEILAVGQVPVND EAGFRKAMD KAGN					
a986	AGITLQTHTDSSGGHLVVVRVSDAERAGLRRGDEILAVGQVPVND EAGFRKAMD KAGN					
	430	440	450	460	470	480
m986.pep	490	500				
	VPLLIMRRGNTLFIALNLQX					
a986	VPLLIMRRGNTLFIALNLQX					
	490	500				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2973>:

g987.seq

1 ATGAAAACAC GCAGCCTCAT TTCCCTTTTA TGCCTCCTTC TCTGTTTCATG

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51  TTCTTCATGG TTGCCCCCAG TGGAAGAAGC GACGGAAAGC CGTCATTTTA
101 ATACTTCCAA ACCTGTCTTC CTGGACAACA TCCTGCAAAT CCGGCACACC
151 CCTCATAACA ACGGGCTATC CGACATCTAC CTGCTCGACG ACCCCACGA
201 AGCCTTTGCC GCCCGCGCCG CCCTTATCGA ATCTGCCGAA CACAGCCTCG
251 ATTTGCAATA CTACATTTGG CGCAACGACA TTCCGGCAG GCTGCTGTTT
301 AACCTCATGT ACCTTGCCGC agaacgcGGC GTGCGCGTAC GCCTGCTGT
351 ggacgacaAC AACAcgcgcg gcttggacga tctcctGCTC GCCCTCGACA
401 GCCATCCCAA TAtctaagtG CGCCTGTTCa ACCCCTtcgt CCTACGCAAA
451 TGGCGCGCAC TCGGCTACCT GACCGACTTC CCCCCTCA ACCGCCGAT
501 GCACAACAAA TCCTTTACCG CCGACAACCG CGCCACCATA CTCGGCGGAC
551 GCAATATCGG CGACGAATAC TTCAAAGTCG GTGAGGACAC CGTTTTCGCC
601 GACCTGGACA TCCTCGCCAC CGGCAGCGTC GTCCGCGAAG TATCGCACGA
651 CTTGACCGC TACTGGGCAA GCCATTCCGC CCACAACGCC ACGCGCATCA
701 TCCGCAGCGG CAACATCGGC AAGGGTCTTC AAGCACTCGG ATACAACGAC
751 GAAACATCCA GACACGCGCT CTGCGCTAC CGCGAAACCG TCGAACAGTC
801 GCCCCTCTAC CAAAAAATAC AGACGGGACG CATCGACTGG CAGAGCGTCC
851 AAACCCGCCT GATCAGCGAC AGCCCTGCAA AAGGACTCGA CCGCGACCGC
901 CGCAAAACGC CGATTGCCGG GAGGCTGCAA GACGCGCTCA AACAGCCGA
951 AAAAAGCGTC TATCTCGTTT CACCCTATTT CGTCCCTACA AAATCCGGCA
1001 CAGACGCACT GGCAAACTG GTGCAGGACG GCATAGACGT TACCGTCTTG
1051 ACCAATCTGC TACAGGCGAC CGACGTTGCC GCCGTCCATT CCGGCTACGT
1101 CAAATACGCA AAACCGCTGC TCAAAGCCGG CATCAAATC TACGAGCTGC
1151 AACCCAACCA TGCCGTCCCC GCCACAAAAG ACAAAGGCCT GACCGCGAGC
1201 TCCGTAACCA GCCTGCATGC CAAAACCTTC ATTGTGGacg gCAAACGCA
1251 CTTTCATCGG TCATTCAACC TCGACCCCG TTCCGCGACG CTCAATACCG
1301 AAATGGGCGT CGTCATCGAA AGCCCCAAA TCGCAGAACA GATGCGCGC
1351 AccctCGCCG AtacCACACC CGAATACGCC TACCGCGTTA CCTCGACAA
1401 ACACAACCGC CTGCAATGGC ACGATCCGCG CACCCGAAAA ACCTACCCGA
1451 ACGAACCCGA AGCCAACTT TGGAAACGCA TCGCCGCAAA AATCCTATCC
1501 CTGCTGCCCA TCGAAGGTTT ATTATAG

```

This corresponds to the amino acid sequence <SEQ ID 2974; ORF 987.ng>:

g987.pep

```

1  MKTRSLISLL CLLLSCSSW LPPLEERTES RHFNTSKPVL LDNIQIRIIT
51  PHNGLSDIY LLDDPHEAFA ARAALIESAE HSLDLQYYIW RNDISGRLLF
101 NIMYLAERG VRVRLLLDN NTRGLDLLLL ALDSHPNI*V RLFNPFVLRK
151 WRALGYLTDF PRLNRRMHNK SFTADNRATI LGGRNIGDEY FKVGEDTVFA
201 DLDILATGSV VGEVSHDFDR YWASHSAHNA TRIIRSGNIG XGLQALGYND
251 ETSRHALLRY RETVEQSPLY OKIQTGRIDW QSVQTRLISD SPAKGLDRDR
301 RKPPIAGRLO DALKQPEKSV YLVSPYFVPT KSGTDALAKI VQDGIDIVTL
351 TNSLQATDVA AVHSGYVKYR KPLLKAGIKL YELQPNHAVP ATKDKGLTGS
401 SVTSLHAKTF IVDGKRIFIG SFNLDPRSAR LNTEMGVIE SPKIAEQMER
451 TLADTTPEYA YRVTLDKHNR LQWHPATRK TYPNEPEAKL WKRIAARKILS
501 LLPIEGLL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2975>:

m987.seq

```

1  ATGAAAACAC GCAGCCTAAT TTCCCTTTTA TGCCTCCTTC TCTGTTTCATG
51  TTCTTCATGG TTGCCCCCAG TGGAAGAAGC GACGGAAAGC CGTCATTTCA
101 ATACTTCCAA ACCCGTCCGC CTGGACAACA TCCTGCAAAT CCGGCACACC
151 CCTCATAACA ACGGGCTATC CGATATCTAT CTGTGGAACG ACCCCACGA
201 AGCCTTTGCC GCCCGCGCCG CCCTTATCGA ATCTGCCGAA CACAGCCTCG
251 ATTTGCAATA CTACATCTGG CGCAACGACA TTCCGGCAG GCTGCTGTTT
301 AACCTCGTGT ACCTTGCCGC AGAACGCGGT GTGCGCGTAC GCCTGCTGTT
351 GGACGACAAC AACACGCGCG GATTGGACGA CCTCCTGCTT GCCCTCGACA
401 GCCATCCCAA TATCGAAGTG CGCCTGTTCa ACCCCTTCGT CTTACGAAAA
451 TGGCGCGCAC TCGGCTACCT GACCGACTTC CCCCCTCA ACCGCCGAT
501 GCACAACAAA TCCTTTACCG CCGACAACCG CGCCACCATA CTCGGCGGAC
551 GCAATATCGG CGACGAATAC TTCAAAGTCG GTGAGGACAC CGTTTTCGCC
601 GATTTGACGA TCCTCGCCAC CGGCAGCGTC GTCCGCGAAG TATCGCACGA
651 CTTGACCGC TACTGGGCAA GCCATTCCGC CCACAACGCC ACGCGCATCA
701 TCCGCAGCGG CGACATCGGC AAGGGTCTTC AAGCACTCGG ATACAACGAC
751 GAAACGTCCA GACACGCGCT CTGCGCTAC CGCGAAACCG TCGAACAGTC
801 GCCCCTCTAC CAAAAAATAC AGACAGGATG CATCGACTGG CAGAGCGTCC
851 GAACCCGCCT CATCAGCGAC GACCCTGCAA AAGGACTCGA CCGCGACCGC

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1395

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901 CGCAAACCGC CGATTGCCGG GCGGCTGCAA GACGCGCTCA AACAGCCCGA
951 AAAAAGCGTC TATCTGGTTT CACCTATTT CGTCCCCA AAATCCGGCA
1001 CAGACGCACT GGCAAACTG GTGCAGGACG GCATAGACGT TACCGTTCTG
1051 ACCAACTCGC TGCAGGCGAC CGACGTTGCC GCCGTCCATT CCGGCTATGT
1101 CAAATACCGA AAACCGCTGC TCAAAGCCGG CATCAAATC TACGAGCTGC
1151 AACCCAACCA TGCCGTCCCC GCCACAAAG ACAAAGGCCT GACCGGCAGC
1201 TCCGTAACCA GCCTGCACGC CAAAACCTTC ATTGTGGACG GCAAACGCAT
1251 CTTTCATCGT TCGTTCAACC TCGACCCCG TTCCGCGCGT CTCAACACCG
1301 AAATGGGCGT TGTATCGAA AGCCCCAAA TCGCAGAACA GATGGAGCGC
1351 ACCCTTGCCG ATACCACACC CGCCTACGCC TACCGCGTTA CCCTCGACAG
1401 GCACAACCGC CTGCAATGGC ACGATCCCGC CACCCGAAA ACCTACCGA
1451 ACGAACCCGA AGCCAACTT TGGAAACGCA TCGCCGCAA AATCCTATCC
1501 CTGCTGCCCA TAGAAGGTTT ATTATAG

```

This corresponds to the amino acid sequence <SEQ ID 2976; ORF 987>:

```

m987.pep
1 MKTRSLISLL CLLCSCSSW LPPLEERTES RHFNSTSKPVR LDNILQIRHT
51 PHTNGLSDIY LLNDPHEAFA ARAALIESAE HSLDLQYYIW RNDISGRLLF
101 NLVYLAERG VRVRLLLDDN NTRGLDDLLL ALDHPNIEV RLFNFFVLRK
151 WRALGYLTDF PRLNRRMHNK SFTADNRATI LGGRNIGDEY FKVGEDTVFA
201 DLDILATGSV VGEVSHDFDR YWASHAHNA TRIIRSGDIG KGLQALGYND
251 ETSRHALRY RETVEQSPLY QKIQTGCIDW QSVRTRLISD DPAKGLDRDR
301 RKPIIAGRLQ DALKQPEKSV YLVSPYFVPT KSGTDALAKL VQDGIDVTVI
351 TNSLQATDVA AVHSGYVKYR KPLLKAGIKL YELQPNHAVP ATKDKGLTGS
401 SVTSLHAKTF IVDGKRIFIG SFNLDPRSAR LNTEMGVIE SPKIAEQMER
451 TLADTTPAYA YRVTLDRHNR LQWHPATRK TYPNEPEAKL WKRIAAILK
501 LLPIEGLL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m987/g987 97.8% identity in 508 aa overlap

	10	20	30	40	50	60
m987.pep	MKTRSLISLLCLLLCSCSSWLPPLEERTESRHFNSTSKPVRLDNILQIRHTPHTNGLSDIY					
g987	MKTRSLISLLCLLLCSCSSWLPPLEERTESRHFNSTSKPVLLDNILQIRHTPHNGLSDIY					
	10	20	30	40	50	60
m987.pep	LLNDPHEAFAARAALIESAEHSLDLQYYIWRNDISGRLLFNVLVYLAERGVRVRLLLDDN					
g987	LLDDPHEAFAARAALIESAEHSLDLQYYIWRNDISGRLLFNMYLAERGVRVRLLLDDN					
	70	80	90	100	110	120
m987.pep	NTRGLDDLLLALDHPNIEVRLFNPFVLRKWRALGYLTDFPRLNRRMHNKSFTADNRATI					
g987	NTRGLDDLLLALDHPNIXVRLFNPFVLRKWRALGYLTDFPRLNRRMHNKSFTADNRATI					
	130	140	150	160	170	180
m987.pep	LGGRNIGDEYFKVGEDTVFADLDILATGSVVGEVSHDFDRYWASHAHNATRIIRSGDIG					
g987	LGGRNIGDEYFKVGEDTVFADLDILATGSVVGEVSHDFDRYWASHAHNATRIIRSGNIG					
	190	200	210	220	230	240
m987.pep	KGLQALGYNDETSRHALRYRETVEQSPLYQKIQTGCIDWQSVRTRLISDPAKGLDRDR					
g987	KGLQALGYNDETSRHALRYRETVEQSPLYQKIQTGRIDWQSVQTRLISDSPAKGLDRDR					
	250	260	270	280	290	300
m987.pep	RKPIIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGIDVTVLNSLQATDVA					
g987	RKPIIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGIDVTVLNSLQATDVA					
	310	320	330	340	350	360
m987.pep	RKPIIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGIDVTVLNSLQATDVA					
g987	RKPIIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGIDVTVLNSLQATDVA					

1396

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|||||
g987      RKPPPIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGDVTVLTNSLQATEVA
          310      320      330      340      350      360

          370      380      390      400      410      420
m987.pep  AVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTSLHAKTFIVDGKRIFIG
          370      380      390      400      410      420
g987      AVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTSLHAKTFIVDGKRIFIG
          370      380      390      400      410      420

          430      440      450      460      470      480
m987.pep  SFNLDPRSARLNTMGVVIESPKIAEQMERTLADTTPAYAYRVTLDRHNLQWHPATRK
          430      440      450      460      470      480
g987      SFNLDPRSARLNTMGVVIESPKIAEQMERTLADTTPEYAYRVTLDKHNLQWHPATRK
          430      440      450      460      470      480

          490      500      509
m987.pep  TYPNEPEAKLWKRIAANKILSLPIEGLLX
          490      500
g987      TYPNEPEAKLWKRIAANKILSLPIEGLLX
          490      500

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2977>:

```

a987.seq
1  ATGAAACAC GCAGCCTAAT TTCCCTTTTA TGCCTCCTTC TCTGTTTCATG
51  TTCTTCATGG TTGCCCCCAC TGAAGAAGC GACGGAAGC CGTCATTTCA
101 ATACTTCCAA ACCCGTCCGC CTGGACAACA TCCTGCAAAAT CCGGCACACC
151 CCTCATACCA ACGGGCTATC CGATATCTAT CTGTTGAACG ACCCCCACGA
201 AGCCTTTGCC GCCCGCGCCG CCCTTATCGA ATCTGCCGAA CACAGCCTCG
251 ATTTGCAATA CTACATCTGG CGCAACGACA TTCCCGGCCG ACTGCTGTTC
301 AACCTCGTGT ACCTTGCCGC AGAACGCGGT GTGCGCGTAC GCCTGTGTGT
351 GGACGACAAC AACACGCGCG GATTGGACGA CCTCCTGCTC GCCCTCGACA
401 GCCATCCCAA TATCGAAGTG CGCCTGTTCA ACCCCTTCGT CTTACGAAAA
451 TGGCGCGCAC TCGGCTACCT GACCGACTTC CCCCGCCTCA ACCGCCGCAT
501 GCACAACAAA TCCTTTACCG CCGACAACCG CGCCACCATA CTCGGCGGAG
551 GCAATATCGG CGACGAATAC TTCAAAGTCG GTGAGGACAC CGTTTTCGCC
601 GACCTGGACA TCCTCGCCAC CGGCAGCGTC GTCGGCGAAG TATCGCACGA
651 CTTCGACCGC TACTGGGCAA GCCATTCCGC CCACAACGCC ACGCGCATCA
701 TCCGCAGCGG CAACATCGGC AAGGGTCTTC AAGCACTCGG ATACAACGAC
751 GAAACGTCCA GACACGCGCT CCGCGCTAC CGCGAAACCG TCGAACAGTC
801 GCCCCTCTAC CAAAAATAC AGACAGGACG CATCGACTGG CAGAGCGTCC
851 AAACCCGCCT CATCAGCGAC GACCCTGCAA AAGGACTCGA CCGCGACCGC
901 CGCAAACCGC CGATTGCGCG GCGGCTGCAA GACGCGCTCA AACAGCCCGA
951 AAAAAGCGTC TATCTGTTT CACCCTATT CGTCCCACA AAATCCGGCA
1001 CAGACGCACT GGCAAACTG GTGCAGGACG GCATAGACGT TACCGTCTG
1051 ACCAACTCGC TACAGGCGAC CGACGTTGCC GCCGTCCATT CCGGCTATGT
1101 CAAATACCGA AAACCGCTGC TCAAAGCCGG CATCAAACTC TACGAGCTGC
1151 AACCCTAACCA TGCCGTCCCT GCCACAAAAG ACAAGGCCT GACCGGCAGC
1201 TCCGTAACCA GCCTGCATGC CAAAACCTTC ATTGTGGACG GCAAACGCAT
1251 CTTCATCGGC TCATTCAACC TCGACCCCGG TTCCGCACGG CTCAATACTG
1301 AAATGGGCGT TGTATCGAA AGCCCCAAAA TCGCAGAACA GATGGAGCGC
1351 ACCCTTGCCG ATACCTCACC CGAATACGCC TACCGCGTTA CCCTCGACAG
1401 GCACAACCGC CTGCAATGGC ACGATCCCGC CACCCGAAAA ACCTACCCGA
1451 ACGAACCCGA AGCCAACTT TGGAACGCA TCGCCGCAAA AATCCTATCC
1501 CTGCTGCCCA TAGAAAGTTT ATTATAG

```

This corresponds to the amino acid sequence <SEQ ID 550; ORF 2978.a>:

```

a987.pep
1  MKTRSLISLL CLLLCSSSW LPPLERTES RHFNTSKPVR LDNILQIRHT
51  PHTNGLSDIY LLNDPHEAFA ARAALIESAE HSLDLQYIYW RNDISGRLLF
101 NLVYLAERG VRVRLLLDDN NTRGLDLLLL ALDSHPNIEV RLFNPFVLRK
151 WRALGYLTD FRLNRRMHNK SFTADNRATI LGGRNIGDEY FKVGEDTVFA
201 DLDILATGSV VGEVSHDFDR YWASHSAHNA TRIIRSGNIG KGLQALGYND
251 ETSRHALLRY RETVEQSPLY QKIQTGRIDW QSVQTRLISD DPAKGLDRDR
301 RKPPPIAGRLQ DALKQPEKSV YLVSPYFVPT KSGTDALAKL VQDGDVTVL

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1397

351 TNSLQATDVA AVHSGYVKYR KPLLKAGIKL YELQPNHAVP ATKDKGLTGS
 401 SVTSLHAKTF IVDGKRIFIG SFNLDPRSAR LNTMGVVIE SPKIAEQMER
 451 TLAOTSPEYA YRVTLDRHNR LQWHPATRK TYPNEPEAKL WKRIAAILLS
 501 LLPIESLL*

m987/a987 98.8% identity in 508 aa overlap

m987.pep	10	20	30	40	50	60
	MKTRSLISLLCLLLCSCSSWLPPLEERTESRHFNTSKPVRLDNILQIRHTPHTNGLSDIY					
a987	10	20	30	40	50	60
	MKTRSLISLLCLLLCSCSSWLPPLEERTESRHFNTSKPVRLDNILQIRHTPHTNGLSDIY					
m987.pep	70	80	90	100	110	120
	LLNDPHEAFAARAALIESAEHSLDLQYYIWRNDISGRLLFNLVYLAERGVRVRLLLDDN					
a987	70	80	90	100	110	120
	LLNDPHEAFAARAALIESAEHSLDLQYYIWRNDISGRLLFNLVYLAERGVRVRLLLDDN					
m987.pep	130	140	150	160	170	180
	NTRGLDDLLALDSHPNIEVRLFNPFVLRKWRALGYLTDFFRLNRRMHNKSFTADNRATI					
a987	130	140	150	160	170	180
	NTRGLDDLLALDSHPNIEVRLFNPFVLRKWRALGYLTDFFRLNRRMHNKSFTADNRATI					
m987.pep	190	200	210	220	230	240
	LGGRNIGDEYFKVGEDTVFADLDILATGSVVGEVSHDFDRYWASHSAHNATRIIRSGDIG					
a987	190	200	210	220	230	240
	LGGRNIGDEYFKVGEDTVFADLDILATGSVVGEVSHDFDRYWASHSAHNATRIIRSGNTG					
m987.pep	250	260	270	280	290	300
	KGLQALGYNDETSRHALLRYRETVEQSPLYQKIQTGCIDWQSVTRTLISDDPAKGLDRDR					
a987	250	260	270	280	290	300
	KGLQALGYNDETSRHALLRYRETVEQSPLYQKIQTGRIDWQSVQTRLISDDPAKGLDRDR					
m987.pep	310	320	330	340	350	360
	RKPPIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGDVTVLTNSLQATDVA					
a987	310	320	330	340	350	360
	RKPPIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGDVTVLTNSLQATDVA					
m987.pep	370	380	390	400	410	420
	AVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTSLHAKTFIVDGKRIFIG					
a987	370	380	390	400	410	420
	AVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTSLHAKTFIVDGKRIFIG					
m987.pep	430	440	450	460	470	480
	SFNLDPRSARLNTMGVVIESPKIAEQMERTLADTTPAYAYRVTLDRHNRQLQWHPATRK					
a987	430	440	450	460	470	480
	SFNLDPRSARLNTMGVVIESPKIAEQMERTLADTSPEYAYRVTLDRHNRQLQWHPATRK					
m987.pep	490	500	509			
	TYPNEPEAKLWKRIAAILLSLLPIEGLLX					
a987	490	500	509			
	TYPNEPEAKLWKRIAAILLSLLPIESLLX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2979>:

g988.seq
 1 ATGAATAAAA ATATTAAATC TTAAATTTC CGGGAAAAAG ACCCGTTTTT

1398

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51  AAGTCGTGAA AAACAGCGTT ATGAACATCC TTTGCCCAGT CGGgaATGGA
101 TAATCGAATT GTTGGAGCGC AAAGGTGTGC CTTCAAAAAT CGAATCGCTT
151 GCACGCGAGC TGTCGATTAC GGAAGacgag tATGTCTTTT TTGAACGCCG
201 TCTGAaggCG atgGCGCGGG AcggtCAGGT TTTAATCAAC CGCCgaggcg
251 CagtTTGCGc gGCggacaag ctgGATTTGG TCAAATGccg Cgtcgaggcg
301 catAAgGAcg gtttcggctt cgcCGTGCCG CTCATGCCGA TGGACGAAGG
351 GGATTTCGTT TTATACGAAC GCCAgatgcy tggTgtcatG CAcggcgaca
401 ccgttACCGT CCGTCCTGCg ggtatggaCC GCAGGGGccg ccgcGAAGgg
451 acgtttctGG ATATTGT'CGA ACGCGCGCAA AGCAAAGTTG TCGGCCGTTT
501 CTATATGGAT AGGGGCGTGG CGATTTTGA GCGGAAGAC AAGCGTCTGA
551 ACCAAAGCAT CGTGTGGA CCGGACGGCG TGGCGCGTTT CAAACCCGAA
601 TCCGGTCAGG TTATCGTCGG CAAAATTGAG GTTTATCCCG AGCAAAACCG
651 GCCTGCAGTG GCAAAAATCA ITGAAGTTT GGGCGATTAT GCCGACAGCG
701 GGATGGAAAT cgAAATTGCC GTGCGCAAGC ATCATTGGCC GCaccgaTTC
751 AGTGAagcgt gtGcCAAATC CGcgaaAAAA ATtcccgacc ATGTACGCAA
801 AAGCGATTTG AAAGGCCGCG TCGATTTGTG CGACCTTCTT TTGGTAACGA
851 TAGACGGCGA AACGGCGCGC GATTTTCGACG ACGCGGTGTT TGCCGAAAAA
901 TCGGACGCA ATTACCGCCT GGTCTGGCG ATTGCGGATG TCAGCCATTA
951 TGTCCGCCCT GACGATGCGA TTGATGCAGA TGCTCAAGAA CGCACTACCA
1001 GCGTGTATTT CCGCGCCGT ATGATTCCGA TGCTGCCGA AAACCTGTCC
1051 AACGGCATCT GCTCGCTCAA TCCCGATGTC GAGCGT'TGT GTATGGTGTG
1101 CGATATGGTC GTTACCTATG CGGGCAATAT CAAAGAATAC CGCTTCTATC
1151 CCGCCGTGAT GCGCTCTCAT GCCCGCTGA CCTACAACCA AGTTTGGAAA
1201 TGGCTTTCAG ACGGCATCGG GAATCCGCAC AAAGCCCAA TCGACACGCT
1251 TTACAAGCTG TTTAAAATTT TGCAGAAAAA ACGTCTGGCG CGCGGGGCGG
1301 TGGAGTTTGA AAGCGTCGAA ACCCAGATGA TTTTCGACGA CAACGGCAAA
1351 ATCGAAAAAA TTGTCCCGT CGTCCGCAAC gatGCCACA AGCTGATTGA
1401 AGAATGTATG CTGGCGGCGA ATGTTTGC GC CGGATTTT CTGTTGAAAA
1451 ACAACATAC GGCTTTGTTC CGCAACCATT TGGGCCCCAC GCCCGAAAAA
1501 CTCGCCACCC TCGCGGAGCA GCTCGGTCTG TTGGGGCTTC AACTTGGCGG
1551 CCGCGACAAC CCGTCGCGCA AAGACTATGC CGCGCTTGCC GAACAATTCA
1601 AAGGCAGGCC GGATGCCGAA TTGCTGCAAG TCATGATGTT GCGCTCCATG
1651 CAGCAGCGCG TTTACGAACC GCATTGCGAA GGGCATTTTCG GTTTGGCTTA
1701 TGAAGCATAC GCCCACTTTA CCTCGCCCAT CCGCCGCTAT CCCGACCTGA
1751 CCGTCCACCG TGCCATCAAA GCCGTATTGA ACCGGAAGAC CTACACGCCA
1801 AACAAAAGCT GGCAGGCTTT GGGCGTGCAT ACTTCGTTTT GCGAACGCCG
1851 TGCCGACGAT GCTGGCCGCG ATGTGGAAAA CTGGCTGAAA ACTTATTATA
1901 TGCGCGATAA GGTGGGTGAA ATATTGAAG GcaaatCtc ccggggtgtg
1951 gcaaatTttg gaATATTGT CACTTTGGAC GATATccata tcgacggtct
2001 ggtacaTATC AGCGatttgg gcgaAGATTA TTTCaacttc cgccccgAAA
2051 TCATGGCAAT CGAAGGCGAA CGCAGCGGCA TCCGTTTCAA TATGGGGGAC
2101 AGGGTTGCCG TCCGGGTCGC GCGTGCCGAT TTGGATGATG GAAAAATCGA
2151 CTTTGTCTTA ATTGCCGGAG AAAGCGGCAG GCGGCGAAG GTCAAATTAT
2201 CCGCATCTGC CAAACCGGCA GGGGCGGCGG GGAAGGGGAA ATCGAAAACC
2251 ACCGCCGAGA AAAAAACAGC CCGATCGGCG AAAGTAAGGG GAAGGGGCGT
2301 GCCTGCCGTT GCCGAATCGG GGAAAAAGGC AAAGAAACCG GTTCCGATTA
2351 AGGTCAAAAA ACGGAAAGGC AAATCATAA

```

This corresponds to the amino acid sequence <SEQ ID 2980; ORF 988.ng>:

g988.pep

```

1  MNKNIKSLNL REKDPFLSRE KORYEHPLPS REWIIELLER KGVPSKIESL
51  ARELSITEDE YVFFERRLKA MARDGQVLIN RRGAVCAADK LDLVKCRVEA
101 HKDGFGEFVP LMPMDEGDFV LYERQMRGVM HGDVTVVRPA GMDRRGRREG
151 TFLDIVERAQ SKVVGRFYMD RGVAILEPED KRLNQSIVLE PDGVARFKPE
201 SGQVIVGKIE VYPEQNRPAV AKIIEVLGDY ADSGMEIEIA VRKHHLPFRF
251 SEACAKSAKK IPDHVRKSDL KGRVOLDCLP LVTIDGETAR DFDDAVFAEK
301 VGRNYRLVVA IADVSHYVRP DDAIDADAQE RSTSVYFPRR MIPMLPENLS
351 NGICSLNPDV ERLCMVCDMV VTYAGNIKEY RFYPVMRSH ARLTYNQVWK
401 WLSDGIGNPH KAQIDTLYKL FKILQKKRLA RGAVEFESVE TQMIFDDNGK
451 IEKIVPVVRN DAHKLIEECM LAANVCAADF LLKNKHTALF RNHLGPTPEK
501 LATLREQLGL LGLQLGGGDN PSPKDYAALA EQFKGRPDAE LLQVMMLRSM
551 QQAVYEPHCE GHFGLAYEAY AHFTSPIRRY PDLTVHRAIK AVLNRKTYTP
601 NKSWQALGVH TSFCERRADD AGRDVENWLK TTYMRDKVGE IFEGKISRGV
651 ANFGIFVTLT DIHIDGLVHI SDLGEDYFNF RPEIMAIEGE RSGIRFNMGD
701 RVAVRVARAD LDDGKIDFVL IAGESGRRRK VKLSASAKPA GAAGKGKSKT
751 TAEKKTARCG KVRGRGVPVAV AESGKKAKKP VPIKVKKRKG KS*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2981>:

```
m988.seq (partial)
1 ..ACAGTTCTGG ATATGTCTGA ACGCGCGCAA AGCAAAGTGG TCGGCCGTTT
51 CTATATGGAT AGGGGCGTGG CGATTTTGGG GCCGGAAGAC AAGCGTCTGA
101 ACCAAAGCAT CGTATTGGAA CCGGACGGCG TGGCGCGTTT CAAACCTGAA
151 TCCGGTCAGG TCATCGTCGG CGAAATTGAG GTTTATCCTG AGCAAAACCG
201 GCCGGCAGTG GCAAAAATCA TCGAAGTTTT GGGCGATTAT GCCGACAGCG
251 GCATGGAGAT TGAATTGCC GTGCGCAAGC ATCATTTGCC GCACCAATTC
301 AGTGAAGCGT GTGCCAAAGC TCGGAAAAAA ATTCCCGTCC ATGTACGCAA
351 AAGCGATTTC AAAGGCCGCG TCGATTGCG CGACCTGCCT TTGGTAACGA
401 TAGACGGCGA AACGGCGCGC GATTTCGACG ACGCGGTGTT TGCCGAAAAA
451 TCGGGACGCA ATTACCGTCT GGTCTGGCG ATTGCGGATG TCAGCCATTA
501 TGTCCGCCCT GACGATGTGA TTGATGCAGA TGCTCAAGAA CGCAGTACCA
551 GCGTATATTT CCCGCGCCGT GTGATTCCGA TGCTGCCGGA AAACCTGTCT
601 AACGGCATTT GCTCGCTCAA TCCCGATGTC GAGCGTTTGT GTATGTTGTG
651 CGATATGGTC GTTACCTATG CGGGCAATAT CAAAGAATAC CGCTTCTACC
701 CCGCCGTAAT GCGCTCTCAT GCCGCGCTGA CCTACAACCA AGTTTGGA
751 TGGATTTCAG ACGGCATCGA CCAATCCGTAC AAAGCCCAAA TCGACACCCT
801 TTACAAATC TTCAAATCC TTCAGAAAAA GCGTTTCGAA CGCGGCGCGG
851 TGGAGTTTGA AAGCGTCGAA ACCCAGATGA TTTTCGATGA CAACGGCAAA
901 ATCGAAAAAA TCGTCCCCGT TGTCCGCAAC GATGCCACA AGCTGATTGA
951 AGAATGTATG CTGGCGGCGA ATGTTTGCGC AGCGGATTTT CTGTTGAAAA
1001 ACAAGCATAC GGCTTTGTTC CGCAACCATT TGGGCCCCAC GCCCGAAAAA
1051 CTCGCCACCC TGCGCGAGCA GTCGGTCTG TTGGGGCTTC AACTTGGCGG
1101 CGGCGACAAC CCGTCGCCGA AAGACTATGC CGCGCTTGTG GAACAATTCA
1151 AAGGCAGACC TGATGCCGAA TTGCTGCAAG TCATGATGTT GCGCTCCATG
1201 CAGCAGGCGG TTTACGAACC GCATTGCGAC GGACACTTTG GTCTTGCCTA
1251 CGAAGCATAC GCCCACTTCA CCTCGCCCAT CCGCCGCTAT CCCGACCTGA
1301 CCGTACACCG CGCCATCAAA GCCGTGTTGA ATCAGCAAAC CTACACGCCA
1351 AAAAAAAGCT GGCAGGCTTT GGGCGTGCAT ACCTCGTTCT GTGAGCGCCG
1401 TGCCGACGAC GCCAGCCGCG ACGTGGAAAA CTGGCTGAAA ACCTATTATA
1451 TGCGCGATAA GGTGCGCGAA GTATCGAAG GTAAAATCTC CGGCATGACC
1501 AGTTTTGGTA TCTTTGTAAC ACTGGACGGC ATCCACATTG ACGGCTTGGT
1551 GCATATCAGC GATTTGGGCG AAGACTATTT CAACTCCGC CCCGAAATCA
1601 TGGCAATCGA AGGCGAACGC AGCGGCATCC GTTTCACAT GGGGGACAGG
1651 GTTGCCGTCC GGGTCGCCC TGCCGATTG GATGACGGAA AAATCGATTT
1701 TGTCCTGATT GCCGGGGGGA GCGGCAGGGG GCGGAAAGTT AAATCATCCG
1751 CGTCTGCCAA ACCGCGAGGG ACGGCGGGGA AAGGAAGCC GAAAACCGCC
```


1400

1801 GCCGAGAAAA AACAGCCCG AGGCGGCAAA GTAAGGGGAA GGGGCGCGTC
 1851 TGCCGCCGCA GAATCGAGGA AAAAGGCAAA GAAACCGGT CCGATTAAGG
 1901 TAAAAAACG GAAAGGCAAA TCATAA

This corresponds to the amino acid sequence <SEQ ID 2982; ORF 988>:

m988.pep (partial)
 1 ..TVLDIVERAQ SKVVGRFYMD RGVAILEPED KRLNQSIVLE PDGVARFKPE
 51 SGQVIVGEIE VYPEQNRPAV AKIEVLGDY ADSGMEIEIA VRKHHLP HQF
 101 SEACAKAAKK IPVHVRKSDL KGRVDLRDLP LVTIDGETAR DFDDAVFAEK
 151 VGRNYRLVVA IADVSHYVRP DDVIDADAQE RSTSVYFPRR VIPMLPENLS
 201 NGICSLNPDV ERLCMVCDMV VTYAGNIKEY RFYPAVMRSH ARLTYNQVWK
 251 WISDGIDHPY KAQIDTLYKL FKILQKKRFE RGAVEFESVE TQMIFDDNGK
 301 IEKIVPVVRN DAHKLIEECM LAANVCAADF LLKNKHTALF RNHLGPTPEK
 351 LATLREQLGL LGLQLGGGDN PSPKDYAALV EQFKGRPD AE LLQVMMLRSM
 401 QOAVYEPHCD GHFGLAYEAY AHFTSPIRRY PDLTVHRAIK AVLNQQTYP
 451 KKSQALGVH TSFCERRADD ASRDVENWLK TYMRDKVGE VFEGKISGMT
 501 SFGIFVTL DG IHIDGLVHIS DLGEDYFNFR PEIMAIEGER SGIRENMGDR
 551 VAVRVARADL DDGKIDFVLI AGGSGRGRKV KSSASAKPAG TAGKGKPKTA
 601 AEKKTARGGK VRGRGASAAA ESRKAKKPV PIKVKRRKGK S*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m988/g988 94.2% identity in 642 aa overlap

m988.pep				10	20	30
				TVLDIVERAQSKVVGRFYMDRGVAILEPED		
g988	LYERQMRGMHGDVTVVRPAGMDRRGRREGTFLDIVERAQSKVVGRFYMDRGVAILEPED					
	130	140	150	160	170	180
m988.pep		40	50	60	70	80
		KRLNQSIVLEPDGVARFKPESGQVIVGEIEVYPEQNRPAVAKIEVLGDYADSGMEIEIA				
g988		KRLNQSIVLEPDGVARFKPESGQVIVGKIEVYPEQNRPAVAKIEVLGDYADSGMEIEIA				
	190	200	210	220	230	240
m988.pep		100	110	120	130	140
		VRKHHLP HQFSEACAKAAKKIPVHVRKSDLKGRVDLRDLP LVTIDGETARDFDDAVFAEK				
g988		VRKHHLP HRFSEACAKSAKKIPDHVRKSDLKGRVDLCLDLP LVTIDGETARDFDDAVFAEK				
	250	260	270	280	290	300
m988.pep		160	170	180	190	200
		VGRNYRLVVAIADVSHYVRPDDVIDADAQERSTSVYFPRRVI PMLPENLSNGICSLNPDV				
g988		VGRNYRLVVAIADVSHYVRPDDAIDADAQERSTSVYFPRRMIPMLPENLSNGICSLNPDV				
	310	320	330	340	350	360
m988.pep		220	230	240	250	260
		ERLCMVCDMVV TYAGNIKEYRFYPAVMRSHARLTYNQVWKWISDGIDHPYKAQIDTLYKL				
g988		ERLCMVCDMVV TYAGNIKEYRFYPAVMRSHARLTYNQVWKWLSDGIGNPHKAQIDTLYKL				
	370	380	390	400	410	420
m988.pep		280	290	300	310	320
		FKILQKKRFERGAVEFESVETQMIFDDNGKIEKIVPVVRNDAHKLIEECMLAANVCAADF				
g988		FKILQKKRLARGAVEFESVETQMIFDDNGKIEKIVPVVRNDAHKLIEECMLAANVCAADF				
	430	440	450	460	470	480
m988.pep		340	350	360	370	380
		LLKNKHTALFRNHLGPTPEKLATLREQLGLLGLQLGGGDNPSPKDYAALVEQFKGRPD AE				
g988		LLKNKHTALFRNHLGPTPEKLATLREQLGLLGLQLGGGDNPSPKDYAALAEQFKGRPD AE				

1401

	490	500	510	520	530	540
	400	410	420	430	440	450
m988 . pep	LLQVMMLRSMQQAVYEPHCDGHFGLAYEAYAHFTSPIRRYPDLTVHRAIKAVLNQOTYTP					
g988	LLQVMMLRSMQQAVYEPHCEGHFGLAYEAYAHFTSPIRRYPDLTVHRAIKAVLNKRKTYTP					
	550	560	570	580	590	600
	460	470	480	490	500	509
m988 . pep	KKSWQALGVHTSFCERRADDASRDVENWLKTYMMDKVGEVFEGKIS-GMTSFGIFVTLD					
g988	NKSQWALGVHTSFCERRADDAGRDVENWLKTYMMDKVGEVFEGKISRGVANFGIFVTLD					
	610	620	630	640	650	660
	510	520	530	540	550	569
m988 . pep	GIHIDGLVHISDLGEDYFNFRPEIMAIEGERSGIRENMGDRVAVRVARADLDDGKIDFVL					
g988	DIHIDGLVHISDLGEDYFNFRPEIMAIEGERSGIRENMGDRVAVRVARADLDDGKIDFVL					
	670	680	690	700	710	720
	570	580	590	600	610	629
m988 . pep	IAGSGRGRKVKSSASAKPAGTAGKGPKTAAEKKTARGGKVRGRGASAAESRKKAKKP					
g988	IAGESGRRRKVKLSASAKPAGAAGKGSKTAEKKTARCGKVRGRGVPAAVESGKKAKKP					
	730	740	750	760	770	780
	630	640				
m988 . pep	VPIKVKRRKGKXS					
g988	VPIKVKRRKGKXS					
	790					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2983>:

```

a988 . seq
1  ATGAATAAAA ATATTAAATC TTAAATTTA CGGGAAAAAG ACCCGTTTTT
51  AAGTCGTGAA AAACAGCGTT ATGAACATCC TTTGCCAGT CGGGAATGGA
101 TAATCGAGCT GCTTGAACGT AAAGGCGTAC CATCCAAGAT TGAAGCTTTG
151 GTACGCGAAT TGTCGATTAA GGAAGAAGAG TACGAATTTT TCGAACGTCG
201 TCTGAAGGCG ATGGCGGGG ACGGTCAGGT TTTAATCAAC CGTCGGGGCG
251 CGGTTTTCGC GCGGACAAA TTGGATTGCG TCAAATGCCG TGTCAAGGCG
301 CACAAAGACC GCTTCGGTTT CGCCGTGCCG CTCACGCCCC CCAAAGACGG
351 TGATTTTGTC TTGTACGAAC GCCAGATGCG CGGCATTATG CACGGCGATA
401 TTGTCACTGT TCGTCCTGCC GGCATGGACG GTAGGGGCGG CCGCGAAGGG
451 ACGGTTCTGG ATATTGTCGA ACGCGCGCAA AGCAAAGTGG TCGGCCGTTT
501 CTANATGGAT AGGGGCGTGG CGATTTTGGG GCCGGAAGAC AAGCGTCTGA
551 ACCAAAGCAT CGTATTGGAA CCGGACGGCG TGGCGCGTTT CAAACCTGAA
601 TCCGGTCAGG TCATCGTCGG CGAAATTGAG GTTTATCCTG AGCAAAACCG
651 GCCGGCAGTG GCAAAAATCA TCGAAGTTT GGGCGATTAT GCCGACAGCG
701 GCATGGAGAT TGAAATTGCC GTGCGCAAGC ATCATTTGCC GCACCAATTC
751 AGTGAAGCGT GTGCCAAAGC CGCGAAAAAA ATTCCCGACC ATGTACGCAA
801 AAGCGATTTG AAAGGCGCGC TCGATTTCGG CGACCTGCCT TTGGTAACGA
851 TAGACGGCGA AACGGCTCGA GATTTTGACG ATGCGGTGTT TGCCGAGAAA
901 ATCGGACGCA ATTACCGTCT GGTCTGGCG ATTGCCGATG TCAGCCATTA
951 TGTCCGCCCC GATGACGCTA TCGACACGGA CGCTCAGGAA CGCAGCACCA
1001 GTGTTTACTT CCCGCGCCGC GTGATTCCCA TGTGCGCGGA AAACCTGTCC
1051 AACGGCATCT GCTCGCTCAA TCCTCATGTC GAGCGTTTGT GTGTGGTGTG
1101 CGATATGGTT ATCACTTACG CGGGCAATAT CAAAGAATAC CGCTTCTACC
1151 CCGCCGTGAT GCGCTCTCAT GCGCGCCTGA CCTACAACCA AGTTTGAAAA
1201 TGGCTTTCAG GCGGCATCGA GCATCCGTTC AAAACCCAAA TCGACACGCT
1251 TTACAAACTC TTCAAAATCC TTCAGAAAAA GCGTTTGGAA CGCGGGGCGG
1301 TGGAGTTTGA CAGCATCGAA ACCCAAATGC TTTTCGACGA CAACGGTAAA
1351 ATTGAAAAAA TCGTCCCGT TGTCGCAAC GATGCCACA AGCTGATTGA
1401 AGAATGTATG TTGGCGGCAA ACGTTTGCAG AGCGGATTTT CTGTTGAAAA
1451 ACAAGCATAC CGCATTTGTC CGCAACCATT TGGGGCCAC GCCGAAAAA
1501 CTCGCCGCTT TGCGCGAGCA GCTCGGTCTG TTGGGGCTTC AACTTGGCGG
1551 CGGCGACAAC CCGTCGCCGA AAGACTATGC CGCGCTTGCC GGACAGTTCA

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1402

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1601 AAGGCAGGCC GGATGCCGAA TTGCTGCAAG TCATGATGTT GCGCTCCATG
1651 CAACAGGCGG TTTACGAACC GCATTGCGAC GGACACITTG GTCTTGCCCTA
1701 CGAAGCATAC GCCCACTTCA CCTCGCCCAT CCGCCGCTAT CCCGACCTGA
1751 CCGTACACCG CGCCATCAAA GCCGTGTTGA ATCAGCAAAC CTACACGCCA
1801 AAAAAAAGCT GGCAGGCTTT GGCCTGTCAT ACCTCGTTCT GTGAGCGCCG
1851 TGCCGACGAC GCCAGCCGCG ACGTGGAAAA CTGGCTGAAA ACCTATTATA
1901 TGCGCGATAA GGTGCGCGAA GTATTGGAAG GTAAAAATCTC CGGCATGACC
1951 AGTTTTGGTA TCTTTGTAACT ACTGGACGGC ATCCACATTG ACGGCTTGGT
2001 GCATATCAGC GATTGCGCG AAGACTATTT CAACTTCCGC CCCGAAATCA
2051 TGGCAATCGA AGGCGAACGC AGCGGCATCC GTTTCACAT GGGGGACAGG
2101 GTTGCCGTCC GGTGCGCCCG TGCCGATTG GATGACGGAA AAATCGATT
2151 TGTCTGATT GCCGGGGGGA GCGGCAGGGG GCGGAAAGTT AAATCATCCG
2201 CGTGTGCCAA ACCGGCAGGG ACGGCGGGGA AAGGGAAGCC GAAACCGCC
2251 GCCGAGAAAA AACAGCCCG AGGCGGCAAA GTAAGGGGAA GGGGCGCGTC
2301 TGCGCCCGCA GAATCGAGGA AAAAGGCAAA GAAACCGGTT CCGATTAAGG
2351 TAAAAAACG GAAAGGCAAA TCATAA

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This corresponds to the amino acid sequence <SEQ ID 2984; ORF 988.a>:

a988.pep

```

1 MNKNIKSLNL REKDFFLSRE KQRYEHPLPS REWIIELLER KGVPSKIEAL
51 VRELSIKEEE YEFFERRLKA MARDGQVLIN RRGAVCAADK LDIVKCRVKA
101 HKDRFGFAVP LTPAKDGFV LYERQMRGIM HGDIVTVRPA GMDGRGRREG
151 TVLDIVERAQ SKVVGFRFXMD RGVAILPEP KRLNQSIVLE PDGVARFKPE
201 SGQVIVGEIE VYPEQNRPAV AKIIEVLGDY ADSGMEIEIA VRKHHLPHQF
251 SEACAKAAKK IPDHVRKSOL KGRVDLRDL LVTIDGETAR DFDDAVFAEK
301 IGRNYRLVVA IADVSHYVRP DDAIDTDAQE RSTSVYFRR VIPMLPENLS
351 NGICSLNPHV ERLCVVCDMV ITYAGNIKEY RFYPAVMRSH ARLTYNQVWK
401 WLSGGIEHPF KTQIDTLYKL FKILQKKRFE RGAVEFDSIE TQMLFDDNGK
451 IEKIVPVVRN DAHKLIEECM LAANVCAADF LLKNKHTALF RNHLGPTPEK
501 LAALREQLGL LGLQLGGGDN PSPKDYAALA GQFKGRPDAE LLQVMMLRSM
551 QQAVYEPHCD GHFGLAYEAY AHFTSPIRRY PDLTVHRAIK AVLNQQTYP
601 KKSQWALGVH TSFCERRADD ASRDVENWLK TYMRDKVGE VFEGKISGMT
651 SFGIFVTLDG IHIDGLVHIS DLGEDYFNFR PEIMAEGER SGIRFNMGRD
701 VAVRVARADL DDGKIDFVLI AGSGRGRKV KSSASAKPAG TAGKGKPKTA
751 AEKKTARGGK VRGRGASAAA ESRKKAKKPV PIKVKRKGK S*

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m988/a988 97.0% identity in 641 aa overlap

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                                10      20      30
m988.pep                                TVLDIVERAQSKVVGFRFYMDRGVAILEPED
                                |||
a988      LYERQMRGIMHGDIVTVRPA GMDGRGRREGTVLDIVERAQSKVVGFRFXMDRGVAILEPED
                                130      140      150      160      170      180

                                40      50      60      70      80      90
m988.pep      KRLNQSIVLEPDGVARFKPESGQVIVGEIEVYPEQNRPAVAKIIEVLGDYADSGMEIEIA
                                |||
a988      KRLNQSIVLEPDGVARFKPESGQVIVGEIEVYPEQNRPAVAKIIEVLGDYADSGMEIEIA
                                190      200      210      220      230      240

                                100      110      120      130      140      150
m988.pep      VRKHHLPHQFSEACAKAAKKIPVHVRKSDLKGRVDLRDLPLVTIDGETARDFDDAVFAEK
                                |||
a988      VRKHHLPHQFSEACAKAAKKIPDHVRKSDLKGRVDLRDLPLVTIDGETARDFDDAVFAEK
                                250      260      270      280      290      300

                                160      170      180      190      200      210
m988.pep      VGRNYRLVVAIADVSHYVRPDDVIDADAQERSTSVYFRRVIPMLFENLSNGICSLNPDV
                                :|||
a988      IGRNYRLVVAIADVSHYVRPDDAIDTDAQERSTSVYFRRVIPMLFENLSNGICSLNPHV
                                310      320      330      340      350      360

                                220      230      240      250      260      270
m988.pep      ERLCMVCDMVITYAGNIKEYRFYPAVMRSHARLTYNQVWKWISDGIDHPYKAQIDTLYKL
                                |||
a988      ERLCVVCDMVITYAGNIKEYRFYPAVMRSHARLTYNQVWKWLSGGIEHPFKTQIDTLYKL

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1403

	370	380	390	400	410	420
	280	290	300	310	320	330
m988.pep	FKILQKKRFERGAVEFESVETQMIFDDNGKIEKIVPVVRNDAHKLIEECMLAANVCAADF					
a988	FKILQKKRFERGAVEFDSIETQMLFDDNGKIEKIVPVVRNDAHKLIEECMLAANVCAADF					
	430	440	450	460	470	480
	340	350	360	370	380	390
m988.pep	LLKNKHTALFRNHLGPTPEKLATLREQLLGLQLGGDNPSPKDYAALVEQFKGRPDAE					
a988	LLKNKHTALFRNHLGPTPEKLAALREQLLGLQLGGDNPSPKDYAALAGQFKGRPDAE					
	490	500	510	520	530	540
	400	410	420	430	440	450
m988.pep	LLQVMMLRSMQQAVYEPHCDGHFGLAYEAYAHFTSPIRRYPDLTVHRAIKAVLNQQTYP					
a988	LLQVMMLRSMQQAVYEPHCDGHFGLAYEAYAHFTSPIRRYPDLTVHRAIKAVLNQQTYP					
	550	560	570	580	590	600
	460	470	480	490	500	510
m988.pep	KKSWQALGVHTSFCERRADDASRDVENWLKTYMRDKVGEVFEGKISGMTSFGIFVTLDG					
a988	KKSWQALGVHTSFCERRADDASRDVENWLKTYMRDKVGEVFEGKISGMTSFGIFVTLDG					
	610	620	630	640	650	660
	520	530	540	550	560	570
m988.pep	IHIDGLVHISDLGEDYFNFRPEIMAIEGERSGIRFNMGDRVAVRVARADLDGKIDFVLI					
a988	IHIDGLVHISDLGEDYFNFRPEIMAIEGERSGIRFNMGDRVAVRVARADLDGKIDFVLI					
	670	680	690	700	710	720
	580	590	600	610	620	630
m988.pep	AGGSGRGRKVKSSASAKPAGTAGKGKPKTAAEKKTARGGKVRGRGASAAESRKKAKKPV					
a988	AGGSGRGRKVKSSASAKPAGTAGKGKPKTAAEKKTARGGKVRGRGASAAESRKKAKKPV					
	730	740	750	760	770	780
	640					
m988.pep	PIKVKKRKGKSX					
a988	PIKVKKRKGKSX					
	790					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2985>:

```

g989.seq
1  ATGACCCCTT TCACACTGAA AAAAACCGTC CTGCTGCTCG GCACTGCCTT
51  TGCCGCCGCA TCTGTCCACG CATCCGGCTA CCACTTCGGC ACACAGTCGG
191 TCAACGCGCA AAGCACGGCA AATGCCGCGG ACGCGTCGAC CATCTTCTAC
151 AATCCCGCCG GCCTGACCAA ACTCGACAGC AGCCAGATTT CCGTCAACGC
291 CAACATCGTG CTGCCAGCA TTCATTATGA AGCAGATTCC GCCACCGACT
251 TTACCGGGCT TCCCGTCCAA GGTTCATAAA ACGGCAAAAT CACCAAAACC
391 ACGGTCGCAC CCCACATTTA CGGCGCATAC AAAGTCAACG ACAATCTGAC
351 CGTGGGCTTG GGCCTGTACG TCCCCTTCGG CTCTGCCACC GAATACGAAA
491 AAGATTCCGT GTTGCGCCAC AACATCAACA AACTCGGTCT GACCAGCATC
451 GCCGTCGAAC CTGTCGCCGC GTGGAAGTCT AACGAACGCC ATTCCTTCGG
591 CGCAGGCATC ATCGCCCAAC ATAATTCCGC CGAAGTCCGC AAATATGCCG
551 ACTGAGGAAT CCCAAAAAAA GCGCAAATGC TGCAAGCAAC ACCTTCTAAT
691 CCTACTGCCG CTGCTCAAAT CAAGGCCGAC GGACACGCCG ATGTCAAAGG
651 CAGCGATTGG GCGCTCGGCT ACCAACTGGC GTGGATGTGG GACATCAACG
791 ACCGCGCGCG CGTGGGCGTG AACTACCGTT CCAAAGTTTC ACACACGCTC
751 AAAGGCGATG CCGAATGGGC GGCAGACGGC GCGGCGGCGA AACAACAGTG
891 GAATGACAAT ATGCTCACAC CGCTCGGTTA CACGGCGAAT GAAAAAGCCA
851 GTGTCAAAAT CGTAACGCCT GAGTCTTTGT CCGTACACGG CATGTACAAA

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1404

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901 GTGTCGACAA AAGCCGACCT GTTCGGCGAC GTAACCTGGA CGCGCCACAG
951 CCGCTTCAAT AAGGCGGAAC TGTTTTTTGA AAAAGAAAAA AATATTGCTA
1001 ATGGCAAAAA ATCCGACCGC ACCACCATCA CCCCCTACTG CGCGCAACACC
1051 TACAAAGTCG GCTTGGGCGG TTCTTATCAA ATCAGCGAAC CGCTGCAACT
1101 GCGCGTCGGC ATCGCTTTTG ACAAACCGCC TGTCGCGAAC GCCGACTAcC
1151 GCATGAACAG CCTGCCCGAC GGCAACCGCA TCTGGTTCTC CGCCGGCATG
1201 AAATACCATA TCGGCAAAAA CCACGTCGTC GATGCCGCTT ACACCCACAT
1251 CCACATCAAC GACACCAGCT ACCGCACGGC GAAGGCAAGC GGCAACGATG
1301 TGGACAGCAA AGGTGCGTCT TCGGCACGTT TCAAAAACCA CGCCGACATC
1351 ATCGGCCTGC AATACACCTA CAAATTCAAA TAA

```

This corresponds to the amino acid sequence <SEQ ID 2986; ORF 989.ng>:

g989.pep

```

1 MTPFTLKKT V LLLGTAFAAA SVHASGYHFG TQSVNAQSTA NAADASTIFY
51 NPAGLTKLDS SQISVNANIV LPSIHYEADS ATDFTGLPVQ GSKNGKITKT
101 TVAPHIYGAY KVNNDLTVGL GVVVPFGSAT EYEKDSVLRH NINKLGLTSI
151 AVEPVAAWKL NERHSFGAGI IAQHNSAELR KYAD*GIFPK AQMLQATPSN
201 PTAAAIKAD GHADVKGS DW GVGQLAWMW DINDRVRGV NYRSKVSHTL
251 KGDAEWAADG AAKQQWNDN MLTPLGYTAN EKASVKIVTP ESLSVHGMK
301 VSDKADLFGD VTWTRHSR FN KAELFFEKEK NIANGKXSDR TTITPNWRNT
351 YKVLGGSYQ ISEPLQLRVG IAFDKPPVRN ADYRMNSLPD GNRIWFSAGM
401 KYHIGKNHVV DAAYTHIHIN DTSYRTAKAS GNDVDSKAS CARFKNHADI
451 IGLQYTYKFK *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2987>:

m989.seq

```

1 ATGACCCCTT CCGCACTGAA AAAAACCCTC CTGCTGCTCG GCACTGCCTT
51 TGCCGCCGCA TCCGTCCACG CATCCGGCTA CCACTTCGGC ACACAGTCGG
101 TCAACGCGCA AAGCACGGCA AATGCCGCGC CGCAGAGAGC CGCCGACGCA
151 TCGACCATCT TCTACAACCC TGCCGGCCTG ACCAACTCG ACAGCAGCCA
201 GATTTCCTGC AACGCCAACA TCGTGCTGCC CAGCATTTCAT TATGAGGCGG
251 ATTCCGCCAC CGACTTTACC GGGCTTCCCG TCCAAGSTTC GAAAAGCGGC
301 AAAATCACCA AAACACGGT CGCGCCAC ATCTACGCG CATACAAAGT
351 CAACGACAAT CTGACCGTGG GCTTGGGCGT GTACGTCCCC TTCGGCTCTG
401 CCACCGAATA CGAAAAAGAT TCCGTGTTGC GCCACAACAT CAACAACTC
451 GGTCTGACCA GCATCGCCGT CGAACCTGTC GCCGCGTGGG AACTCAACGA
501 CCGCCATTCC TTCCGCGCAG GCATCATCGC CCAACATACT TCCGCCGAAC
551 TGCGCAAATA TGCCGACTGG GGGATTAAGA GTAAAGCAGA GATATTGACG
601 GCAAAACCGC CCAACCTAA CGGTGTAGCC GAAGCTGCAA AAATTCAGGC
651 CGACGGACAC GCCGATGTCA AAGGCAGCGA TTGGGGCTTC GGCTACCAAC
701 TGGCGTGGAT GTGGGACATC AACGACCGTG CGCGCGTGGG CGTGAACATC
751 CGTTCCAAAG TCTCGCACAC GCTCAAAGGC GATGCCGAAT GGGCGGCAGA
801 CGGCGCGGCG GCGAAAGCAA TGTGGAGTAC GATGCTTGCA GCAAACGGCT
851 ACACGGCGAA TGAAAAAGCC CGCGTTAAAA TCGTACGCC TGAGTCTTTG
901 TCCGTACACG GTATGTACAA AGTGTCCGAT AAAGCCGACC TGTCGGCGA
951 CGTAACCTGG ACGCGCCACA GCCGCTTCGA TAAGGCGGAA CTGGTTTTTG
1001 AAAAAGAAAA AACCGTCTGC AAAGGCAAAT CCGACCGCAC CACCATCACC
1051 CCCAACTGGC GCAACACCTA CAAAGTCGGC TTCGGCGGTT CTATCAAAAT
1101 CAGCGAACCG CTGCAACTGC GCGCCGGCAT CGCTTTTGAC AAATCGCCCG
1151 TCCGCAACCG CGACTACCGC ATGAACAGCC TACCCGACGG CAACCGCATC
1201 TGGTTCTCCG CCGGTATGAA ATACCATATC GGTAAAAACC ACGTCGTGCA
1251 TGCCGCTTAC ACCCACATCC ACATCAACGA CACCAGCTAC CGCACGGCGA
1301 AGGCAAGCGG CAACGATGTG GACAGCAAAG GCGCGTCTTC CGCACGTTTC
1351 AAAAACCACG CCGCATCATC CGGTCTGCAA TACACCTACA AATCAAATA
1401 A

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This corresponds to the amino acid sequence <SEQ ID 2988; ORF 989>:

m989.pep

```

1 MTPSALKKT V LLLGTAFAAA SVHASGYHFG TQSVNAQSTA NAAAAEAADA
51 STIFYNPAGL TKLDSQISV NANIVLPSIH YEADSATDFT GLPVQGSKSG
101 KITKTTVAPH IYGAYKVDN LTVGLGVYVP FGSATEYEKD SVLRHNINKL
151 GLTSIAVEPV AAWKLNDRHS FGAGIIAQHT SAELRKYADW GIKSKAEILT
201 AKPPKPNQVA EAAKIQADGH ADVKGS DWG GYQLAWMWDI NDRARVGVNY
251 RSKVSHTLKG DAWEAADGAA AKAMWSTMLA ANGYTANEKA RVKIVTPESL
301 SVHGMKVS D KADLFQDVTW TRHSRFDKAE LVFEKEKT VV KGKSDRTTIT

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1405

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351 PNWRNTYKVG FGGSYQISEP LQLRAGIAFD KSPVRNADYR MNSLPDGNRI
401 WFSAGMKYHI GKNHVVDAAI THIHINDTSY RTAKASGNDV DSKGASSARF
451 KNHADIIGLQ YTYKFK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

g989/m989 90.0% identity in 468 aa overlap

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              10      20      30      40      50
g989.pep      MTPFTLKKTVLLLGTAFAAASVHASGYHFGTQSVNAQSTANAA-----DASTIFYNPAGL
              ||| :|||||
m989          MTPSALKKTVLLLGTAFAAASVHASGYHFGTQSVNAQSTANAAAAEADASTIFYNPAGL
              10      20      30      40      50      60

              60      70      80      90      100     110
g989.pep      TKLDSSQISVNANIVLPSIHYEADSATDFTGLPVQGSKNGKITKTTVAPHIYGAYKVNND
              ||| :|||||
m989          TKLDSSQISVNANIVLPSIHYEADSATDFTGLPVQGSKSGKITKTTVAPHIYGAYKVNND
              70      80      90      100     110     120

              120     130     140     150     160     170
g989.pep      LTVGLGVYVPFGSATEYEKDSVLRHNINKLGLTSIAVEPVAAWKLNERHSFGAGIIAQHN
              ||| :|||||
m989          LTVGLGVYVPFGSATEYEKDSVLRHNINKLGLTSIAVEPVAAWKLNDRHSFGAGIIAQHT
              130     140     150     160     170     180

              180     190     200     210     220     230
g989.pep      SAELRKYADXGIPKKAQMLQATPSNPTA---AAQIKADGHADVKGSDWGVGYQLAWMWDI
              ||| :|||||
m989          SAELRKYADWGIKSAEILTAKPPKPNGVAEAAKIQADGHADVKGSDWGVGYQLAWMWDI
              190     200     210     220     230     240

              240     250     260     270     280     290
g989.pep      NDRARVGVNYRSKVSHTLKGDAEWAADGAAAKQQWNDNMLTPLGYTANEKASVKIIVTPES
              ||| :|||||
m989          NDRARVGVNYRSKVSHTLKGDAEWAADGAAAKAMWS-TMLAANGYTANEKARVKIIVTPES
              250     260     270     280     290

              300     310     320     330     340     350
g989.pep      LSVHGMVKVSDKADLFGDVTWTRHSRFNKAELEFFEKEKNIANGKKS DRTTITPNWRNTYK
              ||| :|||||
m989          LSVHGMVKVSDKADLFGDVTWTRHSRFDKAELEFFEKEKT VVKGK-SDRTTITPNWRNTYK
              300     310     320     330     340     350

              360     370     380     390     400     410
g989.pep      VGLGGSYQISEPLQLRVGIAFDKPPVRNADYRMNSLPDGNRIWFSAGMKYHIGKNHVVD
              ||:|||||
m989          VGFSGSYQISEPLQLRAGIAFDKSPVRNADYRMNSLPDGNRIWFSAGMKYHIGKNHVVD
              360     370     380     390     400     410

              420     430     440     450     460
g989.pep      AYTHIHINDTSYRTAKASGNDVDSKGASCARFKNHADIIGLQYTYKFKX
              ||| :|||||
m989          AYTHIHINDTSYRTAKASGNDVDSKGASSARFKNHADIIGLQYTYKFKX
              420     430     440     450     460

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2989>:

```

a989.seq
1   ATGACCCCTT CCGCACTGAA AAAAACCGTC CTA CTGCTCG GCACTGCCTT
51  TGCCGCCGCA TCCGCACAAG CCTCCGGCTA CCA CTTCGGC ACACAGTCGG
101 TCAACGCGCA AAGCACGGCA AATGCCGCG CCG CAGAAGC CGCCGACGCA
151 TCGACCATCT TCTACAACCC TGCCGGCCTG ACCAAACTCG ACAGCAGCCA
201 GATTTCGGTC AACGCCAACA TCGTGCTGCC CAG CATT CAT TATGAGCGG
251 ATTCGCCAC CGACTTTACC GGGCTTCCG TCCAAGGTT CAAAAGCGG

```

1406

```

301 AAAATCACCA AAACCACGGT CGCGCCCCAC ATCTACGGCG CATACAAAGT
351 CAACGACAAT CTGACCGTAG GCTTGGGCGT GTACGTCCCC TTCGGTCTG
401 CCACCGAATA CGAAAAAGAT TCCGTGTTGC GCCACAACAT CAACAACTC
451 GGTCTGACCA GCATCGCCGT CGAACCTGTC GCCGCGTGGA AACTCAACGA
501 ACGCCATTCC TTCGGCGCAG GCATCATCGC CCAACATACT TCCGCCGAGC
551 TGGCCAAATA TGCCGACTGG GGGATTATGG AAAAAGCGAA AGCACTAAAA
601 GAAACACCCC CCAATCCAAC TAAAGCCGCC CAAATCAAAG CCGACGGACA
651 CGCCGATGTC AAAGGCAGCG ATTGGGGCTT CGGCTACCAA CTGGCGTGGA
701 TGTGGGACAT CAACGACCGT GCGCGCGTGG GCGTGAATA CCGTCCAAA
751 GTCTCACACA CGCTCAAAGG CGATGCCGAA TGGGCGGCAG ACGACGCAAT
801 GGCGAACAG TTATGGGATG CAAACAACT CGCACTGCTC GGCTACACGC
851 CAAGCGAAAA AGCCCGCGTT AAAATCGTTA CGCCCGAGTC TTTGTCCGTA
901 CACGGTATGT ACAAAGTGTG CGACAAAGCC GACCTGTTCT GCGACGTAAC
951 TTGGACGCGC CACAGCCGCT TCGATAAGGC GGAAGTGGTT TTTGAAAAAG
1001 AAAAAACCAT CGTCAACGGC AAATCCGACC GCACCACCAT CACCCCCAAC
1051 TGGCGCAACA CCTACAAAGT CGGCTTCGGC GGTCTTTATC AAATCAGCGA
1101 ACCGCTGCAA CTGCGCGCCG GCATCGCTTT TGACAAATCG CCCGTCCGCA
1151 ACGCCGACTA CCGCATGAAC AGCCTGCCCG ACGGCAACCG CATCTGGTTC
1201 TCCGCGGCA TGAAATACCA TATCGGCAAA AACCACGTCG TCGATGCCGC
1251 CTACACCCAC ATCCACATCA ACGACACCAG CTACCGCAG GCGAAGGCAA
1301 GCGGCAACGA TGTGGACAGC AAAGGCGCGT CTCCGCACG TTTCAAAAAC
1351 CACGCCGACA TCATCGGCCT GCAATACACC TACAAATTCA AATAA

```

This corresponds to the amino acid sequence <SEQ ID 2990; ORF 989.a>:

```

a989.pep
1  MTPSALKKTV LLLGTAFAAA SAQASGYHFG TQSVNAQSTA NAAAAEADA
51  STIFYNPAGL TKLDSSQISV NANIVLPSIH YEADSATDFT GLPVQGSKSG
101 KITKTTVAPH IYGAYKVNDN LTVGLGVYVP FGSATEYEKD SVLRHNINKL
151 GLTSIAVEPV AAWKLNERHS FGAGIIAQHT SAELRKYADW GIMEKAKALK
201 ETPNPETKAA QIKADGHADV KGSWGFYQYQ LAWMWDINDR ARVGVNYSK
251 VSHTLKGADE WAADDAMAKQ LWDANKLALL GYTPSEKARV KIVTPESLSV
301 HGMYKVSDKA DLFQDVTWTR HSRFDKAEIV FEKEKTIYNG KSDRTTITN
351 WRNTYKVGFG GSYQISEPLQ LRAGIAFDKS PVRNADYRMN SLPDGNRIWF
401 SAGMKYHIGK NHVVDAAATH IHINDTSYRT AKASGNDVDS KGASSARFKN
451 HADIIGLQYT YKFK*

m989/a989 93.1% identity in 467 aa overlap

          10      20      30      40      50      60
m989.pep  MTPSALKKTVLLLGTAFAAASVHASGYHFGTQSVNAQSTANAAAAEADASTIFYNPAGL
a989      MTPSALKKTVLLLGTAFAAASVHASGYHFGTQSVNAQSTANAAAAEADASTIFYNPAGL
          10      20      30      40      50      60

          70      80      90      100     110     120
m989.pep  TKLDSSQISVNANIVLPSIHYEADSATDFTGLPVQGSKSGKITKTTVAPHIYGAYKVNDN
a989      TKLDSSQISVNANIVLPSIHYEADSATDFTGLPVQGSKSGKITKTTVAPHIYGAYKVNDN
          70      80      90      100     110     120

          130     140     150     160     170     180
m989.pep  LTVGLGVYVPFGSATEYEKDSVLRHNINKLGLTSIAVEPVAAWKLNDRHSGAGIIAQHT
a989      LTVGLGVYVPFGSATEYEKDSVLRHNINKLGLTSIAVEPVAAWKLNERHSGAGIIAQHT
          130     140     150     160     170     180

          190     200     210     220     230     240
m989.pep  SAELRKYADWGIKSKAEILTAKPPKPNGVAEAAKIQADGHADVKGSDWGFYQLAWMWDI
a989      SAELRKYADWGIMEKAKALKETPPNPT---KAAQIKADGHADVKGSDWGFYQLAWMWDI
          190     200     210     220     230

          250     260     270     280     290     299
m989.pep  NDRARVGVNYSKVSHTLKGADEWAADGAAAKAMW-STMLAANGYTANEKARVKIVTPES
a989      NDRARVGVNYSKVSHTLKGADEWAADAMAKQLWDANKLALLGYTPSEKARVKIVTPES

```

1407

	240	250	260	270	280	290
m989.pep	300	310	320	330	340	350
	LSVHGMVKVSDKADLFQDVTWTRHSRFDKAEVFEKEKTIVVKGKSDRTTITPNWRNTYKV					
a989	300	310	320	330	340	350
	LSVHGMVKVSDKADLFQDVTWTRHSRFDKAEVFEKEKTIVVKGKSDRTTITPNWRNTYKV					
m989.pep	360	370	380	390	400	410
	GFGGSYQISEPLQLRAGIAFDKSPVRNADYRMNSLPDGNRIWFSAGMKYHIGKNHVVDAA					
a989	360	370	380	390	400	410
	GFGGSYQISEPLQLRAGIAFDKSPVRNADYRMNSLPDGNRIWFSAGMKYHIGKNHVVDAA					
m989.pep	420	430	440	450	460	
	YTHIHINDTSYRTAKASGNDVDSKGASSARFKNHADIIGLQYTYKFKX					
a989	420	430	440	450	460	
	YTHIHINDTSYRTAKASGNDVDSKGASSARFKNHADIIGLQYTYKFKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2991>:

```

m990.seq
1   ATGTTTCAGAG CTCAGCTTGG TTCAAATACT CGTTCCTACCA AAATCGGCGA
51  CGATGCCGAT TTTTCATTTT CAGACAAGCC GAAACCCGGC ACTTCCCATT
101 ATTTTTCAG  CGGTAAAACC GATCAAAAT CATCCGAATA TGGGTATGAC
151 GAAATCAATA TCCAAGGTAA AAATTACAAT AGCGGCATCC TCGCCGTCGA
201 TAATATGCCC GTTGTCAAAA AATATATTAC AGAGAAGTAT GGGGCTGATT
251 TAAAGCAGGC GGTAAAAAGT CAATTACAGG ATTTATACAA AACAAGACCG
301 GAAGCTTGGG CAGAAAATAA AAAACGGACT GAGGAGGCGT ATATAGCACA
351 GTTTCGAACA AAATTTAGTA CGCTCAAACA GACGATGCCC GATTTAATTA
401 ATAAATTGGT AGAAGATTCC GTACTCACTC CTCATAGTAA TACATCACAG
451 ACTAGTCTCA ACAACATCTT CAATAAAAAA TTACACGTC AATCGAAAA
501 CAAATCCAC  GTCGCCGAC AGGTGTTGGA ACTGACCAAG ATGACGCTGA
551 AAGATTCCCT TTGGGAACCG CGCCGCCATT CCGACATCCA TACGCTGGAA
601 ACTTCCGATA ATGCCCGCAT CCGCCTGAAC ACGAAAGATG AAAAAGTAC
651 CGTCCATAAG GATTATGCGG GCGGCGCGGA TTTCTGTTC GGCTACGACG
701 TGCGGGAGTC GGACGAACCC GCCCTGACCT TTGAAGACAA AGTCAGCGGA
751 CAATCCGGCG TGGTTTGGGA ACGCCGGCCG GAAATCTGA AAACGCTCGA
801 CGGGCGCAAA CTGATTGCGG CAAAACGGC GGATTCCGGT TCGTTTGGCT
851 TTAAACAAAA TTACCGGCAG GGACTGTACG AATTATTGCT CAAGCAATGC
901 GAAGGCGGAT TTTGCTTGGG CGTGCAGCGT TTGGCTATCC CCGAGGCGGA
951 AGCGGTTTTA TATGCCAAC AGGCTTATGC GGCAATACT TTGTTTGGGC
1001 TGCGTGCCCG CGACAGGGGC GACGACGTGT ATGCCGCCGA TCCGTCCCCT
1051 CAAAAATTGT GGCTGCGCTT CATCGCGGCG CGGTCGCATC AAAATATACG
1101 GGGCGGCGCG GCTGCGGACG GGTGGCGCAA AGGCGTGCAA ATCGGCGGCG
1151 AGGTGTTTGT ACGGCAAAAT GAAGGCAGCC GACTGCAAT CCGCGTGATG
1201 GCGGCGAGGG CCGGCCAGCA CGCATCAGTC AACGGCAAAG GCGGTGCGGC
1251 AGGCAGTGAT TTGTATGGTT ATGGCGGGG TGTATTGCT GCGTGGCATC
1301 AGTTGCGCGA TAAACAAACG GGTGCGTATT TGGACGGCTG GTTGCAATAC
1351 CAACGTTTCA AACACCGCAT CAATGATGAA AACCGTGGG AACGTACAA
1401 AACCAAAGGT TGGACGGCTT CTGTCGAAGG CGGCTACAAC GCGCTTGTGG
1451 CGGAAGGCAT TGTCGGAAAA GGCAATAATG TGCGGTTTTA CCTACAACCG
1501 CAGGCGCAGT TTACCTACTT GGGCGTAAAC GCGGCTTTA CCGACAGCGA
1551 GGGGACGGCG GTCGGACTGC TCGGCAGCGG TCAGTGGCAA AGCCGCGCCG
1601 GCATTGCGGC AAAAACCCGT TTTGCTTTGC GTAACGGTGT CAATCTTCAG
1651 CCTTTTGGCG CTTTAAATGT TTTGCACAGG TCAAAATCTT TCGGCGTGGA
1701 AATGGACGGC GAAAAACAGA CGCTGGCAGG CAGGACGGCA CTCGAAGGGC
1751 GGTTCGGTAT TGAAGCCGGT TGGAAAGGCC ATATGTCCGC ACGCATCGGA
1801 TATGGCAAAA GGACGGACGG CGACAAAGAA GCCGATTGT CGCTCAAATG
1851 GCTGTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2992; ORF 990>:

m990.pep

1408

```

1 MFRAQLGSNT RSTKIGDDAD FSFSDKPKPG TSHYFSSGKT DQNSSEYGYD
51 EINIQQKKNYN SGILAVDNMP VVKYITEKY GADLKQAVKS QLQDLYKTRP
101 EAWAENKKRT EEAYIAQFGT KFSTLKQTMP DLINKLVEDS VLTPHSNTSQ
151 TSLNNIFNKK LHVKIENKSH VAGQVLELTK MTLKDSLWEP RRHSDIHTLE
201 TSDNARIRLN TKDEKLTVHK DYAGGADFLF GYDVRESDEP ALTFEDKVSQ
251 QSGVVLERRP ENLKTLDGRK LIAAKTADSG SFAFKQNYRQ GLYELLKQK
301 EGGFCLGVQR LAIPEAEAVL YAQOAYAANT LFGLRAADRG DDVYAADPSR
351 QKLWLRFIGG RSHQNIIRGGA AADGWRKGVQ IGGEVFVRQN EGSRLAIGVM
401 GGRAGQHASV NGKGAAGSD LYGYGGGVYA AWHQLRDKQT GAYLDGWLQY
451 QRFKHRINDE NRAERYKTKG WTASVEGGYN ALVAEGIVGK GNNVRFYLPQ
501 QAQFTYLGVN GGFTDSESTA VLLGSGQWQ SRAGIRAKTR FALRNGVNIQ
551 PFAAFNVLHR SKSFGVEMDG EKQTLAGRTA LEGRFGIEAG WKGHMSARIG
601 YGKRTDGDKE AALSLKWLF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2993>:

a990.seq

```

1 ATGTTTCAGAG CTCAGCTTGG TTCAAATACT CGTTCTACCA AAATCGGCGA
51 CGATGCCGAT TTTTCATTTT CAGACAAGCC GAAACCCGGC ACTTCCCATT
101 ATTTTTCAG CCGTAAACC GATCAAAATT CATCCGAATA TGGGTATGAC
151 GAAATCAATA TCCAAGGTAA AAACATAAT AGCGGCATAC TCGCCGTCGA
201 TAATATGCCC GTTCTTAAGA AATATATTAC AGATACTTAC GGGGATAATT
251 TAAAGGATGC GGTAAAGAAG CAATTACAGG ATTTATACAA AACAGACCC
301 GAAGCTTGGG AAGAAATAA AAAACGGACT GAGGAGGCGT ATATAGAACA
351 GCTTGGACCA AAATTTAGTA TACTCAAACA GAAAAACCCG GATTTAATTA
401 ATAAATTGGT AGAAGATTCC GTACTCACTC CTCATAGTAA TACATCACAG
451 ACTAGTCTCA ACAACATCTT CAATAAAAAA TTACACGTCA AAATCGAAAA
501 CAAATCCAC GTCGCCGAC AGGTGTGGA ACTGACCAAG ATGACGCTGA
551 AAGATTCCCT TTGGGAACCG CGCCGCCATT CCGACATCCA TATGCTGGAA
601 ACTTCCGATA ATGCCCGCAT CCGCCTGAAC ACGAAAGATG AAAAACTGAC
651 CGTCCATAAA GCGTATCAGG GCGGTGCGGA TTTCCTGTTT GGCTACGACG
701 TGCGGGAGTC GGACAAACCC GCCCTGACCT TTGAAGAAAA AGTCAGCGGA
751 CAATCCGCGG TGGTTTGGGA ACGCCGCGCG GAAAATCTGA AAACGCTCGA
801 CGGGCGCAAA CTGATTGCGG CGGAAAAGGC AGACTCTAAT TCGTTTGCCT
851 TTAAACAAAA TTACCGGCAG GGAATGTACG AATTATTGCT CAAGCAATGC
901 GAAGGCGGAT TTTGCTTGGG CGTGACGCGT TTGGCTATCC CCGAGGCGGA
951 AGCGGTTTTA TATGCCCAAC AGGCTTATGC GGCAAAATACT TTGTTCCGGC
1001 TGCGTGCCGC CGACAGGGGC GACGACGTGT ATGCCGCCGA TCCGTCCCGT
1051 CAAAATTGT GGCTGCGCTT CATCGCGGCG CGGTGCGATC AAAATATACG
1101 GGGCGGCGCG GCTGCGGACG GCGCGCGCAA AGGCGTGCAA ATCGGCGGCG
1151 AGGTGTTTGT ACGGCAAAAT GAAGGCAGCC GGCTGGCAAT CGGCGTGATG
1201 GCGGCGAGG CTGGCCAGCA CGCATCAGTC AACGGCAAAG GCGGTGCGGC
1251 AGGCAGTTAT TTGCATGGTT ATGGCGGGGG TGTATTATGCT GCGTGGCATC
1301 AGTTGCGCGA TAAACAAACG GGTGCGTATT TGGACGCGTG GTTGCAATAC
1351 CAACGTTTCA AACACCGCAT CAATGATGAA AACCCTGCGG AACGCTACAA
1401 AACCAAGGT TGGACGGCTT CTGTCGAAGG CGGCTACAAC GCGCTTGTGG
1451 CGGAAGGCGT TGTGCGAAAA GGCAATAATG TGCGGTTTTA CTGCAACCG
1501 CAGGCGCAGT TTACCTACTT GGGCGTAAAC GCGGCTTTA CCGACAGCGA
1551 GGGGACGGCG GTCGGAAGTC TCGGCGAGCG TCAGTGGCAA AGCCGCGCCG
1601 GCATTCGGGC AAAAACCCGT TTTGCTTTGC GTAACGGTGT CAACTCTTCAG
1651 CCTTTTGCCG CTTTAAATGT TTTGCACAGG TCAAAATCTT TCGGCGTGGA
1701 AATGGACGGC GAAAAACAGA CGCTGGCAGG CAGGACGGCG CTCGAAGGGC
1751 GGTTCGGCAT TGAAGCCGGT TGGAAAGGCC ATATGTCCGC ACGCATCGGA
1801 TACGGCAAAA GGACGGACGG CGACAAAGAA GCCGCATTGT CGCTCAAATG
1851 GCTGTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2994; ORF 990.a>:

a990.pep

```

1 MFRAQLGSNT RSTKIGDDAD FSFSDKPKPG TSHYFSSGKT DQNSSEYGYD
51 EINIQQKKNYN SGILAVDNMP VVKYITDIT GDNLDKAVK QLQDLYKTRP
101 EAWAENKKRT EEAYIEQLGP KFSILKQNP DLINKLVEDS VLTPHSNTSQ
151 TSLNNIFNKK LHVKIENKSH VAGQVLELTK MTLKDSLWEP RRHSDIHMLE
201 TSDNARIRLN TKDEKLTVHK AYQGGADFLF GYDVRESDEP ALTFEEKVSG
251 QSGVVLERRP ENLKTLDGRK LIAAEKADSN SFAFKQNYRQ GLYELLKQK
301 EGGFCLGVQR LAIPEAEAVL YAQOAYAANT LFGLRAADRG DDVYAADPSR
351 QKLWLRFIGG RSHQNIIRGGA AADGRRKGVQ IGGEVFVRQN EGSRLAIGVM

```

1409

401 GGRAGQHASV NGKGAAGSY LHGYGGGVYA AWHQLRDKQT GAYLDGWLQY
451 QRFKHRINDE NRAERYKTG WTASVEGGYN ALVAEGVVGK GNNVRFYLQP
501 QAQFTYLGVN GGFTDSEGTA VLLGSGQWQ SRAGIRAKTR FALRNGVNLQ
551 PFAAFNVLHR SKSFGVEMDG EKQTLAGRTA LEGRFGIEAG WKGHMSARIG
601 YGKRTDGDKE AALSLKWLF*

m990/a990 96.0% identity in 619 aa overlap

	10	20	30	40	50	60
m990.pep	M	F	R	A	Q	L
a990	M	F	R	A	Q	L
	70	80	90	100	110	120
m990.pep	S	G	I	L	A	V
a990	S	G	I	L	A	V
	130	140	150	160	170	180
m990.pep	K	F	S	T	L	K
a990	K	F	S	T	L	K
	190	200	210	220	230	240
m990.pep	M	T	L	K	D	S
a990	M	T	L	K	D	S
	250	260	270	280	290	300
m990.pep	A	L	T	F	E	D
a990	A	L	T	F	E	D
	310	320	330	340	350	360
m990.pep	E	G	G	F	C	L
a990	E	G	G	F	C	L
	370	380	390	400	410	420
m990.pep	R	S	H	Q	N	I
a990	R	S	H	Q	N	I
	430	440	450	460	470	480
m990.pep	L	H	G	Y	G	G
a990	L	H	G	Y	G	G
	490	500	510	520	530	540
m990.pep	A	L	V	A	E	G
a990	A	L	V	A	E	G
	550	560	570	580	590	600
m990.pep	F	A	L	R	N	G
a990	F	A	L	R	N	G

1410

	550	560	570	580	590	600
	610	620				
m990 . pep	YGKRTDGDKEAALS	SLKWLFX				
a990	YGKRTDGDKEAALS	SLKWLFX				
	610	620				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2995>:

```

g992 . seq
1  ATGTTTCAGAC GGCATCGGCA TTTGAAAAAT ATGCAGATTA AAAAAATCAT
51  GAAATGGCTT CCCGTCGCCC TGTCGCTTTT GGGCGCGTTG GGTATACGG
101 GATATGACAG TGAGGCGGTG CGGACGGCGG TTGCCGTA CTACGTA CT
151 GGCACGTCAG GGGACGTGGG TTTGACGCGC CCCGTTCCGC GACGGGCATC
201 GCGGAAATCC GGCCACAGCT ACACAGGCAC GGTGTCCAAA GTCTATGACG
251 GCGATACCCCT TCACGTCATC GACGGCGACG GCGCGAAACA TAAATTCGG
301 ATGGCGTATA TCGACGCACC GGAGATGAAA CAGGCTTACG GTACACGTTT
351 GCGCGACAAC CTGCGCGCGG CCGCGGAGGG TAGGAAAGTC AGTGTACGTG
401 TGTTTGAAAC CGACCGCTAT CAGCGCGAAG TGGCGCAGGT ATCCGCCGCG
451 AAAACCGATT TGAACCTGAT GCAGGTGCAG GACGGGCGCG CGTGGCATT
501 TAAAGTTTAT GCTAAAGAAC AGCAGGATAA GCGCGATTTT GCCGACTATG
551 CCGACGCTCA AATTCAGGCG GAAAGGGAAC GCAAAGGATT GTGGAAAGCT
601 AAAAATCCGC AAGCGCCGTG GCGGTACCGC CCGGCAGGCA GGAGCGGCGG
651 GGGCAATAAG GATTGGATGG ATCCCGTGGG CGAATGGTTG GGCATTGGT
701 AA

```

This corresponds to the amino acid sequence <SEQ ID 2996 ORF 992.ng>:

```

g992 . pep
1  MFRRHRHLKN MQIKKIMKWL PVALSLLGAL GYTGVDSEAV RTAVAVLDVL
51  GTAGDVGFDA FVRRRASAKS GHSYTGTVSK VYDGTDLHVI DGDGAKHKIR
101 MAYIDAPEMK QAYGTRSRDN LRAAAEGRKV SVRVFETDRY QREVAQVSAG
151 KTDNLNMQVQ DGAAWHYKSY AKEQQDKADF ADYADAQIQ A ERERKGLWKA
201 KNPQAFWAYR RAGRSGGGNK DWMDSVGEWL GIW*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2997>:

```

m992 . seq
1  ATGTTTCAGAC GGCATCGGCA TTGAAAAAT ATGCAGATTA AAAAAATCAT
51  GAAATGGCTT CCCGTCGCCC TGTCGCTTTT GGGTGCCTTG GGTATACGG
101 GGTACGGCAG CGAGGCGGTG CGGACGGCGG TTGCCGTA CTACGTA CT
151 GCGCGGCGAG GGGACGCGGG TTCCGACGCG CCCGCCCGCC GCCGAGCATC
201 GCGGAAATCC GGCCACCGCT ACACAGGCAC GGTGTCCAAA GTCTATGACG
251 GCGACACCCT TCACGTTATC GACGGCGACG GCGCGAAACA CAAATTCGG
301 ATGGCGTATA TCGACGCGCC GGAGATGAAA CAGGCTTACG GCACGCGTTT
351 GCGCGACAAC CTGCGCGCGG CCGCGGAAGG CAGGAAAGTC AGCGTCCGCG
401 TGTTGCATAC CGACCGCTAC CAGCGCGAAG TGGCGCAGGT TTCTGTCGGC
451 AAAACCGATT TGAACCTGAT GCAGGTGCAG GACGGGCGCG CGTGGCATT
501 TAAAGTTTAT GCTAAAGAAC AGCAGGATAA GCGCGATTTT GCCGATTATG
551 CCGACGCTCA AATTCAGGCG GAAAGGGAAC GCAAAGGATT GTGGAAAGCT
601 AAAAATCCGC AAGCGCCGTG GCGGTACCGC CGAGCAGGCA GGAGCGGCGG
651 GGGCAATAAG GATTGGATGG ATGCCGTGGG CGAATGGTTG GGCATTGGT
701 AA

```

This corresponds to the amino acid sequence <SEQ ID 2998; ORF 992>:

```

m992 . pep
1  MFRRHRHLKN MQIKKIMKWL PVALSLLGAL GYTGVCSEAV RTAVAVLDVL
51  GAAGDAGSDA PARRRASAKS GHRYTGTVSK VYDGTDLHVI DGDGAKHKIR
101 MAYIDAPEMK QAYGTRSRDN LRAAAEGRKV SVRVFETDRY QREVAQVSAG
151 KTDNLNMQVQ DGAAWHYKSY AKEQQDKADF ADYADAQIQ A ERERKGLWKA
201 KNPQAFWAYR RAGRSGGGNK DWMDAVGEWL GIW*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 992 shows 96.1% identity over a 233 aa overlap with a predicted ORF (ORF 992) from *N. gonorrhoeae*

m992/g992 96.1% identity in 233 aa overlap

1411

	10	20	30	40	50	60
m992 .pep	MFRRRHRLKNNMQIKKIMKWL PVALSLLGALGYTGYGSEAVRTAVAVLDVLGAAGDAGSDA					
g992	MFRRRHRLKNNMQIKKIMKWL PVALSLLGALGYTGYDSEAVRTAVAVLDVLGTAGDVGFDA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m992 .pep	PARRRASAKSGHRYTGTVSKVYDGDTLHVIDGDGAKHKIR MAYIDAPEMKQAYGTRSRDN					
g992	PVRRRASAKSGHSYTGTVSKVYDGDTLHVIDGDGAKHKIR MAYIDAPEMKQAYGTRSRDN					
	70	80	90	100	110	120
	130	140	150	160	170	180
m992 .pep	LRAAAEGRKVSVRVFDTRYQREVAQVSVGKTDNLNMQVQDGAAWHYKSYAKEQQDKADF					
g992	LRAAAEGRKVSVRVFETDTRYQREVAQVSAGKTDNLNMQVQDGAAWHYKSYAKEQQDKADF					
	130	140	150	160	170	180
	190	200	210	220	230	
m992 .pep	ADYADAQIQAEERERKGLWKAKNPQAPWAYRRAGRSGGGNKDWM DAVGEWLGIWX					
g992	ADYADAQIQAEERERKGLWKAKNPQAPWAYRRAGRSGGGNKDWM DSVGEWLGIWX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2999>:

```
a992 .seq
1  ATGTTTCAGAC  GGCATCGGCA  TTTGAAAAAT  ATGCAGATTA  AAAAAATCAT
51  GAAATGGCTT  CCCGTCGCCT  TGTGCGTTT  GGGTGCCTTG  GGTATACGG
101 GGTACGGCAG  CGAGGCGGTG  CGGACGGCGG  TTGCCGTACT  CGACGTACTC
151 GGC GCGGCAG  GGGACGCGGG  TTCGACGCG  CCCGCCGCC  GCCGAGCATC
201 GGC GAAATCC  GGCCACCGCT  ACACAGGCAC  GGTGTCCAAA  GTCTATGACG
251 GCGACACCT  TCACGTTATC  GACGCGGACG  GCGCGAAACA  CAAAATCCGG
301 ATGGCGTATA  TCGACCGGCC  GGAGATGAAA  CAGGCTTACG  GCACGCGTTC
351 GCGCGACAAC  CTGCGCGCGG  CGGCGGAAGG  CAGGAAAGTC  AGCGTCCGCG
401 TGTTGCGCAC  CGACCGCTAC  CAGCGCGAAG  TGGCGCAGGT  TTCTGTGCGG
451 AAAACCGATT  TGAACCTGAT  GCAGGTGCAG  GACGGGCGCG  CGTGGCATTG
501 TAAAAGTTAT  GCTAAAGAAC  AGCAGGATAA  GGCGGATTTT  GCCGATTATG
551 CCGACGCTCA  AATTCAGGCG  GAAAGGGAAC  GCAAAGGATT  GTGGAAAGCT
601 AAAAATCCGC  AAGCGCCGTG  GCGGTACCG  CGGGCAGGCA  GGAGCGGCGG
651 GGGCAATAAG  GATTGGATGG  ATGCCGTGG  CGAATGGTTG  GGCATTGGGT
701 AA
```

This corresponds to the amino acid sequence <SEQ ID 3000; ORF 992.a>:

```
a992 .pep
1  MFRRRHRLKN  MQIKKIMKWL  PVALSLLGAL  GYTGYGSEAV  RTAVAVLDVL
51  GAAGDAGSDA  PARRRASAKS  GHRYTGTVSK  VYDGDTLHVI  DGDGAKHKIR
101 MAYIDAPEMK  QAYGTRSRDN  LRAAAEGRKV  SVRVFDTRY  QREVAQVSVG
151 KTDNLNMQVQ  DGAAWHYKSY  AKEQQDKADF  ADYADAQIQA  ERERKGLWKA
201 KNPQAPWAYR  RAGRSGGGK  DWM DAVGEWL  GIW*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 992 shows 100.0% identity over a 233 aa overlap with a predicted ORF (ORF 992) from *N. meningitidis*

a992/m992 100.0% identity in 233 aa overlap

	10	20	30	40	50	60
a992 .pep	MFRRRHRLKNNMQIKKIMKWL PVALSLLGALGYTGYGSEAVRTAVAVLDVLGAAGDAGSDA					
m992	MFRRRHRLKNNMQIKKIMKWL PVALSLLGALGYTGYGSEAVRTAVAVLDVLGAAGDAGSDA					
	10	20	30	40	50	60
	70	80	90	100	110	120
a992 .pep	PARRRASAKSGHRYTGTVSKVYDGDTLHVIDGDGAKHKIR MAYIDAPEMKQAYGTRSRDN					
m992	PARRRASAKSGHRYTGTVSKVYDGDTLHVIDGDGAKHKIR MAYIDAPEMKQAYGTRSRDN					
	70	80	90	100	110	120
	130	140	150	160	170	180

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```

a992.pep    LRAAAEGRKVSVRVFDTRYQREVAQVSVGKTDNLNMQVDGAAWHYKSYAKEQDKADF
m992        LRAAAEGRKVSVRVFDTRYQREVAQVSVGKTDNLNMQVDGAAWHYKSYAKEQDKADF
              130      140      150      160      170      180

              190      200      210      220      230
a992.pep    ADYADAQIQAEERERKGLWKAKNPQAPWAYRRAGRSGGGNKDWM DAVGEWLGIX
m992        ADYADAQIQAEERERKGLWKAKNPQAPWAYRRAGRSGGGNKDWM DAVGEWLGIX
              190      200      210      220      230

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3001>:

```

g993.seq
1   CTGAAAGTCG TATTGGGCAG TTTCAAGGC CCTTTGGATC TGCTGCTCTA
51  CCTTATCCGC AAGCAGAACA TCGATGTTCT CGATATTCCG ATGGTGGAAG
101 TTACCGGGCA GTATCTGCAC TATATTGCC AAATGGAAGC CTATCAGTTT
151 GATTTGGCGG CGGAATATCT TTTGATGGCG GCAATGCTGA TTGAAATCAA
201 ATCGCGCCTG CTGCTGCCGC GTACCGAAGC CGTCGAAGAC GAAGAGGCGG
251 ACCCGCGTGC CGAGTTGGTG CGCGCTCTGC TTGCCACGA GCAAATGAAA
301 CTGGCGGCGC AGGGTTTGGA CGCGCTGCCG CGTGGGGGAC GGGATTTGCG
351 GTGGGCTTAC CTGCCGCTGG AAATTGCAGC CGAGACGAAG CTGCCCGAGG
401 TTTACATCGC CGATTTGATG CAGGCATGGT TGGGCATTCT TTCTCGGGCA
451 AAACATACGC GCAGCCACGA AGTAATCCAA GAAACCCCTT CCGTGGCGGC
501 GCAAATGACG GCAATCCTGC GCCGTTTGAA CGAACACGGG ATATGCAGGT
551 TTCACGCCCT GTTCAATCCC GAACAGGGCG CGGCTTACGT GATCGTCAAC
601 TTCATCGCCC TGTGGAGCT TGCCAAAGAA GGATTGGTCG GAATCGTACA
651 GGAAGACGGT TTCGGAGAAA TCCGAATCAG CCTCAATCAT GAGGGGGCGC
701 ATTCAGACGG CATTTTCGGC ACACGGGGCG GCGCGATGT GTTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 3002 ORF 993.ng>:

```

g993.pep
1   LKVVLSFGQ PLDLLLYLIR KQNI DVLDIP MVEITGQYLH YIAQMEAYQF
51  DLAAEYLLMA AMLIEIKSRL LLPRTAEVD EADPRAELV RRLAYEQMK
101 LAAQGLDALP RAGRDFAWAY LPLEIAAETK LPEVYIADLM QAWLGILSRA
151 KHTRSHEVIQ ETLSVRAQMT AILRLNEHG ICRFHAFNFP EQGAAYVIVN
201 FIALLELAKE GLVGIVQEDG FGEIRISLNH EGAHSDGIFG TRGGRDVF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3003>:

```

m993.seq
1   TTGAAAGTCG TATTGGGCAG CTTCAAGGC CCTTTGGATC TACTGCTGTA
51  TCTGATCCGC AAACAGAATA TCGACGTACT GGATATTCCG ATGGTGGAAG
101 TTACCGGGCA GTATCTGCAC TACATCGCCC AAATAGAAAC CTATCAGTTT
151 GATTTGGCGG CGGAATATCT TTTGATGGCA GCAATGCTGA TTGAAATCAA
201 ATCGCGCCTG CTGCTGCCGC GTACCGAAGC CGTCGAAGAC GAAGAAGCCG
251 ACCCGCGTGC CGAGTTGGTG CGCGCCTGCG TGGCTTACGA ACAGATGAAG
301 CTGGCGGCGC AGGGTTTGGA CGCGCTGCCG CGAGCCGGAC GGGATTTGCG
351 GTGGGCTTAC CTGCCGCTGG AAATTGCCGT CGAAGCCGAG CTGCCCGAAG
401 TCTATATTAC CGACTTGACG CAAGCGTGGC TGGGTATTTT GTCTCGGGCA
451 AAACACACGC GCAGCCACGA AGTAATCAAA GAAACCATCT CCGTGGCGGC
501 GCAAATGACG GCAATCCTGC GCCGTTTGAA CGGACACGGA ATATGCAGGT
551 TTCACGACCT GTTCAATCCC AAACAGGGCG CGGCTTACGT GGTCTGCAAC
601 TTCATCGCAC TGTGGAGCT TGCCAAAGAA GGATTGGTCA GAATCGTGCA
651 GGAAGACGGT TTCGGAGAAA TCCGAATCAG CCTCAATCAT GAGGGGGCGC
701 ATTCAGACGG CATTTCCGGC ACACGAGGCG GCGCGATGT GTTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 3004; ORF 993>:

```

m993.pep
1   LKVVLSFGQ PLDLLLYLIR KQNI DVLDIP MVRKITEQYLH YIAQIETIQF
51  DLAAEYLLMA AMLIEIKSRL LLPRTETVED EADPRAELV RRLAYEQMK
101 LAAQGLDALP RAGRDFAWAY LPLEIAVEAK LPEVYITDLT QAWLGILSRA
151 KHTRSHEVIK ETISVRAQMT AILRLNGHG ICRFHDLFNP KQGAAYVVVN
201 FIALLELAKE GLVRIVQEDG FGEIRISLNH EGAHSDGISG TRGGRDVF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 993 shows 93.1% identity over a 248 aa overlap with a predicted ORF (ORF 993) from *N. gonorrhoeae*

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m993/g993 93.1% identity in 248 aa overlap

	10	20	30	40	50	60
m993.pep	LKVVLSFQGPLDLLLYLIRKQ	NIDVLDIPMVKITEQYLHYIAQ	ITYQFDLAAEYLLMA			
g993	LKVVLSFQGPLDLLLYLIRKQ	NIDVLDIPMVEITGQYLHYIAQ	MEAYQFDLAAEYLLMA			
	10	20	30	40	50	60
m993.pep	70	80	90	100	110	120
m993.pep	AMLEIKSRLLLPRTETVEDEEADPRAELV	RRLLAYEQMKLAAQGLDALPRAGRDFAWAY				
g993	AMLEIKSRLLLPRTAEVEDEEADPRAELV	RRLLAYEQMKLAAQGLDALPRAGRDFAWAY				
	70	80	90	100	110	120
m993.pep	130	140	150	160	170	180
m993.pep	LPLEIAVEAKLPEVYITDLTQAWLGILSRAKH	TRSHEVIKETISVRAQMTAILRRNLNCHG				
g993	LPLEIAAETKLPEVYIADLMQAWLGILSRAKH	TRSHEVIQETLSVRAQMTAILRRNLNEHG				
	130	140	150	160	170	180
m993.pep	190	200	210	220	230	240
m993.pep	ICRFHDLFNPQGAAYVVVNFIALLELAKEGLV	RIVQEDGFGEIRISLNHEGAHSDGISG				
g993	ICRFHALFNPQGAAYVIVNFIALLELAKEGLV	GIVQEDGFGEIRISLNHEGAHSDGIEG				
	190	200	210	220	230	240
m993.pep	249					
m993.pep	TRGGRDVFX					
g993	TRGGRDVFX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3005>:

a993.seq

1	CTGAAAGTCG	TATTGAGCAG	TTTCAAGGC	CCTTTGGATC	TGCTGCTCTA
51	CCTTATCCGC	AAGCAGAACA	TCGATGTTCT	CGATATCCG	ATGGTGAAGA
101	TTACCGAACA	GTATCTGCAC	TACATCGCCC	AAATAGAAAC	CTATCAGTTT
151	GATTTGGCGG	CGGAATATCT	TTTGATGGCA	GCAATGCTGA	TTGAAATCAA
201	ATCGCGCCTG	CTGCTGCCGC	GTACCGAAAC	CGTCGAAGAC	GAAGAAGCCG
251	ACCCGCGTGC	CGAGTTGGTG	CGCCGCTGTC	TGGCTTACGA	GCAGATGAAG
301	CTGGCGGCAC	AAGGGTTGGA	TGCGCTTCCT	CGTGCGGGCC	GGGATTTCSC
351	ATGGGCATAC	CTGCCACTGG	AAATTGCCGT	CGAAGCCAAG	CTGCCCGAAG
401	TCTATATTAC	CGACTTGACG	CAGGCGTGGC	TGAGTATTTT	GTCTCGGGCA
451	AAACATACGC	GCAGCCACGA	AGTTATCAAA	GAAACCATCT	CCGTGCCGCG
501	GCAATGACG	GCAATCTGCG	GCCGTTTGAA	CAAACACGGG	ATATGCAGGT
551	TTCACGACCT	GTTCAATCCC	GAACAGGGCG	CGGCTTACGT	GGTCGTCAAC
601	TTCATCGCAC	TGTTGGAGCT	TGCCAAAGAA	GGTTGGTTCG	GAATCGTACA
651	GGAGTCGGT	TTCGGAGAAA	TCCGAATCAG	CCTCAATCAT	GAGGGGGCGC
701	ATTCAGACGG	CATTCCGGC	ACACGGGGCG	GGCGGATGT	GTTCTAA

This corresponds to the amino acid sequence <SEQ ID 3006; ORF 993.a>:

a993.pep

1	LKVVLSFQGPLDLLLYLIRKQ	NIDVLDIPMVKITEQYLHYIAQ	ITYQFDLAAEYLLMA
51	DLAAEYLLMA	AMLEIKSRLLLPRTETVED	EADPRAELVRRLLAYEQMK
101	LAAQGLDALP	RAGRDFAWAYLPLEIAVEAK	LPEVYITDLTQAWLSILSRA
151	KHTRSHEVIK	ETISVRAQMTAILRRNLNKHG	ICRFHDLFNP
201	EQGAAYVVVN	FIALLELAKEGLVGIVQEVG	FGEIRISLNHEGAHSDGISG

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 993 shows 97.6% identity over a 248 aa overlap with a predicted ORF (ORF 993) from *N. meningitidis*

a993/m993 97.6% identity in 248 aa overlap

	10	20	30	40	50	60
a993.pep	LKVVLSFQGPLDLLLYLIRKQ	NIDVLDIPMVKITEQYLHYIAQ	ITYQFDLAAEYLLMA			
m993	LKVVLSFQGPLDLLLYLIRKQ	NIDVLDIPMVKITEQYLHYIAQ	ITYQFDLAAEYLLMA			

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	10	20	30	40	50	60
a993.pep	70	80	90	100	110	120
	AMLEIEIKSRLLLPRTETVEDEEADPRAELVRRLLAYEQMKLAAQGLDALPRAGRDFAWAY					
m993	70	80	90	100	110	120
	AMLEIEIKSRLLLPRTETVEDEEADPRAELVRRLLAYEQMKLAAQGLDALPRAGRDFAWAY					
a993.pep	130	140	150	160	170	180
	LPLEIAVEAKLPEVYITDLTQAWLSILSRKHTRSHEVIKETISVRAQMTAILRRLNKHG					
m993	130	140	150	160	170	180
	LPLEIAVEAKLPEVYITDLTQAWLGILSRKHTRSHEVIKETISVRAQMTAILRRLNGHG					
a993.pep	190	200	210	220	230	240
	ICRFHDLFNPQGAAYVVVNFIALLELAKEGLVGIVQEVGFGEIRISLNHEGAHSDGISG					
m993	190	200	210	220	230	240
	ICRFHDLFNPQGAAYVVVNFIALLELAKEGLVRIVQEDGFGEIRISLNHEGAHSDGISG					
a993.pep	249					
	TRGGRDVFX					
m993	TRGGRDVFX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3007>:

g996.seq

```

1  ATGAACAGAA  GAACCTTCCT  CCTCGGCGCA  GCGCGTTGCG  TTCTTACCGC
51  CTGCGGCAGA  AAATCCGCC  GAACCCACGC  CAAATTTCCC  GAAGGAAGCA
101  CCGTGCTTGC  CTTGGGCGAT  TCGCTCACCT  TCGGCTACGG  AGCAAACCC
151  GCGGAATCCT  ACCCGCGCA  ACTGCAAAA  CTGACGGGTT  GGAATATTGT
201  CAACGGCGGC  GTATCGGGCG  ATACGTCCGC  GCAAGCCCTA  TCGCGCCTGC
251  CCGCGCTGTT  GGCACGCAA  CCAAGCTTG  TGATTGTCGG  CATAGGCGGC
301  AACGACTTTC  TCGCAAAGT  TCCGAGGAG  CAGACCGCG  CCAATATCGC
351  GAAATCATC  GAAACCGTGC  AAAAGGAAA  CATTCCTCGC  GTCTCGTCG
401  GCGTGCCGCA  CATCACTG  GCGCGTTGT  TCGGCGATT  GAGCGACCAT
451  CCGCTGTATG  AGGATTGTC  CGAGGAATAC  GGCATTCCGT  TGTTCGGCGG
501  CCGTGCGGCG  GAAATTTGG  GCAATAATA  TCTGAAATCC  GACCAAATCC
551  ACGCCAACGG  CAAAGGTAT  CGGAAATTC  CCGAAATTT  GAATCAATTT
601  TTGAGAAAAC  ATGGGTTTAG  ATAA

```

This corresponds to the amino acid sequence <SEQ ID 3008 ORF 996.ng>:

g996.pep

```

1  MNRRTFLLGA  GALLLTACGR  KSARTEAKIP  EGSTVLALGD  SLTFYGANP
51  GESYPALQK  LTGNIVNGG  VSGDTSALQ  SRLPALLARK  PKLVIVGIGG
101  NDFLRKVPEE  QTRANIAKII  ETVQKENIPA  VLVGVPHITL  GALFGHLSHD
151  PLYEDLSEY  GIPLFGGAWA  EILGNLNLKS  DOIHANGKGY  RKFAENLNQF
201  LRKHGER*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3009>:

m996.seq

```

1  ATGAACAGAA  GAACCTTCCT  CCTCGGCGCA  GCGCGTTGCG  TGCTTACCGC
51  CTGCGGCAGA  AAATCCGCC  GAACCCACGC  CAAATTTCCC  GAAGGAAGCA
101  CCGTACTTGC  CTTGGGCGAT  TCGCTTACCT  TCGGCTACGG  CGCAAACCTT
151  GCGGAATCCT  ACCCGCGCA  ACTGCAAAA  CTGACGGGTT  GGAATATTGT
201  CAACGGCGGC  GTATCGGGCG  ATACATCTGC  CCAAGCCCTG  TCGCGCCTGC
251  CCGCGCTGTT  GGCACGCAA  CCAAGCTTG  TGATTGTCGG  CATAGGCGGC
301  AACGACTTTC  TCGCAAAGT  TCCCAAGGAG  CAGACCGCG  CCAATATCGC
351  GAAATCATC  GAAACCGTGC  AGAAGGAAA  CATCCCGGCC  GTCTCGTCG
401  GCGTGCCGCA  CATCACTG  GGTGCGTTGT  TCGGCGATT  GAGCGATCAT
451  CCGCTGTATG  AGGATTGTC  CGAGGAATAC  GGCATTCCGC  TGTTCGGCGG
501  CCGTGCGGCG  GAAATTTGG  GCGATAATA  TCTGAAATCC  GACCAAATCC
551  ACGCCAACGG  CAAAGGTAT  CGGAAATTT  CCGAAGATT  GAATCAATTT
601  TTGAGAAAAC  AGGGTTTAG  ATAA

```

This corresponds to the amino acid sequence <SEQ ID 3010; ORF 996>:

m996.pep

```

1  MNRRTFLLGA  GALLLTACGR  KSARTEAKIP  EGSTVLALGD  SLTFYGANP
51  GESYPALQK  LTGNIVNGG  VSGDTSALQ  SRLPALLARK  PKLVIVGIGG

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101 NDFLRKVPKE QTRANIAKII ETVQKENIPA VLVGVPHITL GALFGHLSDH
 151 PLYEDLSEY GIPFEGGAWA EILGDNNLKS DQIHANGKGY RKFAEDLNQF
 201 LRKQGFR

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 996 shows 98.1% identity over a 207 aa overlap with a predicted ORF (ORF 996) from *N. gonorrhoeae*

m996/g996 98.1% identity in 207 aa overlap

m996.pep	10	20	30	40	50	60
	MNRRTFLLGAGALLLTACGRKSARTHAKIPEGSTVLALGDSLTFGYGANPGESYPAQLQK					
g996	MNRRTFLLGAGALLLTACGRKSARTHAKIPEGSTVLALGDSLTFGYGANPGESYPAQLQK					
	10	20	30	40	50	60
m996.pep	70	80	90	100	110	120
	LTGWNIVNGGVSGDTSAQALSRLPALLARKPKLVIVGIGGNDFLRKVPKEQTRANIAKII					
g996	LTGWNIVNGGVSGDTSAQALSRLPALLARKPKLVIVGIGGNDFLRKVPKEQTRANIAKII					
	70	80	90	100	110	120
m996.pep	130	140	150	160	170	180
	ETVQKENIPAVLVGVPHITLALFGHLSHDHPLYEDLSEYGIPLFGGAWAEILGDNNLKS					
g996	ETVQKENIPAVLVGVPHITLALFGHLSHDHPLYEDLSEYGIPLFGGAWAEILGNNNLKS					
	130	140	150	160	170	180
m996.pep	190	200				
	DQIHANGKGYRKFAEDLNQFLRKQGR					
g996	DQIHANGKGYRKAENLNQFLRKHGFRX					
	190	200				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3011>:

a996.seq

1	ATGAACAGAA	GAACCTTCCT	CCTCGGCGCA	GGCGCGTTGC	TCCTTACCGC
51	CTGCGGCAGA	AAATCCGCC	GAACCCACGC	CAAAATTCCC	GAAGGAAGCA
101	CCGTACTTGC	CTTGGGCGAT	TCGCTTACCT	TCGGCTACGG	CGCAAACCCC
151	GGCGAATCCT	ACCCGCGCA	ACTGCAAAA	CTGACGGGTT	GGAATATTGT
201	CAACGGCGGC	GTATCGGGCG	ATACATCCGC	CCAAGCCCTG	TCGCGCCTGC
251	CCGCGCTGTT	GGCAGCGAAA	CCCAAGCTTG	TGATTGTCGG	CATAGGCGGC
301	AACGACTTTC	TGCGCAAAGT	TCCCAAGGAG	CAGACCCGCG	CCAATATCGC
351	GAAAATCATC	GAAACCGTGC	AGAAGGAAA	CATCCCGGCC	GTCCTCGTCG
401	CGGTGCCGCA	CATTACCTTG	GGCGCGTTGT	TCGGGCATTT	GAGCGATCAT
451	CCGTGTATG	AGGATTTGTC	CGAGGAATAC	GGCATTCCGC	TGTTGCGCGG
501	CGCGTGGCG	GAATTTTGG	GCGATAATA	TCTGAAATCC	GACCAATCC
551	ACGCCAACGG	CAAGGCTAT	CGGAAATTTG	CCGAAGATT	GAATCAATTT
601	TTGAGAAAAC	AGGGTTTAG	ATAA		

This corresponds to the amino acid sequence <SEQ ID 3012; ORF 996.a>:

a996.pep

1	MNRRTFLLGA	GALLLTACGR	KSARTHAKIP	EGSTVLALGD	SLTFGYGANP
51	GESYPAQLQK	LTGWNIVNGG	VSGDTSAQAL	SRLPALLARK	PKLVIVGIGG
101	NDFLRKVPKE	QTRANIAKII	ETVQKENIPA	VLVGVPHITL	GALFGHLSDH
151	PLYEDLSEY	GIPFEGGAWA	EILGDNNLKS	DQIHANGKGY	RKFAEDLNQF
201	LRKQGFR*				

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 996 shows 100.0% identity over a 207 aa overlap with a predicted ORF (ORF 996) from *N. meningitidis*

a996/m996 100.0% identity in 207 aa overlap

a996.pep	10	20	30	40	50	60
	MNRRTFLLGAGALLLTACGRKSARTHAKIPEGSTVLALGDSLTFGYGANPGESYPAQLQK					

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```

|||||
m996      MNRRTFLLGAGALLLTACGRKSARTHAKIPEGSTVLALGDSLTFYGYGANPGESYP AOLQK
          10      20      30      40      50      60
          70      80      90      100     110     120
a996.pep  LTGWNIVNGGVSGD TSAQALSRLPALLARKPKLVIVGIGGNDFLRKVPKEQTRANI AKII
|||||
m996      LTGWNIVNGGVSGD TSAQALSRLPALLARKPKLVIVGIGGNDFLRKVPKEQTRANI AKII
          70      80      90      100     110     120
          130     140     150     160     170     180
a996.pep  ETVQKENIPAVLVGVPHITLGALFGHLS DHP LYEDLSE EYG I PLFGGAWAE ILGDNNLKS
|||||
m996      ETVQKENIPAVLVGVPHITLGALFGHLS DHP LYEDLSE EYG I PLFGGAWAE ILGDNNLKS
          130     140     150     160     170     180
          190     200
a996.pep  DQIHANGKGYRKFAEDLNQFLRKQGF RX
          |||||
m996      DQIHANGKGYRKFAEDLNQFLRKQGF R
          190     200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3013>:

```

g997.seq (partial)
1  ATGATGAACA CGCCGCATCC GCGCCCGAAA ATCGCCGTCA TCGGCGCAGG
51 CTGGGCGGCG TTGTCCGCGG CCGTCACCTT GCGCGGCAC GCCGACGTTA
101 CCCTGTTTGA AGCCGGCCGG CAGGCGGGCG GAAGGCGCGG CACACTGGCC
151 GGAAATACCG ACGGTTTCGG TTTTGTGGAC AACGGGCAGC ACATTTTGCT
201 CGGCGCATAC CGGGCGGTGT TCGCCTGAT GAAAACCATC GGTTCAGACC
251 CCCGTGCCGC CTTTTGCGC GTACCGCTGC ACTGGCATAT GCACGGCGGT
301 TTGCAGTTCC GCGCCCTCCC CCTGCCGCGG CCGCTGCATA TTTGGGCGG
351 CGTGCTGCTT GCCCGGCGCG TACCGTCCGC ATTCAAAGCC AAACGTCTTG
401 CCGATATGTC CGATTGTCAG AAGTCCGCAC GCCTCGGACA GCCCGACACG
451 ACAGTTGCAC AATGGCTGAA ACAGCGGAAC GTGCCGCGTG CCGCCGTAAT
501 GCAGTTTGG CAGCCCTTGG TCTGGGGCGC GCTCAACACG CCTTTGAAA
551 CCGCAAGCCT GCGCGTGTG TGCAACGTTT TGTCCGACGG CGTGCTGACG
601 AAAAAATCCG GCAGCGACTA TCTCTACCC AAACAGGATT TGGGCGCAAT
651 CGTCGCCGAA CCCGCCTTGG CGGAGCTTCA ACGGCTCGGC GCGGACATCC
701 GCCTCGAAAC GCGCGTATGC CGTCTGAACA CCCTCCCGGA CGGAAAAGTC
751 CTCGTCAACG GCGAAGCCTT CGATGCCGCC ATACTTGCCA CCGCGCCCTA
801 CCACGCCGCG GCGCTCCTGC CCGAAGGCAC GCCCGAACAC GTTCAGACGG
851 CATATCAAAA CCTTCGCTAC CAGCCCATCA CCACCGTCTA TCTGCGCTAC
901 GCCGAACCCG TCCGcCTGc cGCCCCGCTG AcCGGcAttg CCGAcggcAC
951 ggcaCaatgG CTGCTTTgcc cgGGCAGGC tccggactgc CcccaaAacg
1001 aagTCTCCGC cGTCAttagc GTTCCGAcc GCGtcggcgC Gtttgcaaac
1051 cga...

```

This corresponds to the amino acid sequence <SEQ ID 3014 ORF 997.ng>:

```

g997.pep (partial)
1  MMNTPHPRPK IAVIGAGWAG LSAAVTLARH ADVTLFEAGR QAGGRARTLA
51 GNTDGFGLD NGQHILLGAY RGVRLMKTI GSDPRAAF LR VPLHWHMHGG
101 LQFRALPLPA FLHILGCVLL ARRVPFAFK KLLADMSDLQ KSARLGQPD
151 TVAQWLKQRN VPRAAVMQFW QPLVWGALNT PLETASLRVL CNVLSGCVLT
201 KKSQSDYLLP KQDLGAIVAE PALAELQRLG ADIRLETRVC RLNTLPDGKV
251 LVNGEAFDAA ILATAPYHAA ALLPEGTPEH VQTAYQNLRY HAITTVYLRY
301 AEPVRLPAPL TGIADGTAQW LCPGQAPDC PQNEVSAVIS VSDRVGAFFAN
351 R...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3015>:

```

m997.seq
1  ATGATGAACA CGCCGCATCC GCGCCCGAAA ATCGCCGTCA TCGGCGCAGG
51 CTGGGCGAGGA CTGTCCGCGG CCGTCACCTT GCGCGGCAC GCCGACGTTA
101 CCCTGTTTGA AGCCGGCCGG CAGGCGGGCG GCAGGCGCGG CACACTGGCC
151 GGAAATACCG ACGGTTTCGG TTTTGTGGAC AACGGGCAGC ACATTTTGCT
201 CGGCGCATAC CGGGCGGTGT TCGCCTGAT GAAAACCATC GGTTCGGATC
251 CCCGTGCCGC CTTTTGCGC GTACCGCTGC ACTGGCATAT GCACGGCGGT
301 TTGCAGTTCC GCGCCCTCCC CCTGCCGCGG CCGCTGCATA TTTGGGCGG
351 CGTGCTGCTT GCCCGGCGTG CACCGACTGC ATTCAAAGCC AAACGTCTTG
401 CCGATATGTC CGATTGTCAG AAGTCCGCAC GCCTCGGACA GCCCGACACG
451 ACAGTGGCGC AATGGCTGAA ACAGCGGAAC GTGCCGCGTG CCGCCGTGAT
501 GCAGTTTGG CAGCCCTTGG TTTGGGCGG GCTCAACACG CCTTTGAAA

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551 CCGCAAGCCT GCGCGTGTG TGCACGTTT TGTCCGACGG CGTGTGACG
601 AAAAAATCCG GCAGCGACTA TCTCTACCC AAGCAGGATT TCGGCGCAAT
651 CGTCGCCGAA CCCGCCCTTG CGGATCTTCA ACGGCTCGGC GCGGACATCC
701 GCCTCGAAAC GCGCGTATGC CGTCTGAACA CCCTCCCGGA CGGGAAAGTG
751 CTCGTCAACG GCGAAGCTTT CGATGCCGCC GTCCCGCCA CCGCGCCCTA
801 CCACGCCGCC GCGCTCCTGC CCGAAGGCAC GCCCGAACAC GTTCAGACGG
851 CATATCAAAA CCTTCGTAC CACGCCATCA CCACCGTCTA TCTGCGCTAC
901 GCCGAACCCG TCCGCTGCC CGCCCGCTG ACCGCGCTG CCGACGGCAC
951 GGTGCAATGG CTGCTTTGCC GGGGCAGGCT CGGACTGCCT GAAACGAAAG
1001 TGTCCGCCGT CATCAGCGTT TCCGACCGCG TCGGCGCGTT TGCAAACCGG
1051 GCGTGGGCGG ACAAAGCCCA CGCCGACCTC AAACGCATCC TTCCGCATTT
1101 GGGCGAACCC GAAGCCGTGC GCGTCATCAC CGAAAAACGC GCCACAACCG
1151 CAGCCGATGC CCCGCCGCGG GACTTSTCGT GGTGACACCG GCACCGCATC
1201 TTCGCCGCGG GCGACTACCT CCACCGGAC TACCCGCCCA CGCTCGAAGC
1251 CGCCGTACAA TCAGGTTTCG CGTCGCGGGA AGCCTGCCTG CAAAGCCTGA
1301 GCGATGCCGT CTGA

```

This corresponds to the amino acid sequence <SEQ ID 3016; ORF 997>:

```

m997.pep
1  MMNTPHPRPK IAVIGAGWAG LSAAVTLARH ADVTLFEAGR QAGGRARTLA
51  GNTDGFGLD NGQHILLGAY RGVLRMLKTI GSDPRAAFLR VPLHWHMHGG
101 LQFRALPLPA PLHILGGVLL ARRAPTAFKA KLLADMSDLQ KSARLGQPD
151 TVAQWLKQRN VPRAAVMQFW QPLVWGALNT PLETASLRVL CNVLS
201 KKS GSDYLLP KODLGAIVAE PALADLQRLG ADIRLETRVC RLNTLPD
251 LVNGEAFDAA VPATAPYHAA ALLPEGTPEH VQTAYQNLRY HAITTVY
301 AEPVRLPAPL TGLADGTQWV LLCRGRGLP ENEVSAVISV SDRVGAFANR
351 AWADKAHADL KRILPHLGEP EAVRVITEKR ATTAADAPP DL
401 FPGDYLHPD YPATLEAAVQ SGFASAEACL QSLSDAV

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 997 shows 96.0% identity over a 351 aa overlap with a predicted ORF (ORF 997) from *N. gonorrhoeae*

g997/m997 96.0% identity in 351 aa overlap

	10	20	30	40	50	60
g997.pep	MMNTPHPRPKIAVIGAGWAGLSAAVTLARHADVTLEAGRQAGGRARTLAGNTDGFGLD					
m997	MMNTPHPRPKIAVIGAGWAGLSAAVTLARHADVTLEAGRQAGGRARTLAGNTDGFGLD					
	10	20	30	40	50	60
g997.pep	70	80	90	100	110	120
	NGQHILLGAYRGVLRMLKTI GSDPRAAFLRVPLHWHMHGG LQFRALPLPAPLHILGGVLL					
m997	NGQHILLGAYRGVLRMLKTI GSDPRAAFLRVPLHWHMHGG LQFRALPLPAPLHILGGVLL					
	70	80	90	100	110	120
g997.pep	130	140	150	160	170	180
	ARRVPSAFKAKLLADMSDLQKSARLGQPDTTVAQWLKQRNVPRAAVMQFWQPLVWGALNT					
m997	ARRAPTAFKAKLLADMSDLQKSARLGQPDTTVAQWLKQRNVPRAAVMQFWQPLVWGALNT					
	130	140	150	160	170	180
g997.pep	190	200	210	220	230	240
	PLETASLRVLCNVLSGDLTKKSGSDYLLPKQDLGAIVAE PALAELQRLGADIRLETRVC					
m997	PLETASLRVLCNVLSGDLTKKSGSDYLLPKQDLGAIVAE PALADLQRLGADIRLETRVC					
	190	200	210	220	230	240
g997.pep	250	260	270	280	290	300
	RLNTLPDGKVLVNGEAFDAA ILATAPYHAA ALLPEGTPEHVQTAYQNLRYHAITTVYLR					
m997	RLNTLPDGKVLVNGEAFDAA VPATAPYHAA ALLPEGTPEHVQTAYQNLRYHAITTVYLR					
	250	260	270	280	290	300
g997.pep	310	320	330	340	350	
	AEPVRLPAPLTGIADGTQWVLLCPGQAPDCPQNEVSAVISVSDRVGAFANR					
m997	AEPVRLPAPLTGLADGTQWVLLCRGRL-GLPENEVSAVISVSDRVGAFANRAWADKAHAD					
	310	320	330	340	350	

1418

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3017>:

```
a997.seq
1  ATGATGAACA CGCCGCATCC GCGCCCGAAA ATCGCCGTCA TCGGCGCAGG
51  CTGGGCGCGG TTGTCCGCGG CCGTTACCTT GCGCGGCGAC GCCGACGTTA
101 CCCTGTTTGA AGCCGCGCGG CAGGCGGGCG GCAGGGCGCG CGCACTGGCC
151 GGAAATACCG ACGGTTTCGG TTTTGTGGAC AACGGGCGAG ATATTTTACT
201 CGGCGGCATAC CGGGCGGTGT TGCGCCTGAT GAAAACCATC GGTTTCAGACC
251 CCCATGCCGC CTTTTTGGCG GTACCGCTGC ACTGGCATAT GCACGGCGGT
301 TTGCAGTTCC GCGCCCTCCC CCTGCCCGCG CCCCTGCATA TTTTGGGCGG
351 CGTGCTGCTT GCCCGGCGCG TACCGTCCCG ATTCAAAGCC AAACCTGCTT
401 CCGATATGTC CGATTTCAG AAGTCCGCAC GCCTCGGACA GCGCGACACG
451 ACAGTGGCGC AATGGCTGAA ACAGCGGAAC GTGCCGCGTG CCGCGCTAAT
501 GCAGTTTGGG CAGCCCTTGG TTTGGGCGCG GCTCAACACG CCTTTGGAAG
551 CCGCAAGCCT GCGCGTGTG TGCAACGTTT TGTCCGACGG CGTGCTGACG
601 AAAAAATCCG GCAGCGACTA TCTCCTACCC AAACAGGATT TGGGCGCAAT
651 CGTCGCGCAA CCCGCCCTGG CGGAGCTTCA ACGGCTCGGC GCGGACATCC
701 GCCTCGAAGC GCGCATATGC CGTCTGAACA CCTCCCGGA CGGGAAGTGT
751 CTCGTCAACG GCGAACCTTT CGATGCCGCC GTCCCGCGCA CCGCGCCCTA
801 CCACGCGGCC GCGCTCCTGC CCGAAGGCAC GCCCGAACAC GTTCAGACGG
851 CATATCAAAA CCTTCGCTAT CACGCCATCA CCACCGTCTA TCTGCGCTAT
901 GCCGAACCCG TCCGCTTGCC TGCCCGCTG ACCGGAAGTG CCGACGGCAC
951 GGTGCAATGG CTGCTTTGCC GGGGCGAGCT CGGACTGCCT GAAAACGAAG
1001 TGTCCGCCCT CATCAGCGTT TCCGACCGCG TCGGCGCGTT TGCAAAACGG
1051 GCGTGGGCGG ACAAAGTTCA CGCCGACCTC AAACGCATCC TTCCGCATTT
1101 GGGCGAACCC GAAGCCGTGC GCGTCATCAC CGAAAAACGC GCCACAACCG
1151 CAGCCGATGC CCGCCGCGCG GATTTGTCGT GGTTCGACCG GCACCGCATC
1201 TTCCCGCGCG GCGACTACCT CCACCCAGAC TACCCGCGCA CGCTCGAAGC
1251 CGCCGTACAA TUAGGTTTCG CGTCGGCGGA AGCCTGCCTG CAAAGCCTGA
1301 GCGATGCCCT CTGA
```

This corresponds to the amino acid sequence <SEQ ID 3018; ORF 997.a>:

```
a997.pep
1  MMNTPHPRPK IAVIGAGWAG LSAAVTLARH ADVTLFEAGR QAGGRARALA
51  GNTDGFGLD NGQHILLGAY RGVLRIMKTI GSDPAAFLR VPLHWHMHGG
101 LQFRALPLPA PLHILGGVLL ARRVPFAFKA KLLADMSDLQ KSARLGQPD
151 TVAQWLKQRN VPRAAVMQFW QPLVWGALNT PLETASLRVL CNVLSDGVL
201 KKSQSDYLLP QDLGAIVAE PALAELQRLG ADIRLETRIC RLNTLPDGKV
251 LVNGEPPDAA VPATAPYHAA ALLPEGTPEH VQTAYQNLRY HAITTVYLYR
301 AEPVRLPAFL TGLADGTVMQ LLCRGRLGLP ENEVSAVISV SDRVGAFAFR
351 AWADKVHADL KRILPHLGEP EAVRVITEKR ATTAADAPPP DLSWLHRRHI
401 FPAGDYLHPD YPATLEAAVO SGFASAEACL QSLSDAV*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 997 shows 98.2% identity over a 437 aa overlap with a predicted ORF (ORF 997) from *N. meningitidis*

a997/m997 98.2% identity in 437 aa overlap

	10	20	30	40	50	60
a997.pep	MMNTPHPRPKIAVIGAGWAGLSAAVTLARHADVTLEAGRQAGGRARALAGNTDGFGLD					
m997	MMNTPHPRPKIAVIGAGWAGLSAAVTLARHADVTLEAGRQAGGRARTLAGNTDGFGLD					
	10	20	30	40	50	60
a997.pep	NGQHILLGAYRGVLRIMKTIGSDPAAFLRVPLHWHMHGGGLQFRALPLPAPLHILGGVLL					
m997	NGQHILLGAYRGVLRIMKTIGSDPAAFLRVPLHWHMHGGGLQFRALPLPAPLHILGGVLL					
	70	80	90	100	110	120
a997.pep	ARRVPFAFAKLLADMSDLQKSARLGQPDTTVAQWLKQRNVPRAAVMQFWQPLVWGALNT					
m997	ARRAPTAFAKLLADMSDLQKSARLGQPDTTVAQWLKQRNVPRAAVMQFWQPLVWGALNT					
	130	140	150	160	170	180
a997.pep	PLETASLRVLCNVLSDGVLTKKSGSDYLLPKQDLGAIVAEPALAELQRLGADIRLETRIC					
m997	PLETASLRVLCNVLSDGVLTKKSGSDYLLPKQDLGAIVAEPALAELQRLGADIRLETRIC					
	190	200	210	220	230	240
a997.pep	PLETASLRVLCNVLSDGVLTKKSGSDYLLPKQDLGAIVAEPALAELQRLGADIRLETRIC					
m997	PLETASLRVLCNVLSDGVLTKKSGSDYLLPKQDLGAIVAEPALAELQRLGADIRLETRIC					

1419

```

m997      PLETASLRVLCNVLSDGVLTKKSGSDYLLPKQDLGAIVAEPALADLQRLGADIRLETRVC
           190      200      210      220      230      240

           250      260      270      280      290      300
a997.pep  RLNTLPDGKVLVNGEPFDAAVPATAPYHAAALLPEGTPEHVQTAYQNLRYHAITTVYLR
           |||||
m997      RLNTLPDGKVLVNGEAFDAAVPATAPYHAAALLPEGTPEHVQTAYQNLRYHAITTVYLR
           250      260      270      280      290      300

           310      320      330      340      350      360
a997.pep  AEPVRLPAPLTGLADGTVQWLLCRGRLGLPENEVSAVISVSDRVGAFANRAWADKVHADL
           |||||
m997      AEPVRLPAPLTGLADGTVQWLLCRGRLGLPENEVSAVISVSDRVGAFANRAWADKAHADL
           310      320      330      340      350      360

           370      380      390      400      410      420
a997.pep  KRILPHLGEPEAVRVITEKRATTAADAPPPDLSSLHRHRIFFAGDYLHPDYPATLEAAVQ
           |||||
m997      KRILPHLGEPEAVRVITEKRATTAADAPPPDLSSLHRHRIFFAGDYLHPDYPATLEAAVQ
           370      380      390      400      410      420

           430
a997.pep  SGFASAEACLSLSDAVX
           |||||
m997      SGFASAEACLSLSDAVX
           430

```

g999.seq Not found yet

g999.pep Not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3019>:

```

m999.seq
1  ATGAATATGA  AAAAATTGAT  TTCCGCAATT  TGTGTTTCAA  TTGTTTATC
51  AGCCTGCAAC  CAACAATCAA  AAACGGCACA  AGCCGAAGAA  CCTGTCCAAA
101  GTATCCAGGC  TGCTGATTGT  ACCGCCCCAA  TGGACATCAC  AGTTGAACAA
151  TATCTCATCA  ATTTGGAGCA  AGCATTTAAA  ACTCAGAACG  TCTCAACAAA
201  AATCCATAAT  AAAAATATTG  TCAAGACCGA  TTGTGGTTAT  GACCTTACTT
251  TGGAATATGA  TTTTGGGGCG  ATTGCGCTCA  AACTGGACGA  GCAGCAAAAA
301  ATTAGAGCTA  TCTCAGTAGG  CTACATTTTA  AAAACCGACG  GAGAGAAAGG
351  ACAAATCTA  GTCAATAATG  CCATAAATGG  ATTACACAGT  ATTCAGGCAG
401  TTCTGTCTTT  AACTACCACA  GACAAATTGG  GCGAATCGGA  AGCAGGAAAA
451  CAACTTTTTA  CAGCTTTAAC  CGAAGTCGTC  AAAGAATCCA  ATCAGACAGG
501  AGCAACAGCG  CAAAAGACG  TTCCGGCAGA  TGGTATTTTA  TATAGCGTTG
551  TTTTGTAAAA  AGAAACAAAC  ACCATTGCAA  TAATCGGCAG  AAAACAACCC
601  TAA

```

This corresponds to the amino acid sequence <SEQ ID 3020; ORF 999>:

```

m999.pep
1  MNMKKLISAI  CVSIVLSACN  QSKTAQAE  PVQSIQAADC  TAPMDITVEQ
51  YLINLEQAFK  TQNVSTKIHN  KNIVKTDG  DLTVMDFGA  IALKLDEQOK
101  IRAISVGYIL  KTDGEKGQNL  VNNAINGL  IQAVLSLTTT  DKLGESEAGK
151  QLFALTVEVV  KESNOTGATA  QKDVPADG  YSVVFEKETN  TIAIIGRKOP

```

a999.seq Not found yet

a999.pep Not found yet

The foregoing examples are intended to illustrate but not to limit the invention.

CLAIMS

1. A protein comprising a fragment of an amino acid sequence from SEQ ID 2790 wherein said fragment comprises at least 7 amino acids from said sequence.
 2. A protein comprising an amino acid sequence selected from the group consisting of even numbered SEQ IDs from SEQ ID number 2 through SEQ ID number 3020.
 3. A protein having 50% or greater homology to a protein according to claim 1.
 4. A protein comprising a fragment of an amino acid sequence selected from the group consisting of even numbered SEQ IDs from SEQ ID number 2 through SEQ ID number 3020, wherein said fragment comprises 7 or more consecutive amino acids from said sequence.
 5. An antibody which binds to a protein according to any one of claims 1 to 3.
 6. A nucleic acid molecule which encodes a protein according to any one of claims 1 to 3.
 7. A nucleic acid molecule according to claim 5, comprising a nucleotide sequence selected from the group consisting of odd numbered SEQ IDs from SEQ ID number 1 through SEQ ID number 3019.
 8. A nucleic acid molecule comprising a fragment of a nucleotide sequence selected from the group consisting of odd numbered SEQ IDs from SEQ ID number 1 through SEQ ID number 3019, wherein said fragment comprises 10 or more consecutive nucleotides from said sequence.
 9. A nucleic acid molecule comprising a nucleotide sequence complementary to a nucleic acid molecule according to claim 5.
 10. A nucleic acid molecule comprising a nucleotide sequence complementary to a nucleic acid molecule according to claim 6.
 11. A nucleic acid molecule comprising a nucleotide sequence complementary to a nucleic acid molecule according to claim 7.
 12. A composition comprising a protein, a nucleic acid molecule, or an antibody according to any preceding claim.
 13. A composition according to claim 11 being a vaccine composition or a diagnostic composition.
 14. A composition according to claim 11 for use as a pharmaceutical.
 15. The use of a composition according to claim 11 in the manufacture of a medicament for the treatment or prevention of infection due to Neisserial bacteria.
-

16. A composition comprising a protein of claim 1 wherein said composition is immunogenic.

17. A composition comprising a protein of claim 2 wherein said composition is immunogenic.

18. A composition comprising a protein of claim 3 wherein said composition is immunogenic.

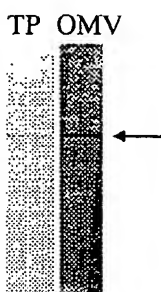
Fig. 2

279 (10.5 kDa)

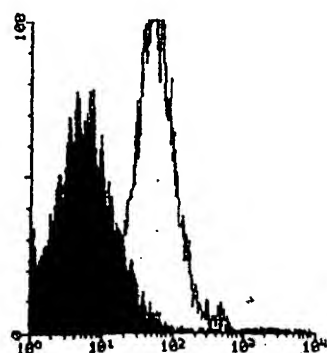
A) PURIFICATION



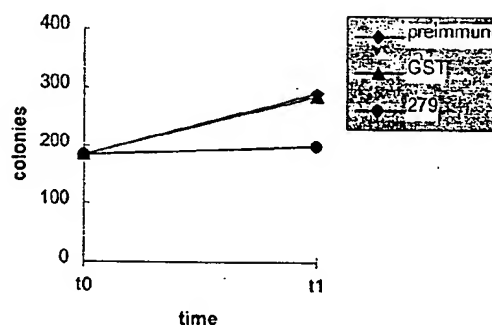
B) WESTERN BLOT



C) FACS



D) BACTERICIDAL ASSAY

E) ELISA assay: positive

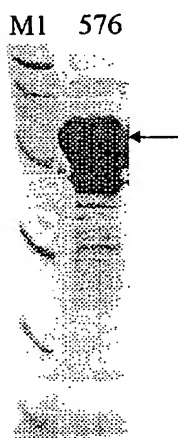
279

The predicted gene 279 was cloned in pGex vector and expressed in *E. coli*. The product of protein expression and purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 279-GST purification. Mice were immunized with the purified 279-GST and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that protein 279 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

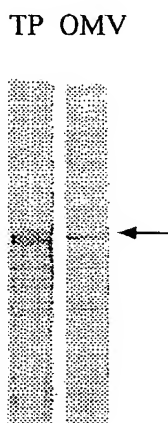
Fig. 3

576 (27.8 kDa)

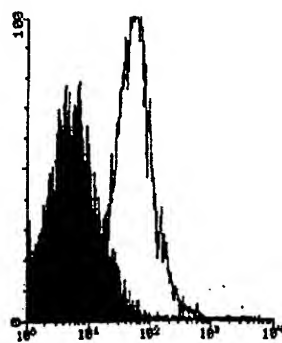
A) PURIFICATION



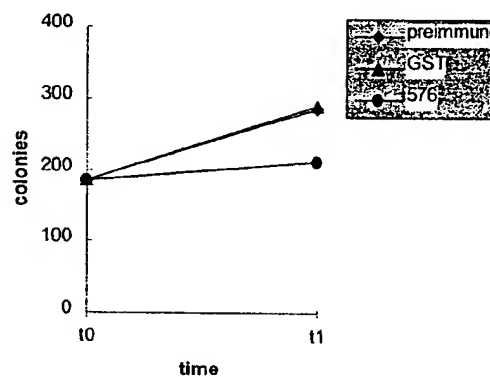
B) WESTERN BLOT



C) FACS

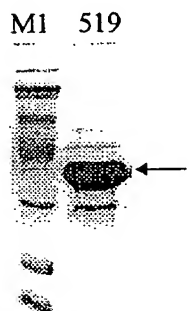
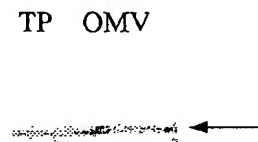
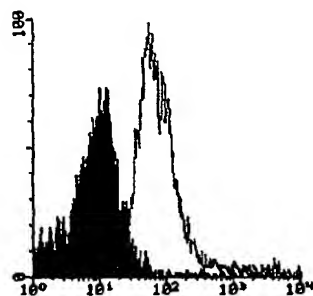
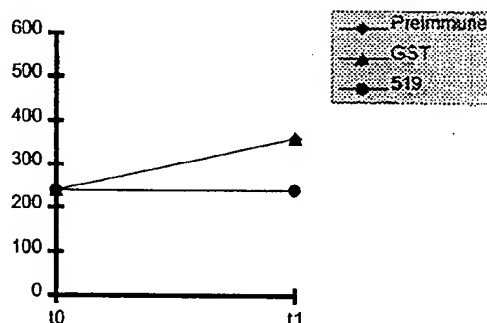


D) BACTERICIDAL ASSAY

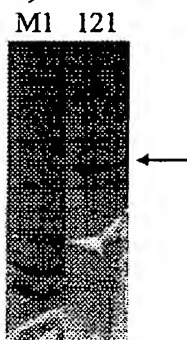
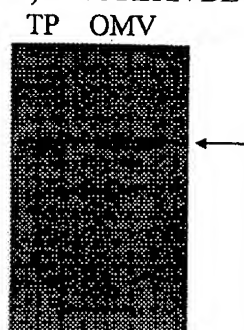
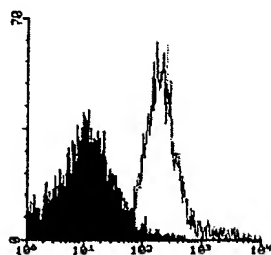
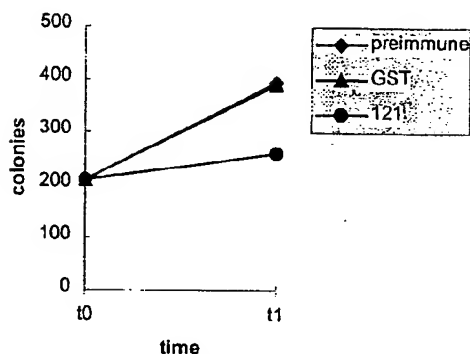
E) ELISA assay: positive

576

The predicted gene 576 was cloned in pGex vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 576-GST fusion protein purification. Mice were immunized with the purified 576-GST and sera were used for Western blot (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that 576 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

519 (33 kDa)**Fig. 4****A) PURIFICATION****B) WESTERN BLOT****C) FACS****D) BACTERICIDAL ASSAY****E) ELISA assay: positive****519**

The predicted gene *519* was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 519-His fusion protein purification. Mice were immunized with the purified 519-His and sera were used for Western blot (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that 519 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

121 (40 kDa)**A) PURIFICATION****B) WESTERN BLOT****C) FACS****D) BACTERICIDAL ASSAY****E) ELISA assay: positive****121**

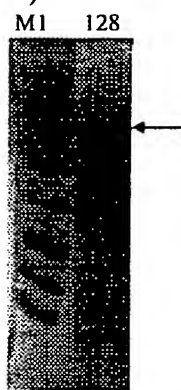
The predicted gene *121* was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 121-His fusion protein purification. Mice were immunized with the purified 121-His and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that 121 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

Fig. 5

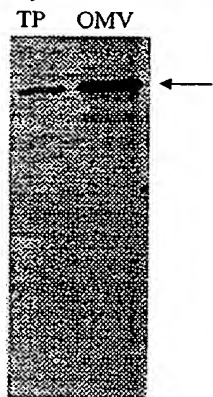
128 (101 kDa)

Fig. 6

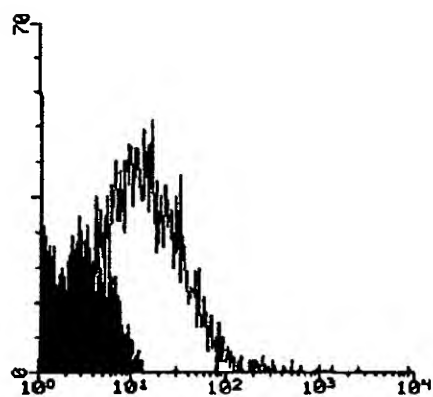
A) PURIFICATION



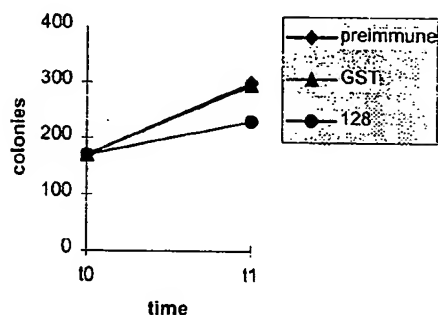
B) WESTERN BLOT



C) FACS



D) BACTERICIDAL ASSAY



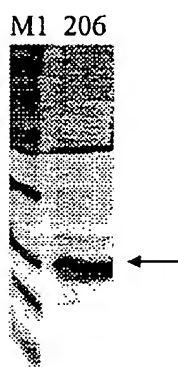
E) ELISA assay: positive

128

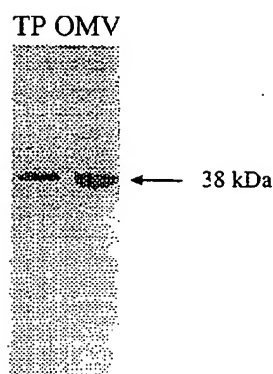
The predicted gene 128 was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 128-His purification. Mice were immunized with the purified 128-His and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D) and ELISA assay (panel E). Results show that 128 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

Fig. 7

A) PURIFICATION



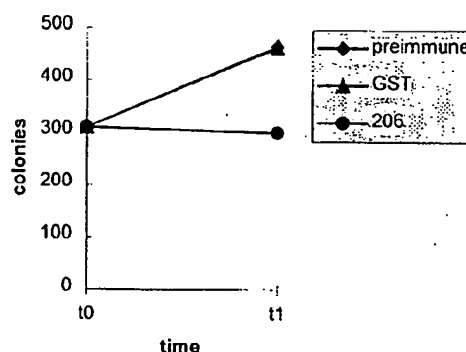
B) WESTERN BLOT



C) FACS



D) BACTERICIDAL ASSAY



E) ELISA assay: positive

206

The predicted gene 206 was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 206-His purification. Mice were immunized with the purified 206-His and sera were used for Western blot analysis (panel B). It is worthnoting that the immunoreactive band in protein extracts from meningococcus is 38 kDa instead of 17 kDa (panel A). To gain information on the nature of this antibody staining we expressed ORF 206 in *E. coli* without the His-tag and including the predicted leader peptide. Western blot analysis on total protein extracts from *E. coli* expressing this native form of the 206 protein showed a recative band at a position of 38 kDa, as observed in meningococcus. We conclude that the 38 kDa band in panel B) is specific and that anti-206 antibodies, likely recognize a multimeric protein complex. In panel C) is shown the FACS analysis, in panel D) the bactericidal assay, and in panel E) the ELISA assay. Results show that 206 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

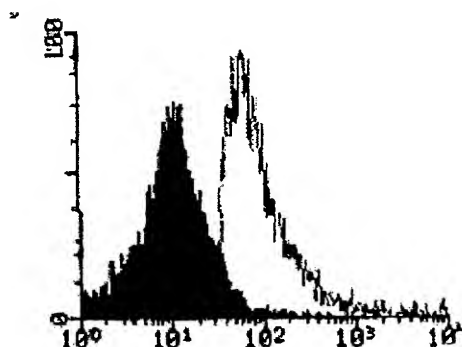
287 (78 kDa)

Fig. 8

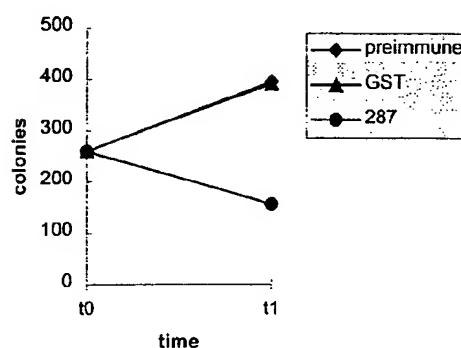
A) PURIFICATION



B) FACS



C) BACTERICIDAL ASSAY

D) ELISA assay : positive

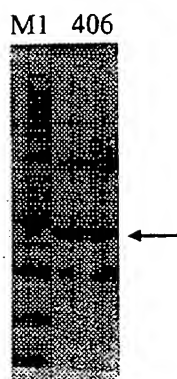
287

The predicted gene 287 was cloned in pGex vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 287-GST fusion protein purification. Mice were immunized with the purified 287-GST and sera were used for FACS analysis (panel B), bactericidal assay (panel C), and ELISA assay (panel D). Results show that 287 is a surface-exposed protein. Symbols: M1, molecular weight marker. Arrow indicates the position of the main recombinant protein product (A).

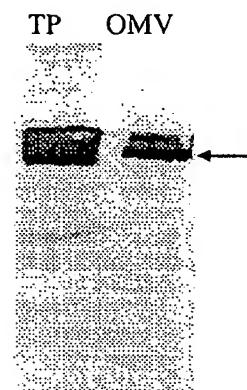
406 (33 kDa)

Fig. 9

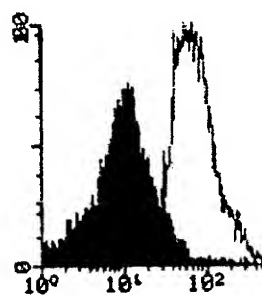
A) PURIFICATION



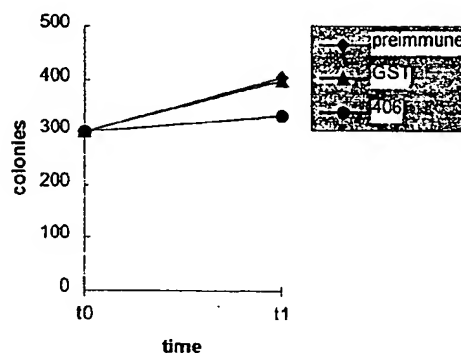
B) WESTERN BLOT



C) FACS



D) BACTERICIDAL ASSAY

E) ELISA assay : positive

406

The predicted gene 406 was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 406-His fusion protein purification. Mice were immunized with the purified 406-His and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that 406 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

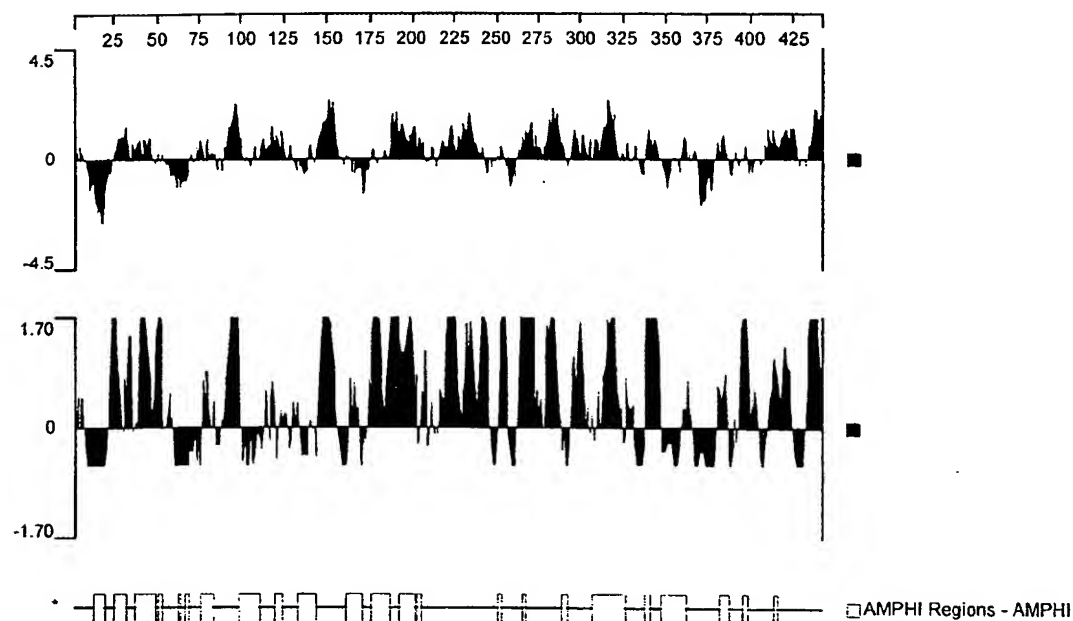
Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 10

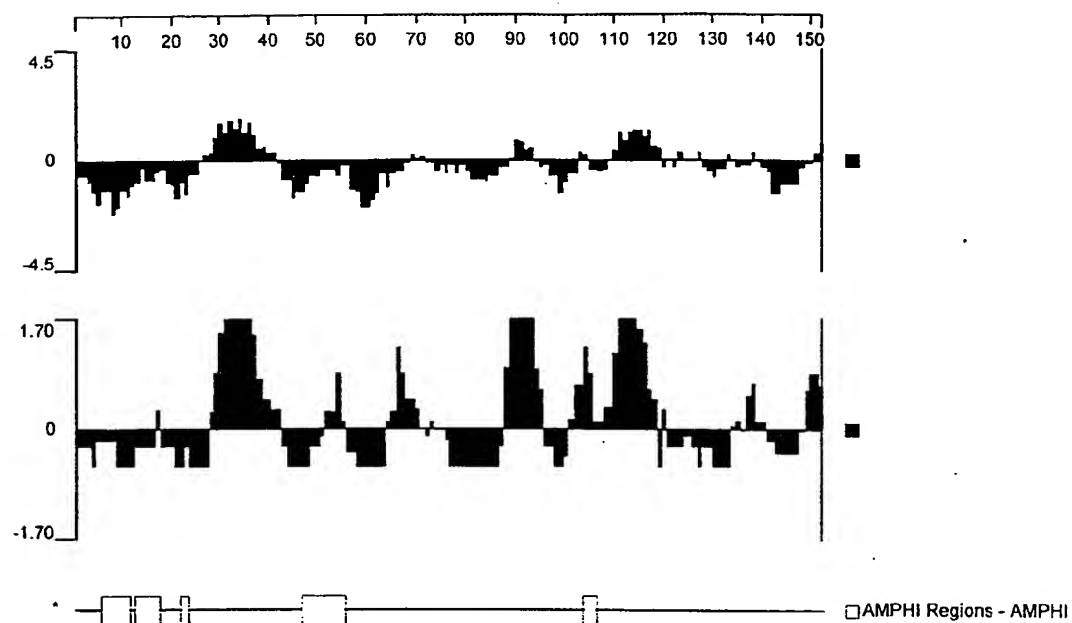
Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 11

11/30

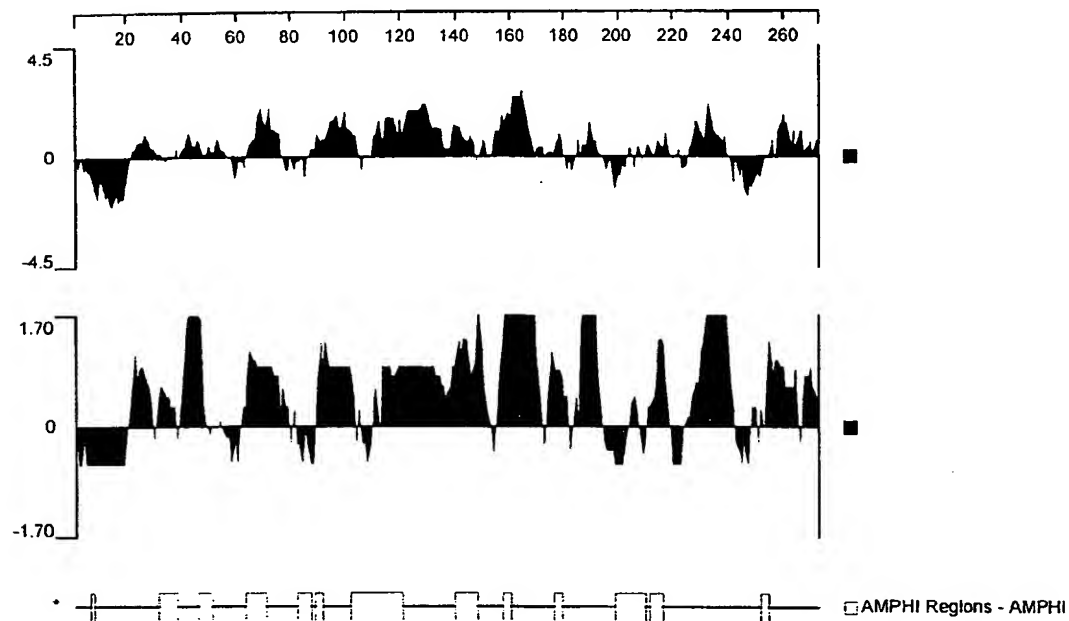
576-1Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 12

12/30

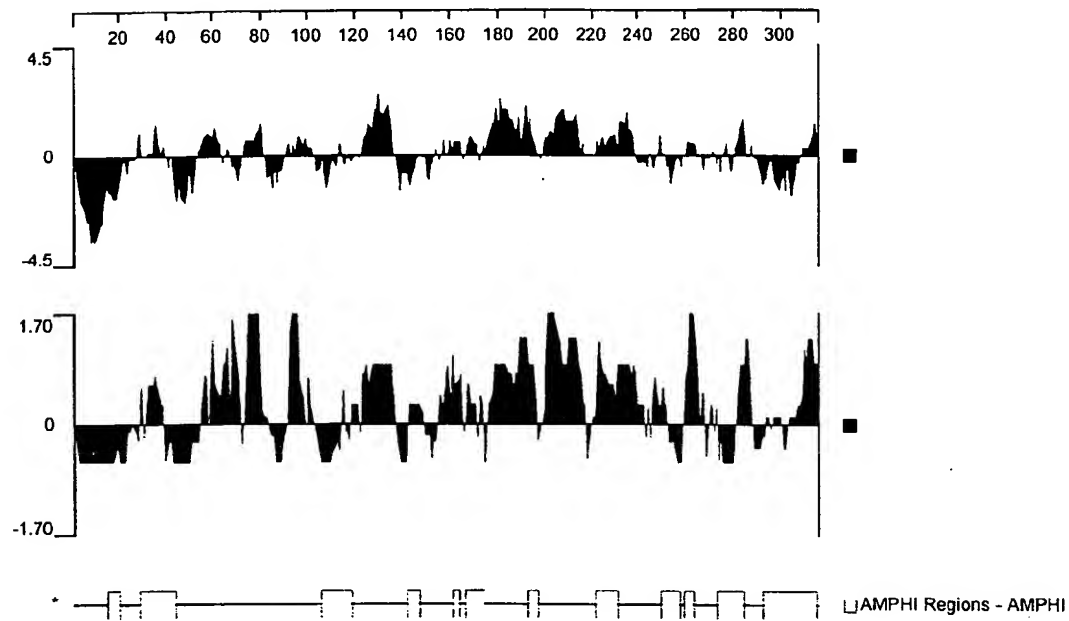
519-1Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 13

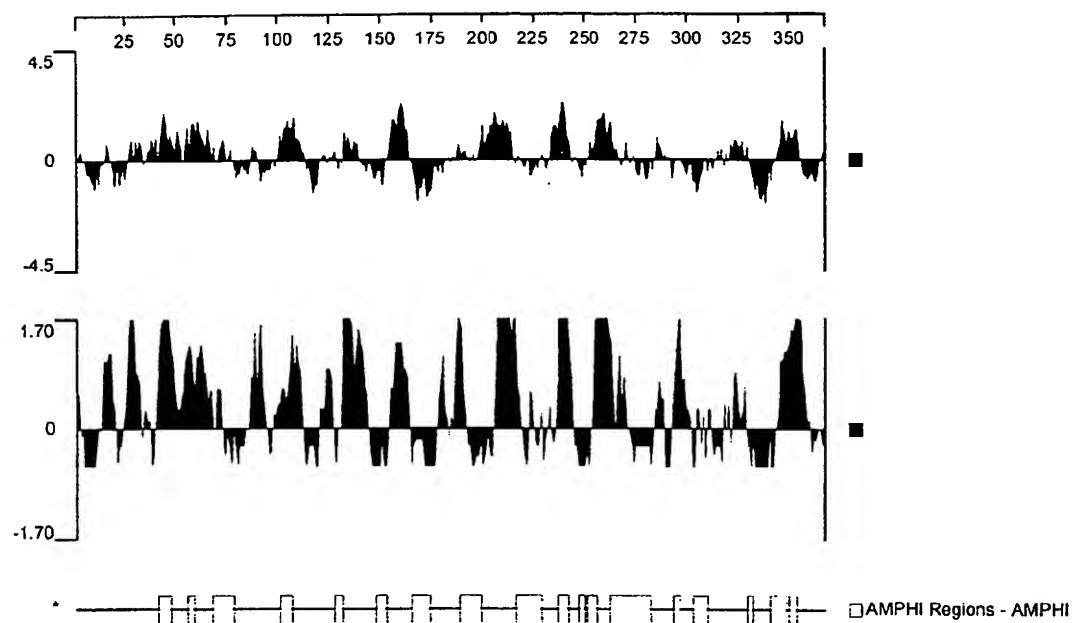
121-1Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 14

14/30

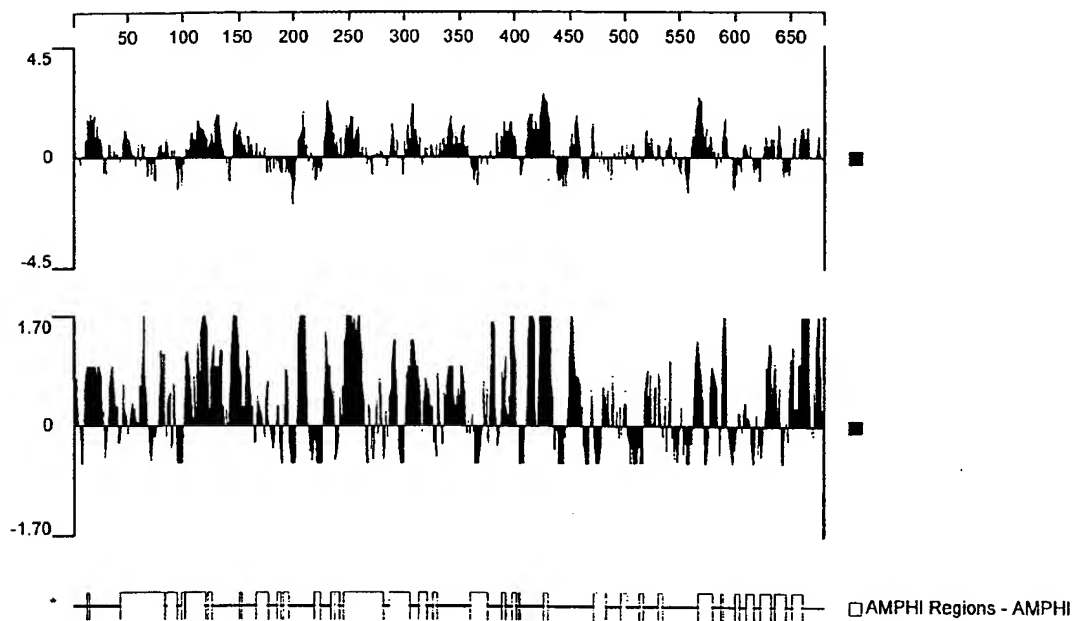
128-1Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 15

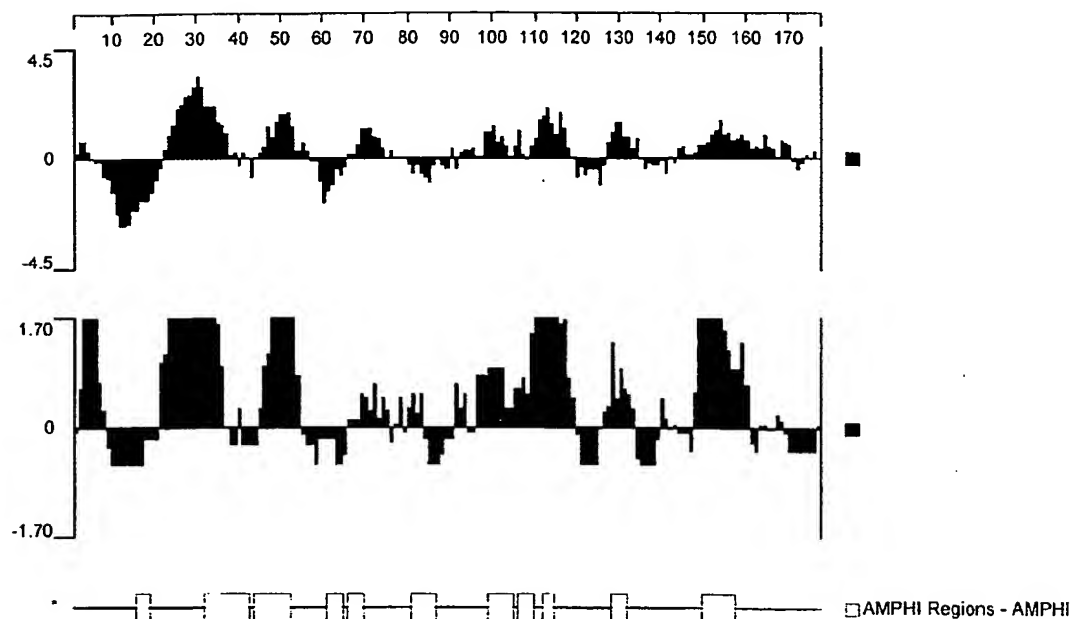
Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 16

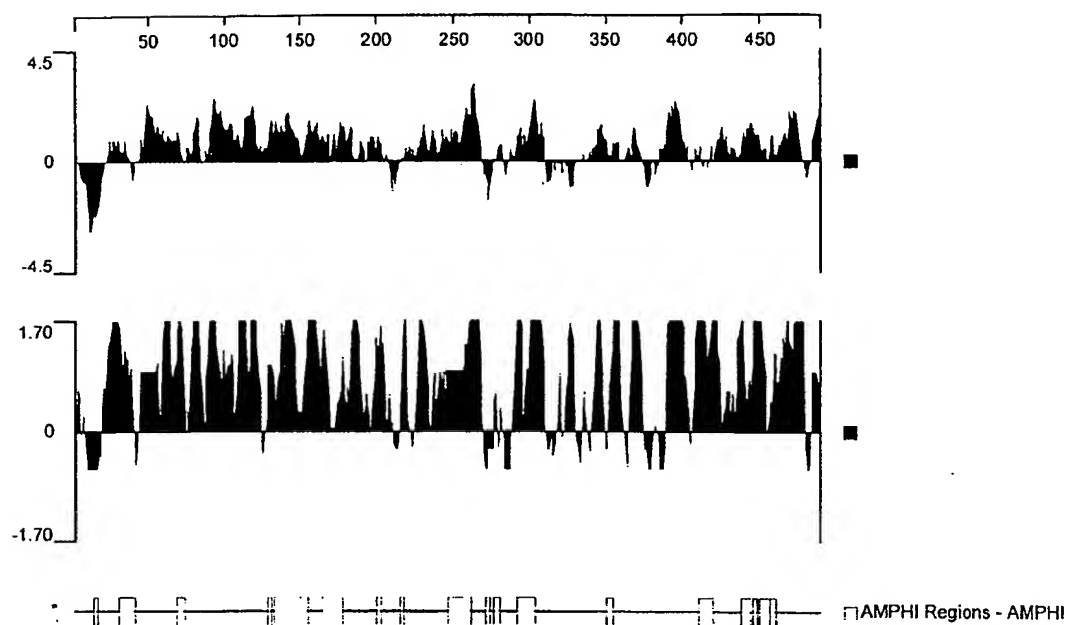
Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 17

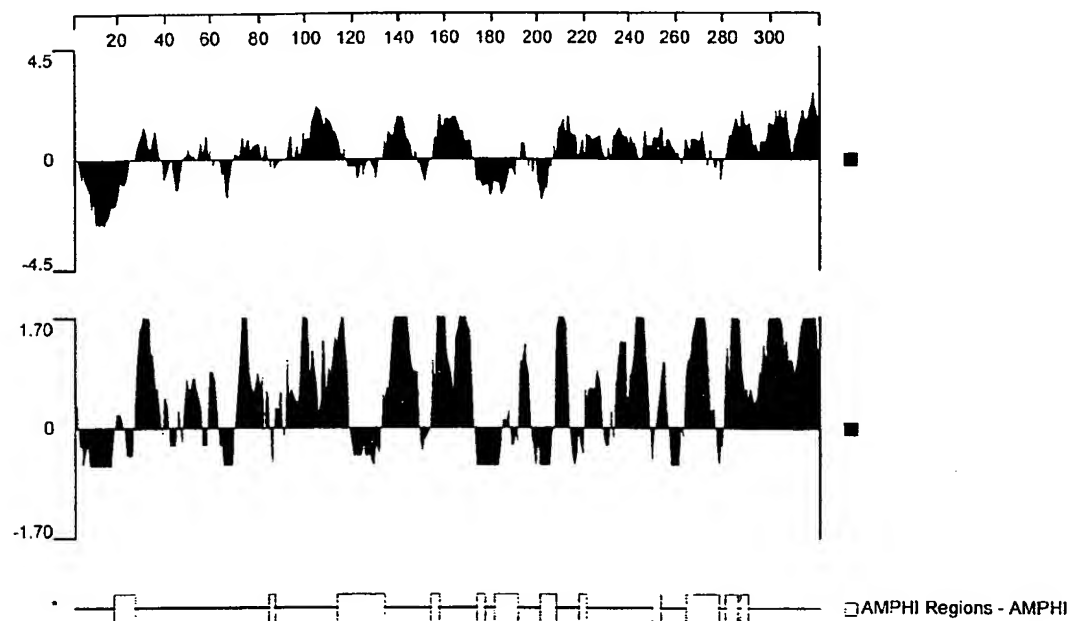
406Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 18

Fig. 19A

Fig. 19B

zo05_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDFSRFLN*
zo08_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDFSRFLN*
zo2491	241	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDFSRFLN*
zo11_225	241	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDFSRFLN*
zo20_225	241	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDFSRFLN*
zo01_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDFSRFLN*
zo09_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDFSRFLN*
zo12_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDFSRFLN*
zo22_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDFSRFLN*
zo23_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDFSRFLN*
zo24_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDFSRFLN*
zo25_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDFSRFLN*
zo26_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDFSRFLN*
zo96_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDFSRFLN*
zo02_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDFSRFLN*
zo04_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDFSRFLN*
zo06_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDFSRFLN*
zo07_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDFSRFLN*
zo10_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDFSRFLN*
zo14_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDFSRFLN*
zo16_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDFSRFLN*
zo17_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDFSRFLN*
zo18_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDFSRFLN*
zo19_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDFSRFLN*
zo21_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDFSRFLN*
zo27_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDFSRFLN*
zo28_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDFSRFLN*
zo29_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDFSRFLN*
zo13_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDFSRFLN*
zo03_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDFSRFLN*
zo15_225	183	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDFSRFLN*
fa1090	183	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDFSRFLN*
zo32_225	183	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDFSRFLN*
zo33_225	183	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDFSRFLN*

Fig. 19C

Fig. 20A

Fig. 20B

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287_14 1 MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSPAAPVVSE ..... KETEA
287_2 1 MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSPAAPVVSE ..... KETEA
287_21 1 MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSPAAPVVSE ..... KETEA
z2491 1 MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSPAAPVVSE ..... KETEA
287_9 1 MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSPAAPVVSE ..... KETEA
fa1090 1 MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSPAAPVVSE ..... KETEA

287_14 50 KEDAPQAGSQGGGAPSQGGQDMAAVSEENTGNGGAAATDRPKNEDEGAQNMPQNAADT
287_2 50 KEDAPQAGSQGGGAPSQGGQDMAAVSEENTGNGGAAATDRPKNEDEGAQNMPQNAADT
287_21 50 KEDAPQAGSQGGGAPSQGGQDMAAVSEENTGNGGAAATDRPKNEDEGAQNMPQNAADT
z2491 50 KEDAPQAGSQGGGAPSQGGQDMAAVSEENTGNGGAAATDRPKNEDEGAQNMPQNAADT
287_9 61 VSGAPQADT...QDATAGKGGQDMAAVSAENTGNGGAAATDRPKNEDEGAQNMPQNAADT
fa1090 61 AGGAPQADT...QDATAGEGSQDMAAVSAENTGNGGAAATDRPKNEDEGAQNMPQNAADT

287_14 110 DSLTPNHPTASNMPAGNMENQAD DAGESE QPANOPDMANTADGMQGGDDPSAGCENAGNTA
287_2 110 DSLTPNHPTASNMPAGNMENQAD DAGESE QPANOPDMANTADGMQGGDDPSAGCENAGNTA
287_21 110 DSLTPNHPTASNMPAGNMENQAD DAGESE QPANOPDMANTADGMQGGDDPSAGCENAGNTA
z2491 110 DSLTPNHPTASNMPAGNMENQAD DAGESE QPANOPDMANTADGMQGGDDPSAGCENAGNTA
287_9 119 DSLTPNHPTASNMPTRDMGNQAD DAGESA QPANOPDMANTADGMQGGDDPSAGCENAGNTA
fa1090 117 .....

287_14 170 AQSTNQAEENQTAGSQNPASSINPSATNSGGDFGRITNNGNSVVIDGSPSONITLTHCKGDS
287_2 170 AQSTNQAEENQTAGSQNPASSINPSATNSGGDFGRITNNGNSVVIDGSPSONITLTHCKGDS
287_21 170 AQSTNQAEENQTAGSQNPASSINPSATNSGGDFGRITNNGNSVVIDGSPSONITLTHCKGDS
z2491 170 AQSTNQAEENQTAGSQNPASSINPSATNSGGDFGRITNNGNSVVIDGSPSONITLTHCKGDS
287_9 178 DQSTNQAEENQTAGSQNPASSINPSATNSGGDFGRITNNGNSVVIDGSPSONITLTHCKGDS
fa1090 117 .ESANQTAGSQNPASSINPSATNSGGDFGRITNNGNSVVIDGSPSONITLTHCKGDS

287_14 230 CSGNFFLDEEVQLKSEFEKLSDAKISNYKKDGKNDGKNEFVGLVADSVQMKGINQYII
287_2 230 CSGNFFLDEEVQLKSEFEKLSDAKISNYKKDGKNDGKNEFVGLVADSVQMKGINQYII
287_21 230 CSGNFFLDEEVQLKSEFEKLSDAKISNYKKDGKNDGKNEFVGLVADSVQMKGINQYII
z2491 230 CSGNFFLDEEVQLKSEFEKLSDAKISNYKKDGKNDGKNEFVGLVADSVQMKGINQYII
287_9 238 QDRD.FLDEEAPPKSEFEKLSDAKISNYKKDGKNDGKNEFVGLVADSVQMKGINQYII
fa1090 176 CSGNFFLDEEVQLKSEFEKLSDAKISNYKKDGKNDGKNEFVGLVADSVQMKGINQYII

287_14 290 FYKPKP...TSARFRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEG
287_2 290 FYKPKP...TSARFRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEG
287_21 286 FYKPKP...TSARFRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEG
z2491 286 FYKPKP...TSARFRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEG
287_9 293 FYKPKP...TSARFRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEG
fa1090 232 FYTDKPPT.....RSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEG

287_14 348 NYRYLTYGAEKLPGGSYALRVQGEPAKGEMLAGTAVYNGEVLHFHTENGRPSPEGRFAA
287_2 348 NYRYLTYGAEKLPGGSYALRVQGEPAKGEMLAGTAVYNGEVLHFHTENGRPSPEGRFAA
287_21 344 NYRYLTYGAEKLPGGSYALRVQGEPAKGEMLAGTAVYNGEVLHFHTENGRPSPEGRFAA
z2491 344 NYRYLTYGAEKLPGGSYALRVQGEPAKGEMLAGTAVYNGEVLHFHTENGRPSPEGRFAA
287_9 353 NYRYLTYGAEKLPGGSYALRVQGEPAKGEMLAGTAVYNGEVLHFHTENGRPSPEGRFAA
fa1090 285 NYRYLTYGAEKLPGGSYALRVQGEPAKGEMLAGTAVYNGEVLHFHTENGRPSPEGRFAA

287_14 408 KVDGFSKSDGIIDSGDLHMGTKQFKAAIDGNGFKGTWTENGCGDVSGFYGPAGEEVA
287_2 408 KVDGFSKSDGIIDSGDLHMGTKQFKAAIDGNGFKGTWTENGCGDVSGFYGPAGEEVA
287_21 404 KVDGFSKSDGIIDSGDLHMGTKQFKAAIDGNGFKGTWTENGCGDVSGFYGPAGEEVA
z2491 404 KVDGFSKSDGIIDSGDLHMGTKQFKAAIDGNGFKGTWTENGCGDVSGFYGPAGEEVA
287_9 413 KVDGFSKSDGIIDSGDLHMGTKQFKAAIDGNGFKGTWTENGCGDVSGFYGPAGEEVA
fa1090 345 KVDGFSKSDGIIDSGDLHMGTKQFKAAIDGNGFKGTWTENGCGDVSGFYGPAGEEVA

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FIG. 21A

287_14	468	GKYSYRPTDAEKGGFGVFAGKKEQD*
287_2	468	GKYSYRPTDAEKGGFGVFAGKKEQD*
287_21	464	GKYSYRPTDAEKGGFGVFAGKKEQD*
z2491	464	GKYSYRPTDAEKGGFGVFAGKKEQD*
287_9	473	GKYSYRPTDAEKGGFGVFAGKKEQD*
fa1090	405	GKYSYRPTDAEKGGFGVFAGKKEQD*

FIG. 21B

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z2491_519 1 MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRLTAGLNILIPFIDRVAYRHS
zv26_519 1 MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRLTAGLNILIPFIDRVAYRHS
zv22_519ass 1 MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRLTAGLNILIPFIDRVAYRHS
fa1090_519 1 MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRLTAGLNILIPFIDRVAYRHS
zv32_519 1 MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRLTAGLNILIPFIDRVAYRHS
zv11_519 1 MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRLTAGLNILIPFIDRVAYRHS
zv28_519 1 MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRLTAGLNILIPFIDRVAYRHS
zv96_519 1 MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRLTAGLNILIPFIDRVAYRHS
zv02_519 1 MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRLTAGLNILIPFIDRVAYRHS
zv03_519 1 MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRLTAGLNILIPFIDRVAYRHS
zv04_519 1 MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRLTAGLNILIPFIDRVAYRHS
zv05_519 1 MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRLTAGLNILIPFIDRVAYRHS
zv01_519 1 MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRLTAGLNILIPFIDRVAYRHS
zv07_519 1 MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRLTAGLNILIPFIDRVAYRHS
zv12_519 1 MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRLTAGLNILIPFIDRVAYRHS
zv18_519 1 MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRLTAGLNILIPFIDRVAYRHS
zv19_519 1 MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRLTAGLNILIPFIDRVAYRHS
zv21_519ass 1 MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRLTAGLNILIPFIDRVAYRHS
zv27_519 1 MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRLTAGLNILIPFIDRVAYRHS
zv20_519ass 1 MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRLTAGLNILIPFIDRVAYRHS
zv06_519ass 1 MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRLTAGLNILIPFIDRVAYRHS
zv29_519ass 1 MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRLTAGLNILIPFIDRVAYRHS

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zv26_519 61 KEIPLDVP SQVCITRDNTQLTV DGIIFYQV TDPKLASYGSSNYIMAITQLAQTTLRSVIG
zv22_519ass 61 KEIPLDVP SQVCITRDNTQLTV DGIIFYQV TDPKLASYGSSNYIMAITQLAQTTLRSVIG
fa1090_519 61 KEIPLDVP SQVCITRDNTQLTV DGIIFYQV TDPKLASYGSSNYIMAITQLAQTTLRSVIG
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zv11_519 61 KEIPLDVP SQVCITRDNTQLTV DGIIFYQV TDPKLASYGSSNYIMAITQLAQTTLRSVIG
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zv96_519 61 KEIPLDVP SQVCITRDNTQLTV DGIIFYQV TDPKLASYGSSNYIMAITQLAQTTLRSVIG
zv02_519 61 KEIPLDVP SQVCITRDNTQLTV DGIIFYQV TDPKLASYGSSNYIMAITQLAQTTLRSVIG
zv03_519 61 KEIPLDVP SQVCITRDNTQLTV DGIIFYQV TDPKLASYGSSNYIMAITQLAQTTLRSVIG
zv04_519 61 KEIPLDVP SQVCITRDNTQLTV DGIIFYQV TDPKLASYGSSNYIMAITQLAQTTLRSVIG
zv05_519 61 KEIPLDVP SQVCITRDNTQLTV DGIIFYQV TDPKLASYGSSNYIMAITQLAQTTLRSVIG
zv01_519 61 KEIPLDVP SQVCITRDNTQLTV DGIIFYQV TDPKLASYGSSNYIMAITQLAQTTLRSVIG
zv07_519 61 KEIPLDVP SQVCITRDNTQLTV DGIIFYQV TDPKLASYGSSNYIMAITQLAQTTLRSVIG
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zv18_519 61 KEIPLDVP SQVCITRDNTQLTV DGIIFYQV TDPKLASYGSSNYIMAITQLAQTTLRSVIG
zv19_519 61 KEIPLDVP SQVCITRDNTQLTV DGIIFYQV TDPKLASYGSSNYIMAITQLAQTTLRSVIG
zv21_519ass 61 KEIPLDVP SQVCITRDNTQLTV DGIIFYQV TDPKLASYGSSNYIMAITQLAQTTLRSVIG
zv27_519 61 KEIPLDVP SQVCITRDNTQLTV DGIIFYQV TDPKLASYGSSNYIMAITQLAQTTLRSVIG
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zv06_519ass 61 KEIPLDVP SQVCITRDNTQLTV DGIIFYQV TDPKLASYGSSNYIMAITQLAQTTLRSVIG
zv29_519ass 61 KEIPLDVP SQVCITRDNTQLTV DGIIFYQV TDPKLASYGSSNYIMAITQLAQTTLRSVIG

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z2491_519 121 RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv26_519 121 RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv22_519ass 121 RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
fa1090_519 121 RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
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zv12_519 121 RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
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zv19_519 121 RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv21_519ass 121 RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv27_519 121 RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv20_519ass 121 RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv06_519ass 121 RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv29_519ass 121 RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE

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FIG. 22A


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z2491_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv26_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv22_519ass 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
fa1090_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv32_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv11_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv28_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv96_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv02_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv03_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv04_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv05_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv01_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv07_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv12_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv18_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv19_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv21_519ass 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv27_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv20_519ass 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv06_519ass 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv29_519ass 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
```

```
z2491_519 241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv26_519 241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv22_519ass 241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
fa1090_519 241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv32_519 241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv11_519 241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv28_519 241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv96_519 241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv02_519 241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv03_519 241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
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zv19_519 241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv21_519ass 241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv27_519 241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv20_519ass 241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv06_519ass 241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv29_519ass 241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
```

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z2491_519 301 ISAGMKIIDSSKTAK*
zv26_519 301 ISAGMKIIDSSKTAK*
zv22_519ass 301 ISAGMKIIDSSKTAK*
fa1090_519 301 ISAGMKIIDSSKTAK*
zv32_519 301 ISAGMKIIDSSKTAK*
zv11_519 301 ISAGMKIIDSSKTAK*
zv28_519 301 ISAGMKIIDSSKTAK*
zv96_519 301 ISAGMKIIDSSKTAK*
zv02_519 301 ISAGMKIIDSSKTAK*
zv03_519 301 ISAGMKIIDSSKTAK*
zv04_519 301 ISAGMKIIDSSKTAK*
zv05_519 301 ISAGMKIIDSSKTAK*
zv01_519 301 ISAGMKIIDSSKTAK*
zv07_519 301 ISAGMKIIDSSKTAK*
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zv18_519 301 ISAGMKIIDSSKTAK*
zv19_519 301 ISAGMKIIDSSKTAK*
zv21_519ass 301 ISAGMKIIDSSKTAK*
zv27_519 301 ISAGMKIIDSSKTAK*
zv20_519ass 301 ISAGMKIIDSSKTAK*
zv06_519ass 301 ISAGMKIIDSSKTAK*
zv29_519ass 301 ISAGMKIIDSSKTAK*
```

Fig. 22B

Fig. 23B


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fa1090      361  IDRRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm33asbc    361  IDRRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm32asbc    361  IDRRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm23asbc    361  VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm27bc      361  VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm09        361  VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm10        361  VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm24        361  VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm25        361  VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm14        361  VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm04        361  VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm11asbc    361  VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm08n       361  VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm96        361  VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm01        361  VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm02        361  VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm03        361  VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm07        361  VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm12        361  VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm18        361  VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm19        361  VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm20        361  VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm21        361  VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm06        361  VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm17        361  VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm13        361  VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm05        361  VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
z2491      361  VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm22        361  VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm26        361  VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm28        361  VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm29asbc    361  VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm16        361  VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm15        361  VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm31asbc    361  VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK

fa1090      421  QKTTGYVWQLLPNGMKPEYRP*
zm33asbc    421  QKTTGYVWQLLPNGMKPEYRP*
zm32asbc    421  QKTTGYVWQLLPNGMKPEYRP*
zm23asbc    421  MKETGYVWQLLPNGMKPEYRP*
zm27bc      421  MKETGYVWQLLPNGMKPEYRP*
zm09        421  QKTTGYVWQLLPNGMKPEYRP*
zm10        421  QKTTGYVWQLLPNGMKPEYRP*
zm24        421  QKTTGYVWQLLPNGMKPEYRP*
zm25        421  QKTTGYVWQLLPNGMKPEYRP*
zm14        421  QKTTGYVWQLLPNGMKPEYRP*
zm04        421  QKTTGYVWQLLPNGMKPEYRP*
zm11asbc    421  QKTTGYVWQLLPNGMKPEYRP*
zm08n       421  QKTTGYVWQLLPNGMKPEYRP*
zm96        421  QKTTGYVWQLLPNGMKPEYRP*
zm01        421  QKTTGYVWQLLPNGMKPEYRP*
zm02        421  QKTTGYVWQLLPNGMKPEYRP*
zm03        421  QKTTGYVWQLLPNGMKPEYRP*
zm07        421  QKTTGYVWQLLPNGMKPEYRP*
zm12        421  QKTTGYVWQLLPNGMKPEYRP*
zm18        421  QKTTGYVWQLLPNGMKPEYRP*
zm19        421  QKTTGYVWQLLPNGMKPEYRP*
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zm17        421  QKTTGYVWQLLPNGMKPEYRP*
zm13        421  QKTTGYVWQLLPNGMKPEYRP*
zm05        421  QKTTGYVWQLLPNGMKPEYRP*
z2491      421  QKTTGYVWQLLPNGMKPEYRP*
zm22        421  QKTTGYVWQLLPNGMKPEYRP*
zm26        421  QKTTGYVWQLLPNGMKPEYRP*
zm28        421  QKTTGYVWQLLPNGMKPEYRP*
zm29asbc    421  QKTTGYVWQLLPNGMKPEYRP*
zm16        421  QKTTGYVWQLLPNGMKPEYRP*
zm15        421  QKTTGYVWQLLPNGMKPEYRP*
zm31asbc    421  QKTTGYVWQLLPNGMKPEYRP*

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Fig. 23D

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